

# Can Yang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4505754/publications.pdf>

Version: 2024-02-01

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	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
2	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
3	GPA: A Statistical Approach to Prioritizing GWAS Results by Integrating Pleiotropy and Annotation. PLoS Genetics, 2014, 10, e1004787.	1.5	189
4	SNPHarvester: a filtering-based approach for detecting epistatic interactions in genome-wide association studies. Bioinformatics, 2009, 25, 504-511.	1.8	182
5	Predictive rule inference for epistatic interaction detection in genome-wide association studies. Bioinformatics, 2010, 26, 30-37.	1.8	156
6	GBOOST: a GPU-based tool for detecting gene-gene interactions in genome-wide case control studies. Bioinformatics, 2011, 27, 1309-1310.	1.8	137
7	Total Variation Regularized Tensor RPCA for Background Subtraction From Compressive Measurements. IEEE Transactions on Image Processing, 2016, 25, 4075-4090.	6.0	135
8	Leveraging functional annotations in genetic risk prediction for human complex diseases. PLoS Computational Biology, 2017, 13, e1005589.	1.5	134
9	Low-Rank Modeling and Its Applications in Image Analysis. ACM Computing Surveys, 2015, 47, 1-33.	16.1	102
10	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
11	Testing and controlling for horizontal pleiotropy with probabilistic Mendelian randomization in transcriptome-wide association studies. Nature Communications, 2020, 11, 3861.	5.8	79
12	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
13	Pervasive pleiotropy between psychiatric disorders and immune disorders revealed by integrative analysis of multiple GWAS. Human Genetics, 2015, 134, 1195-1209.	1.8	72
14	Improving genetic risk prediction by leveraging pleiotropy. Human Genetics, 2014, 133, 639-650.	1.8	71
15	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
16	Implications of pleiotropy: challenges and opportunities for mining Big Data in biomedicine. Frontiers in Genetics, 2015, 6, 229.	1.1	41
17	Bayesian weighted Mendelian randomization for causal inference based on summary statistics. Bioinformatics, 2020, 36, 1501-1508.	1.8	39
18	On high-dimensional misspecified mixed model analysis in genome-wide association study. Annals of Statistics, 2016, 44, .	1.4	38

#	ARTICLE	IF	CITATIONS
19	Accounting for non-genetic factors by low-rank representation and sparse regression for eQTL mapping. <i>Bioinformatics</i> , 2013, 29, 1026-1034.	1.8	37
20	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. <i>Bioinformatics</i> , 2019, 35, 1644-1652.	1.8	36
21	Identifying main effects and epistatic interactions from large-scale SNP data via adaptive group Lasso. <i>BMC Bioinformatics</i> , 2010, 11, S18.	1.2	33
22	Empirical Bayes Correction for the Winner's Curse in Genetic Association Studies. <i>Genetic Epidemiology</i> , 2013, 37, 60-68.	0.6	32
23	Mendelian randomization for causal inference accounting for pleiotropy and sample structure using genome-wide summary statistics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	32
24	On Joint Estimation of Gaussian Graphical Models for Spatial and Temporal Data. <i>Biometrics</i> , 2017, 73, 769-779.	0.8	30
25	CoMM-S2: a collaborative mixed model using summary statistics in transcriptome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 2009-2016.	1.8	30
26	MR-LDP: a two-sample Mendelian randomization for GWAS summary statistics accounting for linkage disequilibrium and horizontal pleiotropy. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa028.	1.5	27
27	Detecting two-locus associations allowing for interactions in genome-wide association studies. <i>Bioinformatics</i> , 2010, 26, 2517-2525.	1.8	23
28	Dissecting ancestry genomic background in substance dependence genome-wide association studies. <i>Pharmacogenomics</i> , 2015, 16, 1487-1498.	0.6	22
29	EPS: an empirical Bayes approach to integrating pleiotropy and tissue-specific information for prioritizing risk genes. <i>Bioinformatics</i> , 2016, 32, 1856-1864.	1.8	19
30	Detection of cell-type-specific risk-CpG sites in epigenome-wide association studies. <i>Nature Communications</i> , 2019, 10, 3113.	5.8	19
31	The complete compositional epistasis detection in genome-wide association studies. <i>BMC Genetics</i> , 2013, 14, 7.	2.7	18
32	ProteinLasso: A Lasso regression approach to protein inference problem in shotgun proteomics. <i>Computational Biology and Chemistry</i> , 2013, 43, 46-54.	1.1	18
33	LSMM: a statistical approach to integrating functional annotations with genome-wide association studies. <i>Bioinformatics</i> , 2018, 34, 2788-2796.	1.8	18
34	A Unified Primal Dual Active Set Algorithm for Nonconvex Sparse Recovery. <i>Statistical Science</i> , 2021, 36, .	1.6	17
35	XPXP: improving polygenic prediction by cross-population and cross-phenotype analysis. <i>Bioinformatics</i> , 2022, 38, 1947-1955.	1.8	16
36	Exploring the genetic architecture of alcohol dependence in African-Americans via analysis of a genomewide set of common variants. <i>Human Genetics</i> , 2014, 133, 617-624.	1.8	15

#	ARTICLE	IF	CITATIONS
37	Computing exact permutation p-values for association rules. <i>Information Sciences</i> , 2016, 346-347, 146-162.	4.0	15
38	A tissue-specific collaborative mixed model for jointly analyzing multiple tissues in transcriptome-wide association studies. <i>Nucleic Acids Research</i> , 2020, 48, e109-e109.	6.5	15
39	IGREX for quantifying the impact of genetically regulated expression on phenotypes. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa010.	1.5	15
40	A Partial Set Covering Model for Protein Mixture Identification Using Mass Spectrometry Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 368-380.	1.9	13
41	Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets. <i>Nature Computational Science</i> , 2022, 2, 317-330.	3.8	13
42	Admixture mapping analysis in the context of GWAS with GAW18 data. <i>BMC Proceedings</i> , 2014, 8, S3.	1.8	12
43	IGESS: a statistical approach to integrating individual-level genotype data and summary statistics in genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 2882-2889.	1.8	12
44	Accurate genetic and environmental covariance estimation with composite likelihood in genome-wide association studies. <i>PLoS Genetics</i> , 2021, 17, e1009293.	1.5	12
45	Analyzing Association Mapping in Pedigree-Based GWAS Using a Penalized Multitrait Mixed Model. <i>Genetic Epidemiology</i> , 2016, 40, 382-393.	0.6	11
46	LPM: a latent probit model to characterize the relationship among complex traits using summary statistics from multiple GWASs and functional annotations. <i>Bioinformatics</i> , 2020, 36, 2506-2514.	1.8	11
47	Prediction Analysis for Microbiome Sequencing Data. <i>Biometrics</i> , 2019, 75, 875-884.	0.8	10
48	Exploring the Relationship Between Psychiatric Traits and the Risk of Mouth Ulcers Using Bi-Directional Mendelian Randomization. <i>Frontiers in Genetics</i> , 2020, 11, 608630.	1.1	10
49	FIRM: Flexible integration of single-cell RNA-sequencing data for large-scale multi-tissue cell atlas datasets. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
50	Leveraging the local genetic structure for trans-ancestry association mapping. <i>American Journal of Human Genetics</i> , 2022, 109, 1317-1337.	2.6	10
51	VIMCO: variational inference for multiple correlated outcomes in genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 3693-3700.	1.8	9
52	Peak bagging for peptide mass fingerprinting. <i>Bioinformatics</i> , 2008, 24, 1293-1299.	1.8	8
53	A Regularized Method for Peptide Quantification. <i>Journal of Proteome Research</i> , 2010, 9, 2705-2712.	1.8	8
54	Automatic mitral leaflet tracking in echocardiography by outlier detection in the low-rank representation. , 2012, , .		7

#	ARTICLE	IF	CITATIONS
55	LPG: A four-group probabilistic approach to leveraging pleiotropy in genome-wide association studies. BMC Genomics, 2018, 19, 503.	1.2	7
56	The choice of null distributions for detecting gene-gene interactions in genome-wide association studies. BMC Bioinformatics, 2011, 12, S26.	1.2	6
57	Identifying disease-associated SNP clusters via contiguous outlier detection. Bioinformatics, 2011, 27, 2578-2585.	1.8	6
58	LLR: a latent low-rank approach to colocalizing genetic risk variants in multiple GWAS. Bioinformatics, 2017, 33, 3878-3886.	1.8	6
59	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
60	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
61	Comments on "An empirical comparison of several recent epistatic interaction detection methods". Bioinformatics, 2012, 28, 145-146.	1.8	3
62	Introduction to Statistical Methods for Integrative Data Analysis in Genome-Wide Association Studies. , 2016, , 3-23.		3
63	Joint analysis of individual-level and summary-level GWAS data by leveraging pleiotropy. Bioinformatics, 2019, 35, 1729-1736.	1.8	3
64	A hidden two-locus disease association pattern in genome-wide association studies. BMC Bioinformatics, 2011, 12, 156.	1.2	2
65	A penalized linear mixed model for genomic prediction using pedigree structures. BMC Proceedings, 2014, 8, S67.	1.8	2
66	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
67	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
68	Adjustment of familial relatedness in association test for rare variants. BMC Proceedings, 2014, 8, S39.	1.8	1
69	Editorial: Genetic Pleiotropy in Complex Traits and Diseases. Frontiers in Genetics, 2022, 13, 897383.	1.1	1
70	GPC Algorithm and Queuing-selecting for Networked Level Control. , 2007, , .		0
71	Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. Nature Precedings, 2008, , .	0.1	0
72	eQTL mapping. , 0, , 208-228.		0

#	ARTICLE	IF	CITATIONS
73	Introduction to statistical methods in genome-wide association studies. , 0, , 26-52.		0
74	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
75	scPI: A Scalable Framework for Probabilistic Inference in Single-Cell RNA-Sequencing Data Analysis. Statistics in Biosciences, 0, , 1.	0.6	0
76	Title is missing!. , 2021, 17, e1009293.		0
77	Title is missing!. , 2021, 17, e1009293.		0
78	Title is missing!. , 2021, 17, e1009293.		0
79	Title is missing!. , 2021, 17, e1009293.		0