

Qiuying Sha

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

532
citations

687363

13
h-index

752698

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47
all docs

47
docs citations

47
times ranked

447
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting Association of Rare and Common Variants by Testing an Optimally Weighted Combination of Variants. <i>Genetic Epidemiology</i> , 2012, 36, 561-571.	1.3	74
2	Transmission/Disequilibrium Test Based on Haplotype Sharing for Tightly Linked Markers. <i>American Journal of Human Genetics</i> , 2003, 73, 566-579.	6.2	73
3	Joint Analysis of Multiple Traits Using "Optimal" Maximum Heritability Test. <i>PLoS ONE</i> , 2016, 11, e0150975.	2.5	25
4	An Adaptive Fisher's Combination Method for Joint Analysis of Multiple Phenotypes in Association Studies. <i>Scientific Reports</i> , 2016, 6, 34323.	3.3	25
5	Two Adaptive Weighting Methods to Test for Rare Variant Associations in Family-Based Designs. <i>Genetic Epidemiology</i> , 2012, 36, 499-507.	1.3	24
6	A new association test using haplotype similarity. <i>Genetic Epidemiology</i> , 2007, 31, 577-593.	1.3	21
7	Genome-wide association reveals three SNPs associated with sporadic amyotrophic lateral sclerosis through a two-locus analysis. <i>BMC Medical Genetics</i> , 2009, 10, 86.	2.1	19
8	An improved score test for genetic association studies. <i>Genetic Epidemiology</i> , 2011, 35, 350-359.	1.3	19
9	Joint Analysis of Multiple Traits in Rare Variant Association Studies. <i>Annals of Human Genetics</i> , 2016, 80, 162-171.	0.8	17
10	Tests of Association Between Quantitative Traits and Haplotypes In A Reduced-Dimensional Space. <i>Annals of Human Genetics</i> , 2005, 69, 715-732.	0.8	15
11	An ensemble learning approach jointly modeling main and interaction effects in genetic association studies. <i>Genetic Epidemiology</i> , 2008, 32, 285-300.	1.3	15
12	A Novel Method to Detect Gene-Gene Interactions in Structured Populations: MDR-SP. <i>Annals of Human Genetics</i> , 2011, 75, 742-754.	0.8	15
13	A Combinatorial Searching Method for Detecting a Set of Interacting Loci Associated with Complex Traits. <i>Annals of Human Genetics</i> , 2006, 70, 677-692.	0.8	14
14	A clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. <i>Bioinformatics</i> , 2019, 35, 1373-1379.	4.1	14
15	Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. <i>European Journal of Human Genetics</i> , 2013, 21, 332-337.	2.8	13
16	Power Comparisons of Methods for Joint Association Analysis of Multiple Phenotypes. <i>Human Heredity</i> , 2015, 80, 144-152.	0.8	13
17	A hierarchical clustering method for dimension reduction in joint analysis of multiple phenotypes. <i>Genetic Epidemiology</i> , 2018, 42, 344-353.	1.3	13
18	A novel method to test associations between a weighted combination of phenotypes and genetic variants. <i>PLoS ONE</i> , 2018, 13, e0190788.	2.5	12

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19	Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. <i>Genetic Epidemiology</i> , 2005, 28, 341-351.	1.3	11
20	Joint Analysis for Genome-Wide Association Studies in Family-Based Designs. <i>PLoS ONE</i> , 2011, 6, e21957.	2.5	11
21	Detecting association of rare and common variants based on cross-validation prediction error. <i>Genetic Epidemiology</i> , 2017, 41, 233-243.	1.3	9
22	A new association test to test multiple-marker association. <i>Genetic Epidemiology</i> , 2009, 33, 164-171.	1.3	8
23	Detecting Association of Rare Variants by Testing an Optimally Weighted Combination of Variants for Quantitative Traits in General Families. <i>Annals of Human Genetics</i> , 2013, 77, 524-534.	0.8	7
24	A Rare Variant Association Test Based on Combinations of Single-Variant Tests. <i>Genetic Epidemiology</i> , 2014, 38, 494-501.	1.3	7
25	Testing an optimally weighted combination of common and/or rare variants with multiple traits. <i>PLoS ONE</i> , 2018, 13, e0201186.	2.5	7
26	Joint Analysis of Multiple Phenotypes in Association Studies based on Cross-Validation Prediction Error. <i>Scientific Reports</i> , 2019, 9, 1073.	3.3	7
27	Joint analysis of multiple phenotypes using a clustering linear combination method based on hierarchical clustering. <i>Genetic Epidemiology</i> , 2020, 44, 67-78.	1.3	7
28	Incorporating multiple-marker information to detect risk loci for rheumatoid arthritis. <i>BMC Proceedings</i> , 2009, 3, S28.	1.6	6
29	Detecting susceptibility genes for rheumatoid arthritis based on a novel sliding-window approach. <i>BMC Proceedings</i> , 2009, 3, S14.	1.6	5
30	A Novel Test for Testing the Optimally Weighted Combination of Rare and Common Variants Based on Data of Parents and Affected Children. <i>Genetic Epidemiology</i> , 2014, 38, 135-143.	1.3	5
31	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. <i>Human Heredity</i> , 2019, 84, 170-196.	0.8	4
32	Testing gene-environment interactions for rare and/or common variants in sequencing association studies. <i>PLoS ONE</i> , 2020, 15, e0229217.	2.5	4
33	A general statistic to test an optimally weighted combination of common and/or rare variants. <i>Genetic Epidemiology</i> , 2019, 43, 966-979.	1.3	3
34	A computationally efficient clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. <i>PLoS ONE</i> , 2022, 17, e0260911.	2.5	3
35	A Powerful Approach to Test an Optimally Weighted Combination of Rare Variants in Admixed Populations. <i>Genetic Epidemiology</i> , 2015, 39, 294-305.	1.3	2
36	Identification of Interacting Genes in Genome-Wide Association Studies Using a Model-Based Two-Stage Approach. <i>Annals of Human Genetics</i> , 2010, 74, 406-415.	0.8	1

#	ARTICLE	IF	CITATIONS
37	A gene based approach to test genetic association based on an optimally weighted combination of multiple traits. PLoS ONE, 2019, 14, e0220914.	2.5	1
38	Gene-based association tests using GWAS summary statistics and incorporating eQTL. Scientific Reports, 2022, 12, 3553.	3.3	1
39	MF \rightarrow OWmuT: Testing an optimally weighted combination of common and rare variants with multiple traits using family data. Genetic Epidemiology, 2021, 45, 64-81.	1.3	0
40	Control for population stratification in genetic association studies based on GWAS summary statistics. Genetic Epidemiology, 0, , .	1.3	0