Shuanglin Zhang

List of Publications by Year
in descending order

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		567281	454955
61	1,114	15	30
papers	citations	h-index	g-index

67	67	67	1093
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gene-based association tests using GWAS summary statistics and incorporating eQTL. Scientific Reports, 2022, 12, 3553.	3.3	1
2	A computationally efficient clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. PLoS ONE, 2022, 17, e0260911.	2.5	3
3	Gene-Based Association Tests Using New Polygenic Risk Scores and Incorporating Gene Expression Data. Genes, 2022, 13, 1120.	2.4	2
4	MFâ€TOWmuT: 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
5	Joint analysis of multiple phenotypes using a clustering linear combination method based on hierarchical clustering. Genetic Epidemiology, 2020, 44, 67-78.	1.3	7
6	A general statistic to test an optimally weighted combination of common and/or rare variants. Genetic Epidemiology, 2019, 43, 966-979.	1.3	3
7	Joint Analysis of Multiple Phenotypes in Association Studies based on Cross-Validation Prediction Error. Scientific Reports, 2019, 9, 1073.	3.3	7
8	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. Human Heredity, 2019, 84, 170-196.	0.8	4
9	A clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. Bioinformatics, 2019, 35, 1373-1379.	4.1	14
10	Testing an optimally weighted combination of common and/or rare variants with multiple traits. PLoS ONE, 2018, 13, e0201186.	2.5	7
11	A hierarchical clustering method for dimension reduction in joint analysis of multiple phenotypes. Genetic Epidemiology, 2018, 42, 344-353.	1.3	13
12	Joint analysis of multiple phenotypes in association studies using allele-based clustering approach for non-normal distributions. Annals of Human Genetics, 2018, 82, 389-395.	0.8	1
13	A novel method to test associations between a weighted combination of phenotypes and genetic variants. PLoS ONE, 2018, 13, e0190788.	2.5	12
14	Detecting association of rare and common variants based on cross-validation prediction error. Genetic Epidemiology, 2017, 41, 233-243.	1.3	9
15	Joint Analysis of Multiple Traits Using "Optimal" Maximum Heritability Test. PLoS ONE, 2016, 11, e0150975.	2.5	25
16	An Adaptive Fisherâ€™s Combination Method for Joint Analysis of Multiple Phenotypes in Association Studies. Scientific Reports, 2016, 6, 34323.	3.3	25
17	A Nonparametric Regression Approach to Control for Population Stratification in Rare Variant Association Studies. Scientific Reports, 2016, 6, 37444.	3.3	14
18	Joint Analysis of Multiple Traits in Rare Variant Association Studies. Annals of Human Genetics, 2016, 80, 162-171.	0.8	17

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19	Power Comparisons of Methods for Joint Association Analysis of Multiple Phenotypes. Human Heredity, 2015, 80, 144-152.	0.8	13
20	A Powerful Approach to Test an Optimally Weighted Combination of Rare Variants in Admixed Populations. Genetic Epidemiology, 2015, 39, 294-305.	1.3	2
21	Test of rare variant association based on affected sib-pairs. European Journal of Human Genetics, 2015, 23, 229-237.	2.8	6
22	A Novel Test for Testing the Optimally Weighted Combination of Rare and Common Variants Based on Data of Parents and Affected Children. Genetic Epidemiology, 2014, 38, 135-143.	1.3	5
23	A Rare Variant Association Test Based on Combinations of Single-Variant Tests. Genetic Epidemiology, 2014, 38, 494-501.	1.3	7
24	Testing optimally weighted combination of variants for hypertension. BMC Proceedings, 2014, 8, S59.	1.6	4
25	Detecting association of rare and common variants by testing an optimally weighted combination of variants with longitudinal data. BMC Proceedings, 2014, 8, S91.	1.6	5
26	Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. European Journal of Human Genetics, 2013, 21, 332-337.	2.8	13
27	Detecting Association of Rare Variants by Testing an Optimally Weighted Combination of Variants for Quantitative Traits in General Families. Annals of Human Genetics, 2013, 77, 524-534.	0.8	7
28	Two Adaptive Weighting Methods to Test for Rare Variant Associations in Familyâ€Based Designs. Genetic Epidemiology, 2012, 36, 499-507.	1.3	24
29	Detecting Association of Rare and Common Variants by Testing an Optimally Weighted Combination of Variants. Genetic Epidemiology, 2012, 36, 561-571.	1.3	74
30	A Novel Method to Detect Gene-Gene Interactions in Structured Populations: MDR-SP. Annals of Human Genetics, 2011, 75, 742-754.	0.8	15
31	Detection of rare variant effects in association studies: extreme values, iterative regression, and a hybrid approach. BMC Proceedings, 2011, 5, S112.	1.6	3
32	An improved score test for genetic association studies. Genetic Epidemiology, 2011, 35, 350-359.	1.3	19
33	A test of Hardy-Weinberg equilibrium in structured populations. Genetic Epidemiology, 2011, 35, 671-678.	1.3	21
34	Joint Analysis for Genome-Wide Association Studies in Family-Based Designs. PLoS ONE, 2011, 6, e21957.	2.5	11
35	A data-driven weighting scheme for family-based genome-wide association studies. European Journal of Human Genetics, 2010, 18, 596-603.	2.8	7
36	A combinatorial approach for detecting gene-gene interaction using multiple traits of Genetic Analysis Workshop 16 rheumatoid arthritis data. BMC Proceedings, 2009, 3, S43.	1.6	4

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37	A new association test to test multipleâ€marker association. Genetic Epidemiology, 2009, 33, 164-171.	1.3	8
38	Genome-wide association reveals three SNPs associated with sporadic amyotrophic lateral sclerosis through a two-locus analysis. BMC Medical Genetics, 2009, 10, 86.	2.1	19
39	A Variableâ€Sized Slidingâ€Window Approach for Genetic Association Studies via Principal Component Analysis. Annals of Human Genetics, 2009, 73, 631-637.	0.8	27
40	An ensemble learning approach jointly modeling main and interaction effects in genetic association studies. Genetic Epidemiology, 2008, 32, 285-300.	1.3	15
41	A method dealing with a large number of correlated traits in a linkage genome scan. BMC Proceedings, 2007, 1, S84.	1.6	3
42	A new association test using haplotype similarity. Genetic Epidemiology, 2007, 31, 577-593.	1.3	21
43	A multi-marker test based on family data in genome-wide association study. BMC Genetics, 2007, 8, 65.	2.7	6
44	Two-stage association tests for genome-wide association studies based on family data with arbitrary family structure. European Journal of Human Genetics, 2007, 15, 1169-1175.	2.8	19
45	A Combinatorial Searching Method for Detecting a Set of Interacting Loci Associated with Complex Traits. Annals of Human Genetics, 2006, 70, 677-692.	0.8	14
46	Tests of Association Between Quantitative Traits and Haplotypes In A Reducedâ€Dimensional Space. Annals of Human Genetics, 2005, 69, 715-732.	0.8	15
47	Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. Genetic Epidemiology, 2005, 28, 341-351.	1.3	11
48	A Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. Annals of Human Genetics, 2005, 69, 455-467.	0.8	11
49	Reply to Knapp and Becker. American Journal of Human Genetics, 2004, 74, 591-593.	6.2	8
50	On a semiparametric test to detect associations between quantitative traits and candidate genes using unrelated individuals. Genetic Epidemiology, 2003, 24, 44-56.	1.3	95
51	Transmission/Disequilibrium Test Based on Haplotype Sharing for Tightly Linked Markers. American Journal of Human Genetics, 2003, 73, 566-579.	6.2	73
52	Linkage disequilibrium mapping with genotype data. Genetic Epidemiology, 2002, 22, 66-77.	1.3	4
53	Association mapping, using a mixture model for complex traits. Genetic Epidemiology, 2002, 23, 181-196.	1.3	128
54	On a family-based haplotype pattern mining method for linkage disequilibrium mapping. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 100-11.	0.7	2

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55	Quantitative Similarity-Based Association Tests Using Population Samples. American Journal of Human Genetics, 2001, 69, 601-614.	6.2	24
56	The Power of Transmission Disequilibrium Tests for Quantitative Traits. Genetic Epidemiology, 2001, 21, S632-7.	1.3	11
57	Test of Association for Quantitative Traits in General Pedigrees: The Quantitative Pedigree Disequilibrium Test. Genetic Epidemiology, 2001, 21, S370-5.	1.3	23
58	Linkage disequilibrium mapping in populations of variable size using the decay of haplotype sharing and a stepwise-mutation model. Genetic Epidemiology, 2000, 19, S99-S105.	1.3	10
59	Transmission/Disequilibrium Tests Using Multiple Tightly Linked Markers. American Journal of Human Genetics, 2000, 67, 936-946.	6.2	159
60	On the best equivariant estimator of covariance matrix of a multivariate normal population. Communications in Statistics - Theory and Methods, 1997, 26, 2021-2034.	1.0	2
61	Control for population stratification in genetic association studies based on GWAS summary statistics. Genetic Epidemiology, 0, , .	1.3	0