

Shuanglin Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6930584/publications.pdf>

Version: 2024-02-01

61
papers

1,114
citations

567281

15
h-index

454955

30
g-index

67
all docs

67
docs citations

67
times ranked

1093
citing authors

#	ARTICLE	IF	CITATIONS
1	Transmission/Disequilibrium Tests Using Multiple Tightly Linked Markers. <i>American Journal of Human Genetics</i> , 2000, 67, 936-946.	6.2	159
2	Association mapping, using a mixture model for complex traits. <i>Genetic Epidemiology</i> , 2002, 23, 181-196.	1.3	128
3	On a semiparametric test to detect associations between quantitative traits and candidate genes using unrelated individuals. <i>Genetic Epidemiology</i> , 2003, 24, 44-56.	1.3	95
4	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
5	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
6	A Variable-Sized Sliding Window Approach for Genetic Association Studies via Principal Component Analysis. <i>Annals of Human Genetics</i> , 2009, 73, 631-637.	0.8	27
7	Joint Analysis of Multiple Traits Using "Optimal" Maximum Heritability Test. <i>PLoS ONE</i> , 2016, 11, e0150975.	2.5	25
8	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
9	Quantitative Similarity-Based Association Tests Using Population Samples. <i>American Journal of Human Genetics</i> , 2001, 69, 601-614.	6.2	24
10	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
11	Test of Association for Quantitative Traits in General Pedigrees: The Quantitative Pedigree Disequilibrium Test. <i>Genetic Epidemiology</i> , 2001, 21, S370-5.	1.3	23
12	A new association test using haplotype similarity. <i>Genetic Epidemiology</i> , 2007, 31, 577-593.	1.3	21
13	A test of Hardy-Weinberg equilibrium in structured populations. <i>Genetic Epidemiology</i> , 2011, 35, 671-678.	1.3	21
14	Two-stage association tests for genome-wide association studies based on family data with arbitrary family structure. <i>European Journal of Human Genetics</i> , 2007, 15, 1169-1175.	2.8	19
15	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
16	An improved score test for genetic association studies. <i>Genetic Epidemiology</i> , 2011, 35, 350-359.	1.3	19
17	Joint Analysis of Multiple Traits in Rare Variant Association Studies. <i>Annals of Human Genetics</i> , 2016, 80, 162-171.	0.8	17
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	A Nonparametric Regression Approach to Control for Population Stratification in Rare Variant Association Studies. <i>Scientific Reports</i> , 2016, 6, 37444.	3.3	14
23	A clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. <i>Bioinformatics</i> , 2019, 35, 1373-1379.	4.1	14
24	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
25	Power Comparisons of Methods for Joint Association Analysis of Multiple Phenotypes. <i>Human Heredity</i> , 2015, 80, 144-152.	0.8	13
26	A hierarchical clustering method for dimension reduction in joint analysis of multiple phenotypes. <i>Genetic Epidemiology</i> , 2018, 42, 344-353.	1.3	13
27	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
28	The Power of Transmission Disequilibrium Tests for Quantitative Traits. <i>Genetic Epidemiology</i> , 2001, 21, S632-7.	1.3	11
29	Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. <i>Genetic Epidemiology</i> , 2005, 28, 341-351.	1.3	11
30	A Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. <i>Annals of Human Genetics</i> , 2005, 69, 455-467.	0.8	11
31	Joint Analysis for Genome-Wide Association Studies in Family-Based Designs. <i>PLoS ONE</i> , 2011, 6, e21957.	2.5	11
32	Linkage disequilibrium mapping in populations of variable size using the decay of haplotype sharing and a stepwise-mutation model. <i>Genetic Epidemiology</i> , 2000, 19, S99-S105.	1.3	10
33	Detecting association of rare and common variants based on cross-validation prediction error. <i>Genetic Epidemiology</i> , 2017, 41, 233-243.	1.3	9
34	Reply to Knapp and Becker. <i>American Journal of Human Genetics</i> , 2004, 74, 591-593.	6.2	8
35	A new association test to test multiple marker association. <i>Genetic Epidemiology</i> , 2009, 33, 164-171.	1.3	8
36	A data-driven weighting scheme for family-based genome-wide association studies. <i>European Journal of Human Genetics</i> , 2010, 18, 596-603.	2.8	7

#	ARTICLE	IF	CITATIONS
37	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
38	A Rare Variant Association Test Based on Combinations of Single-Variant Tests. <i>Genetic Epidemiology</i> , 2014, 38, 494-501.	1.3	7
39	Testing an optimally weighted combination of common and/or rare variants with multiple traits. <i>PLoS ONE</i> , 2018, 13, e0201186.	2.5	7
40	Joint Analysis of Multiple Phenotypes in Association Studies based on Cross-Validation Prediction Error. <i>Scientific Reports</i> , 2019, 9, 1073.	3.3	7
41	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
42	A multi-marker test based on family data in genome-wide association study. <i>BMC Genetics</i> , 2007, 8, 65.	2.7	6
43	Test of rare variant association based on affected sib-pairs. <i>European Journal of Human Genetics</i> , 2015, 23, 229-237.	2.8	6
44	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
45	Detecting association of rare and common variants by testing an optimally weighted combination of variants with longitudinal data. <i>BMC Proceedings</i> , 2014, 8, S91.	1.6	5
46	Linkage disequilibrium mapping with genotype data. <i>Genetic Epidemiology</i> , 2002, 22, 66-77.	1.3	4
47	A combinatorial approach for detecting gene-gene interaction using multiple traits of Genetic Analysis Workshop 16 rheumatoid arthritis data. <i>BMC Proceedings</i> , 2009, 3, S43.	1.6	4
48	Testing optimally weighted combination of variants for hypertension. <i>BMC Proceedings</i> , 2014, 8, S59.	1.6	4
49	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. <i>Human Heredity</i> , 2019, 84, 170-196.	0.8	4
50	A method dealing with a large number of correlated traits in a linkage genome scan. <i>BMC Proceedings</i> , 2007, 1, S84.	1.6	3
51	Detection of rare variant effects in association studies: extreme values, iterative regression, and a hybrid approach. <i>BMC Proceedings</i> , 2011, 5, S112.	1.6	3
52	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
53	A computationally efficient clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. <i>PLoS ONE</i> , 2022, 17, e0260911.	2.5	3
54	On the best equivariant estimator of covariance matrix of a multivariate normal population. <i>Communications in Statistics - Theory and Methods</i> , 1997, 26, 2021-2034.	1.0	2

#	ARTICLE	IF	CITATIONS
55	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
56	On a family-based haplotype pattern mining method for linkage disequilibrium mapping. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 100-111.	0.7	2
57	Gene-Based Association Tests Using New Polygenic Risk Scores and Incorporating Gene Expression Data. <i>Genes</i> , 2022, 13, 1120.	2.4	2
58	Joint analysis of multiple phenotypes in association studies using allele-based clustering approach for non-normal distributions. <i>Annals of Human Genetics</i> , 2018, 82, 389-395.	0.8	1
59	Gene-based association tests using GWAS summary statistics and incorporating eQTL. <i>Scientific Reports</i> , 2022, 12, 3553.	3.3	1
60	MF ϵ TOWmuT: Testing an optimally weighted combination of common and rare variants with multiple traits using family data. <i>Genetic Epidemiology</i> , 2021, 45, 64-81.	1.3	0
61	Control for population stratification in genetic association studies based on GWAS summary statistics. <i>Genetic Epidemiology</i> , 0, , .	1.3	0