

# Rare-Variant Association Testing for Sequencing Data v Association Test

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A parametric Bayesian method to test the association of rare variants. , 2011, , .		0
2	Tests of Selection in Pooled Case-Control Data: An Empirical Study. <i>Frontiers in Genetics</i> , 2011, 2, 83.	1.1	3
3	A General Framework for Detecting Disease Associations with Rare Variants in Sequencing Studies. <i>American Journal of Human Genetics</i> , 2011, 89, 354-367.	2.6	251
4	Finding Disease Variants in Mendelian Disorders By Using Sequence Data: Methods and Applications. <i>American Journal of Human Genetics</i> , 2011, 89, 701-712.	2.6	50
5	Incorporating biological information into association studies of sequencing data. <i>Genetic Epidemiology</i> , 2011, 35, S29-34.	0.6	4
6	Assessing the Impact of Non-Differential Genotyping Errors on Rare Variant Tests of Association. <i>Human Heredity</i> , 2011, 72, 153-160.	0.4	18
7	Mining the LIPG Allelic Spectrum Reveals the Contribution of Rare and Common Regulatory Variants to HDL Cholesterol. <i>PLoS Genetics</i> , 2011, 7, e1002393.	1.5	32
8	Predicting Signatures of "Synthetic Associations" and "Natural Associations" from Empirical Patterns of Human Genetic Variation. <i>PLoS Computational Biology</i> , 2012, 8, e1002600.	1.5	14
9	A Unified Method for Detecting Secondary Trait Associations with Rare Variants: Application to Sequence Data. <i>PLoS Genetics</i> , 2012, 8, e1003075.	1.5	6
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11	"Location, Location, Location"™: a spatial approach for rare variant analysis and an application to a study on non-syndromic cleft lip with or without cleft palate. <i>Bioinformatics</i> , 2012, 28, 3027-3033.	1.8	22
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16	A powerful test for multiple rare variants association studies that incorporates sequencing qualities. <i>Nucleic Acids Research</i> , 2012, 40, e60-e60.	6.5	26
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19	Two-Stage Extreme Phenotype Sequencing Design for Discovering and Testing Common and Rare Genetic Variants: Efficiency and Power. <i>Human Heredity</i> , 2012, 73, 139-147.	0.4	15

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20	A Unified Framework for Detecting Rare Variant Quantitative Trait Associations in Pedigree and Unrelated Individuals via Sequence Data. <i>Human Heredity</i> , 2012, 73, 105-122.	0.4	14
21	Regression Modeling of Allele Frequencies and Testing Hardy Weinberg Equilibrium. <i>Human Heredity</i> , 2012, 74, 71-82.	0.4	5
22	Rare Variant Association Testing for Next-Generation Sequencing Data via Hierarchical Clustering. <i>Human Heredity</i> , 2012, 74, 165-171.	0.4	5
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40	Single-Variant and Multi-Variant Trend Tests for Genetic Association with Next-Generation Sequencing That Are Robust to Sequencing Error. <i>Human Heredity</i> , 2012, 74, 172-183.	0.4	10
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55	Exome sequencing and the genetic basis of complex traits. <i>Nature Genetics</i> , 2012, 44, 623-630.	9.4	340
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91	Adjustment for Population Stratification via Principal Components in Association Analysis of Rare Variants. Genetic Epidemiology, 2013, 37, 99-109.	0.6	38
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94	Complex Rare Variation and Its Role in Endophenotypic Variation in Schizophrenia. <i>Biological Psychiatry</i> , 2013, 73, 499-500.	0.7	0
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113	Optimal Methods for Using Posterior Probabilities in Association Testing. <i>Human Heredity</i> , 2013, 75, 2-11.	0.4	8
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1015	A general statistic to test an optimally weighted combination of common and/or rare variants. <i>Genetic Epidemiology</i> , 2019, 43, 966-979.	0.6	3
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1017	Identifying and exploiting gene-pathway interactions from RNA-seq data for binary phenotype. <i>BMC Genetics</i> , 2019, 20, 36.	2.7	2
1018	Discovering genetic interactions bridging pathways in genome-wide association studies. <i>Nature Communications</i> , 2019, 10, 4274.	5.8	52

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1022	eQTL mapping of rare variant associations using RNA-seq data: An evaluation of approaches. <i>PLoS ONE</i> , 2019, 14, e0223273.	1.1	2
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1033	Jackknife Model Averaging Prediction Methods for Complex Phenotypes with Gene Expression Levels by Integrating External Pathway Information. <i>Computational and Mathematical Methods in Medicine</i> , 2019, 2019, 1-8.	0.7	7
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1071	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	9.4	592
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1074	A generalized model for combining dependent SNP-level summary statistics and its extensions to statistics of other levels. <i>Scientific Reports</i> , 2019, 9, 5461.	1.6	7
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1086	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. <i>Human Heredity</i> , 2019, 84, 170-196.	0.4	4
1087	Novel risk genes and mechanisms implicated by exome sequencing of 2572 individuals with pulmonary arterial hypertension. <i>Genome Medicine</i> , 2019, 11, 69.	3.6	86
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1102	A novel association of rs13334070 in the RPGRI1L gene with adiposity factors discovered by joint linkage and linkage disequilibrium analysis in Iranian pedigrees: Tehran Cardiometabolic Genetic Study (TCGS). <i>Genetic Epidemiology</i> , 2019, 43, 342-351.	0.6	6
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1107	An optimal kernel-based U-statistic method for quantitative gene-environment association analysis. <i>Genetic Epidemiology</i> , 2019, 43, 137-149.	0.6	7
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1113	Mitochondrial DNA variants and pulmonary function in older persons. <i>Experimental Gerontology</i> , 2019, 115, 96-103.	1.2	4
1114	Enabling genome-wide association testing with multiple diseases and no healthy controls. <i>Gene</i> , 2019, 684, 118-123.	1.0	8
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1124	A weighted burden test using logistic regression for integrated analysis of sequence variants, copy number variants and polygenic risk score. <i>European Journal of Human Genetics</i> , 2019, 27, 114-124.	1.4	24
1125	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. <i>Platelets</i> , 2019, 30, 164-173.	1.1	15
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1142	Gene-based association analysis for bivariate time-to-event data through functional regression with copula models. <i>Biometrics</i> , 2020, 76, 619-629.	0.8	6
1143	Population genetic simulation study of power in association testing across genetic architectures and study designs. <i>Genetic Epidemiology</i> , 2020, 44, 90-103.	0.6	7
1144	An efficient integrative resampling method for gene-trait association analysis. <i>Genetic Epidemiology</i> , 2020, 44, 197-207.	0.6	1



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1148	Powerful rare variant association testing in a copula-based joint analysis of multiple phenotypes. <i>Genetic Epidemiology</i> , 2020, 44, 26-40.	0.6	5
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1150	Male-specific association of the 2p25 region with suicide attempt in bipolar disorder. <i>Journal of Psychiatric Research</i> , 2020, 121, 151-158.	1.5	7
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1152	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020, 126, 350-360.	2.0	41
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1155	A multi-ethnic meta-analysis identifies novel genes, including ACSL5, associated with amyotrophic lateral sclerosis. <i>Communications Biology</i> , 2020, 3, 526.	2.0	49
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1157	Explaining the Genetic Causality for Complex Phenotype via Deep Association Kernel Learning. <i>Patterns</i> , 2020, 1, 100057.	3.1	6
1158	A Minimax Optimal Ridge-Type Set Test for Global Hypothesis With Applications in Whole Genome Sequencing Association Studies. <i>Journal of the American Statistical Association</i> , 2022, 117, 897-908.	1.8	4
1159	Meta-analysis of whole-exome sequencing data from two independent cohorts finds no evidence for rare variant enrichment in Parkinson disease associated loci. <i>PLoS ONE</i> , 2020, 15, e0239824.	1.1	11
1160	PWAS: proteome-wide association study linking genes and phenotypes by functional variation in proteins. <i>Genome Biology</i> , 2020, 21, 173.	3.8	52
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1166	A telescope GWAS analysis strategy, based on SNPs-genes-pathways ensemble and on multivariate algorithms, to characterize late onset Alzheimer’s disease. <i>Scientific Reports</i> , 2020, 10, 12063.	1.6	11
1167	A rank-based normalization method with the fully adjusted full-stage procedure in genetic association studies. <i>PLoS ONE</i> , 2020, 15, e0233847.	1.1	8
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1923	Longitudinal Associations Between TPO Gene Variants and Thyroid Peroxidase Antibody Seroconversion in a Population-Based Study: Tehran Thyroid Study. <i>Genetic Testing and Molecular Biomarkers</i> , 2023, 27, 65-73.	0.3	0
1924	Gene Association Analysis of Quantitative Trait Based on Functional Linear Regression Model with Local Sparse Estimator. <i>Genes</i> , 2023, 14, 834.	1.0	0
1925	Scalable mixed model methods for set-based association studies on large-scale categorical data analysis and its application to exome-sequencing data in UK Biobank. <i>American Journal of Human Genetics</i> , 2023, 110, 762-773.	2.6	0
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