Resource Summary Report

Generated by RRID on Apr 18, 2025

SKAT

RRID:SCR_009396
Type: Tool

Proper Citation

SKAT (RRID:SCR_009396)

Resource Information

URL: https://www.hsph.harvard.edu/skat/

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Description: Software application that is a SNP-set (e.g., a gene or a region) level test for association between a set of rare (or common) variants and dichotomous or quantitative phenotypes. SKAT aggregates individual score test statistics of SNPs in a SNP set and efficiently computes SNP-set level p-values, e.g. a gene or a region level p-value, while adjusting for covariates, such as principal components to account for population stratification. SKAT also allows for power/sample size calculations for designing for sequence association studies. (entry from Genetic Analysis Software)

Synonyms: SNP-set (Sequence) Kernel Association Test

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, bio.tools

Funding:

Resource Name: SKAT

Resource ID: SCR_009396

Alternate IDs: nlx_154634, biotools:skat

Alternate URLs: https://bio.tools/skat

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063546+0000

Ratings and Alerts

No rating or validation information has been found for SKAT.

No alerts have been found for SKAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 255 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Ali A, et al. (2025) Genetic variants associated with age-related episodic memory decline implicate distinct memory pathologies. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14379.

Zheng D, et al. (2024) radioGWAS links radiome to genome to discover driver genes with somatic mutations for heterogeneous tumor image phenotype in pancreatic cancer. Scientific reports, 14(1), 12316.

Leger BS, et al. (2024) Rare and Common Variants Associated with Alcohol Consumption Identify a Conserved Molecular Network. bioRxiv : the preprint server for biology.

Loomis SJ, et al. (2024) Genome-Wide Association Studies of ARIA From the Aducanumab Phase 3 ENGAGE and EMERGE Studies. Neurology, 102(3), e207919.

Zhao Y, et al. (2024) Genetic analysis of transcription factors in dopaminergic neuronal development in Parkinson's disease. Chinese medical journal, 137(4), 450.

Clarke B, et al. (2024) Integration of variant annotations using deep set networks boosts rare variant association testing. Nature genetics, 56(10), 2271.

Littleton SH, et al. (2024) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. Cell genomics, 4(5), 100556.

Kars ME, et al. (2024) The landscape of rare genetic variation associated with inflammatory bowel disease and Parkinson's disease comorbidity. Genome medicine, 16(1), 66.

Yuan H, et al. (2024) Two-stage association study of mitochondrial DNA variants in allergic

rhinitis. Allergy, asthma, and clinical immunology : official journal of the Canadian Society of Allergy and Clinical Immunology, 20(1), 16.

Wang H, et al. (2024) Whole-Genome Sequencing Analysis Reveals New Susceptibility Loci and Structural Variants Associated with Progressive Supranuclear Palsy. medRxiv : the preprint server for health sciences.

Cao C, et al. (2024) RAVAR: a curated repository for rare variant-trait associations. Nucleic acids research, 52(D1), D990.

Guo H, et al. (2024) Prioritizing disease-related rare variants by integrating gene expression data. bioRxiv : the preprint server for biology.

Hop PJ, et al. (2024) Systematic rare variant analyses identify RAB32 as a susceptibility gene for familial Parkinson's disease. Nature genetics, 56(7), 1371.

Alade A, et al. (2024) Rare variants analyses suggest novel cleft genes in the African population. Scientific reports, 14(1), 14279.

Sun X, et al. (2024) Association analysis of mitochondrial DNA heteroplasmic variants: methods and application. medRxiv : the preprint server for health sciences.

Guo H, et al. (2024) Prioritizing disease-related rare variants by integrating gene expression data. PLoS genetics, 20(9), e1011412.

Benitez BA, et al. (2024) Haploinsufficiency of lysosomal enzyme genes in Alzheimer's disease. bioRxiv : the preprint server for biology.

Kimura T, et al. (2024) Whole-genome sequencing to identify rare variants in East Asian patients with dementia with Lewy bodies. npj aging, 10(1), 52.

Zhu L, et al. (2024) Integrating External Controls by Regression Calibration for Genome-Wide Association Study. Genes, 15(1).

Acharya S, et al. (2024) Multi-omics Integration Identifies Genes Influencing Traits Associated with Cardiovascular Risks: The Long Life Family Study. medRxiv : the preprint server for health sciences.