Resource Summary Report

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SNPTEST

RRID:SCR_009406
Type: Tool

Proper Citation

SNPTEST (RRID:SCR_009406)

Resource Information

URL: https://mathgen.stats.ox.ac.uk/genetics_software/snptest/snptest.html

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Description: Software program for the analysis of single SNP association in genome-wide studies. The tests implemented can cater for binary (case-control) and quantitative phenotypes, can condition upon an arbitrary set of covariates and properly account for the uncertainty in genotypes. The program is designed to work seamlessly with the output of both the genotype calling program CHIAMO, the genotype imputation program IMPUTE and the program GTOOL. This program was used in the analysis of the 7 genome-wide association studies carried out by the Wellcome Trust Case-Control Consortium (WTCCC). (entry from Genetic Analysis Software)

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, bio.tools

Resource Name: SNPTEST

Resource ID: SCR_009406

Alternate IDs: nlx_154651, biotools:snptest

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

Old URLs: http://www.stats.ox.ac.uk/~marchini/software/gwas/snptest.html

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260805T044222+0000

Ratings and Alerts

No rating or validation information has been found for SNPTEST.

No alerts have been found for SNPTEST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 396 mentions in open access literature.

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

Zheng SL, et al. (2025) Evaluation of polygenic scores for hypertrophic cardiomyopathy in the general population and across clinical settings. Nature genetics, 57(3), 563.

Leu C, et al. (2025) Genome-wide association meta-analyses of drug-resistant epilepsy. EBioMedicine, 115, 105675.

Wei J, et al. (2025) Integrative proteomic analysis provides novel therapeutic insights for etiological subtypes of diabetes. Diabetes, obesity & metabolism, 27(12), 6894.

Zhao SS, et al. (2025) Modifiable risk factors and inflammation-related proteins in polymyalgia rheumatica: genome-wide meta-analysis and Mendelian randomization. Rheumatology (Oxford, England), 64(5), 3012.

Roshandel D, et al. (2025) Genetics of C-Peptide and Age at Diagnosis in Type 1 Diabetes. Diabetes, 74(2), 223.

Binks SNM, et al. (2025) Novel risk loci in LGI1-antibody encephalitis: genome-wide association study discovery and validation cohorts. Brain : a journal of neurology, 148(3), 737.

Rajabli F, et al. (2025) Multi-ancestry genome-wide meta-analysis of 56,241 individuals identifies known and novel cross-population and ancestry-specific associations as novel risk loci for Alzheimer's disease. Genome biology, 26(1), 210.

Obry L, et al. (2025) Identification of gene-sun exposure interactions of GWAS-identified variants in perceived facial aging progression. Frontiers in aging, 6, 1519799.

Power GM, et al. (2025) The role of body image dissatisfaction in the relationship between body size and disordered eating and self-harm: complimentary Mendelian randomization and mediation analyses. Molecular psychiatry, 30(2), 521.

Leppilahti JM, et al. (2025) Genome-Wide Association Study of Temporomandibular Disorder-Related Pain in Finnish Populations. Journal of oral rehabilitation, 52(2), 151.

Yang G, et al. (2025) Investigation of Genomic and Transcriptomic Risk Factors of Clopidogrel Response in African Americans. Clinical pharmacology and therapeutics,

117(5), 1313.

Valo E, et al. (2025) Genome-wide characterization of 54 urinary metabolites reveals molecular impact of kidney function. Nature communications, 16(1), 325.

Kalafati IP, et al. (2025) Development and validation of a polygenic risk score for height in a Greek cohort: Association with blood pressure measurements. Frontiers in genetics, 16, 1538975.

Sadler MC, et al. (2025) Genetic determinants of zinc homeostasis and its role in cardiometabolic diseases. PLoS genetics, 21(12), e1011928.

Le Borgne J, et al. (2025) X-chromosome-wide association study for Alzheimer's disease. Molecular psychiatry, 30(6), 2335.

Hernangomez-Laderas A, et al. (2025) Impact of placental and peripheral blood DNA methylation on celiac disease susceptibility. Journal of pediatric gastroenterology and nutrition, 81(3), 587.

Salminen A, et al. (2025) Genome-wide association study of pulpal and apical diseases. Nature communications, 16(1), 6774.

Thomassen JQ, et al. (2025) APOE stratified genome-wide association studies provide novel insights into the genetic etiology of Alzheimers's disease. medRxiv : the preprint server for health sciences.

Qin W, et al. (2025) The genetic landscape of early-onset Alzheimer's disease in China. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(2), e14486.

Zhu Q, et al. (2025) Appraising the causal role of cathepsins in genitourinary carcinoma: a two-sample mendelian randomization and prospective study based on 36,225 individuals. Discover oncology, 16(1), 435.