

Resource Summary Report

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GSA-SNP

RRID:SCR_013109

Type: Tool

Proper Citation

GSA-SNP (RRID:SCR_013109)

Resource Information

URL: <http://sourceforge.net/projects/gsa-snp/>

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Description: A tool for the gene-set (or pathway) analysis of a genome-wide association study result. It accepts a genome-wide list of SNPs and their association P-values. It summarizes the SNP P-values into nearby genes. The gene-by-gene summary results are then further summarized by gene-sets such as Gene Ontology, KEGG pathways, or user-created gene-sets. Various standardization and statistical tests can be performed and the resulting gene-sets that pass a significance level after multiple-testing correction are reported. The tool is written in Java and is available as a standalone version.

Abbreviations: GSA-SNP

Resource Type: software resource, software application, data processing software

Defining Citation: [PMID:20501604](https://pubmed.ncbi.nlm.nih.gov/20501604/)

Keywords: clinical neuroinformatics, computational neuroscience, imaging genomics, bio.tools

Funding:

Availability: GNU General Public License v2

Resource Name: GSA-SNP

Resource ID: SCR_013109

Alternate IDs: nlx_155765, biotools:gsa-snp

Alternate URLs: <https://bio.tools/gsa-snp>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250421T053919+0000

Ratings and Alerts

No rating or validation information has been found for GSA-SNP.

No alerts have been found for GSA-SNP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Nho K, et al. (2024) CYP1B1-RMDN2 Alzheimer's disease endophenotype locus identified for cerebral tau PET. Nature communications, 15(1), 8251.

Ma Y, et al. (2020) Identification of 34 genes conferring genetic and pharmacological risk for the comorbidity of schizophrenia and smoking behaviors. Aging, 12(3), 2169.

Jiao H, et al. (2019) Genome-Wide Interaction and Pathway Association Studies for Body Mass Index. Frontiers in genetics, 10, 404.

Horgusluoglu-Moloch E, et al. (2019) Genome-wide association analysis of hippocampal volume identifies enrichment of neurogenesis-related pathways. Scientific reports, 9(1), 14498.

Yoon S, et al. (2018) Efficient pathway enrichment and network analysis of GWAS summary data using GSA-SNP2. Nucleic acids research, 46(10), e60.

Primes G, et al. (2018) Real-life helping behaviours in North America: A genome-wide association approach. PloS one, 13(1), e0190950.

Zhao H, et al. (2017) Improving the detection of pathways in genome-wide association studies by combined effects of SNPs from Linkage Disequilibrium blocks. *Scientific reports*, 7(1), 3512.

Deters KD, et al. (2017) Genome-wide association study of language performance in Alzheimer's disease. *Brain and language*, 172, 22.

Szefer E, et al. (2017) Multivariate association between single-nucleotide polymorphisms in Alzgene linkage regions and structural changes in the brain: discovery, refinement and validation. *Statistical applications in genetics and molecular biology*, 16(5-6), 349.

Witt SH, et al. (2017) Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. *Translational psychiatry*, 7(6), e1155.

Below JE, et al. (2016) Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs. *Scientific reports*, 6, 19429.

Li WD, et al. (2015) Pathway-Based Genome-wide Association Studies Reveal That the Rac1 Pathway Is Associated with Plasma Adiponectin Levels. *Scientific reports*, 5, 13422.

Wojcik GL, et al. (2015) Relative performance of gene- and pathway-level methods as secondary analyses for genome-wide association studies. *BMC genetics*, 16, 34.

Kwon JS, et al. (2014) Gene-set based genome-wide association analysis for the speed of sound in two skeletal sites of Korean women. *BMB reports*, 47(6), 348.

Vinayagamoorthy N, et al. (2014) New variants including ARG1 polymorphisms associated with C-reactive protein levels identified by genome-wide association and pathway analysis. *PLoS one*, 9(4), e95866.

Kim J, et al. (2013) Gene set analyses of genome-wide association studies on 49 quantitative traits measured in a single genetic epidemiology dataset. *Genomics & informatics*, 11(3), 135.

Kwon JS, et al. (2012) Performance Comparison of Two Gene Set Analysis Methods for Genome-wide Association Study Results: GSA-SNP vs i-GSEA4GWAS. *Genomics & informatics*, 10(2), 123.

Wang L, et al. (2011) Gene set analysis of genome-wide association studies: methodological issues and perspectives. *Genomics*, 98(1), 1.