Resource Summary Report

Generated by ASWG on Aug 4, 2026

MAGMA

RRID:SCR_005757
Type: Tool

Proper Citation

MAGMA (RRID:SCR_005757)

Resource Information

URL: http://snp-magma.sourceforge.net

Proper Citation: MAGMA (RRID:SCR_005757)

Description: Software that utilizes a multiobjective evolutionary algorithm for genetic mapping. It is based on a the ECJ evolutionary software package written by Sean Luke and includes the Strength Pareto Evoluationary Algorithm Version 2 changes for multiobjective analysis. The code runs on any platform with Java Version 2. A genetic mapping project, typically implemented during a search for genes responsible for a disease, requires the acquisition of a set of data from each of a large number of individuals. This data set includes the values of multiple genetic markers. These genetic markers occur at discrete positions along the genome, which is a collection of one or more linear chromosomes. Typing the value of a marker in an individual carries a cost; one seeks to minimize the number of markers typed without excessively jeopardizing the probability of detecting an association between a marker and a disease phenotype. MAGMA is a project which employ"s a multiobjective evolutionary algorithm to solve this problem.

Abbreviations: MAGMA

Synonyms: Multiobjective Analyzer for Genetic Marker Acquisition, MAGMA: Multiobjective Analyzer for Genetic Marker Acquisition

Resource Type: software resource

Defining Citation: PMID:12875658

Keywords: gene, genetic mapping, algorithm, genomics, single nucleotide polymorphism, population study, haplotype-block elucidation, java

Funding: Juvenile Diabetes Research Foundation

Availability: Open unspecified license

Resource Name: MAGMA

Resource ID: SCR_005757

Alternate IDs: nlx_149220

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260801T190258+0000

Ratings and Alerts

No rating or validation information has been found for MAGMA.

No alerts have been found for MAGMA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 456 mentions in open access literature.

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

Eising E, et al. (2026) De novo protein-coding gene variants in developmental stuttering. Molecular psychiatry, 31(1), 104.

Bj??rndal LD, et al. (2026) Prevalence, Characteristics, and Genetic Architecture of Avoidant/Restrictive Food Intake Phenotypes. JAMA pediatrics, 180(1), 45.

Zhou X, et al. (2026) Single-Cell RNA Sequencing of Thyroid Tissues Reveals Pathogenesis of Graves' Disease. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e08449.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. EBioMedicine, 113, 105569.

Gaertner Z, et al. (2025) Molecular and spatial transcriptomic classification of midbrain dopamine neurons and their alterations in a LRRK2G2019S model of Parkinson's disease. eLife, 13.

Wright SN, et al. (2025) Common and rare genetic variants show network convergence for a majority of human traits. medRxiv : the preprint server for health sciences.

Bai W, et al. (2025) Shared genetic architecture between stroke and blood lipids: a large-scale genome-wide cross-trait analysis. Human genomics, 19(1), 75.

Kim MS, et al. (2025) Genomics reveals eleven obesity endotypes with distinct biological and phenotypic signatures. medRxiv : the preprint server for health sciences.

Zhou F, et al. (2025) The shared genetic etiology of autoimmune disorders and interstitial lung disease: insights from large-scale genome-wide cross-trait analysis. Clinical and experimental medicine, 25(1), 305.

Zhu T, et al. (2025) Mitochondrial FIS1 As a Novel Drug Target for the Treatment of Erectile Dysfunction: A Multi-Omic and Epigenomic Association Study. The world journal of men's health, 43(3), 669.

Pottier C, et al. (2025) Deciphering distinct genetic risk factors for FTLD-TDP pathological subtypes via whole-genome sequencing. Nature communications, 16(1), 3914.

Oliva M, et al. (2025) Integration of GWAS, QTLs and keratinocyte functional assays reveals molecular mechanisms of atopic dermatitis. Nature communications, 16(1), 3101.

Cho S, et al. (2025) Genome-wide interaction study of physical activity and genetic susceptibility on colorectal cancer using UK biobank data. Scientific reports, 15(1), 30180.

Lai Q, et al. (2025) Disentangling associations between complex traits and cell types with seismic. Nature communications, 16(1), 8744.

Wilhelm K, et al. (2025) Meta-evolutionary exome analysis identifies novel type 2 diabetes mellitus genes in the UK Biobank and all of us. PLoS genetics, 21(9), e1011889.

Antonyan L, et al. (2025) Polygenic Risk Scores for Pediatric Obsessive-Compulsive Symptoms and their Mediating Effect in Clinically Diagnosed Samples of Obsessive-Compulsive Disorder, Attention-Deficit/Hyperactivity Disorder, Anxiety, Depression, Autism and Tourette syndrome. Research square.

Newbury A, et al. (2025) Multi-domain rule-based phenotyping algorithms enable improved GWAS signal. NPJ digital medicine, 8(1), 499.

Wang R, et al. (2025) Neural Spectral Prediction for Structure Elucidation with Tandem Mass Spectrometry. bioRxiv : the preprint server for biology.

Liu SA, et al. (2025) Plume-induced emissions of deep methane linked to the end-Guadalupian mass extinction. Nature communications, 16(1), 5865.

Willis C, et al. (2025) Gene expression differences associated with alcohol use disorder in human brain. Molecular psychiatry, 30(4), 1617.