Resource Summary Report

Generated by dkNET on Apr 28, 2025

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: 20250420T014301+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 299 mentions in open access literature.

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

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

Nguyen PT, et al. (2025) Genome-wide association studies are enriched for interacting genes. BioData mining, 18(1), 3.

Li X, et al. (2025) Genetic Nurture Effects on Type 2 Diabetes Among Chinese Han Adults: A Family-Based Design. Biomedicines, 13(1).

Jung S, et al. (2025) Rare Variant Analyses in Ancestrally Diverse Cohorts Reveal Novel ADHD Risk Genes. medRxiv : the preprint server for health sciences.

Huang SY, et al. (2025) Genome-wide association study unravels mechanisms of brain glymphatic activity. Nature communications, 16(1), 626.

Ding H, et al. (2025) Integrating genetics and transcriptomics to characterize shared

mechanisms in digestive diseases and psychiatric disorders. Communications biology, 8(1), 47.

Zhang Y, et al. (2025) A multiscale functional map of somatic mutations in cancer integrating protein structure and network topology. Nature communications, 16(1), 975.

Weng LC, et al. (2025) The impact of common and rare genetic variants on bradyarrhythmia development. Nature genetics, 57(1), 53.

Zhang M, et al. (2025) Multi-ancestry genome-wide meta-analysis with 472,819 individuals identifies 32 novel risk loci for psoriasis. Journal of translational medicine, 23(1), 133.

Dong ZY, et al. (2025) Integrative genetics and multiomics analysis reveal mechanisms and therapeutic targets in vitiligo highlighting JAK STAT pathway regulation of CTSS. Scientific reports, 15(1), 2245.

Herrera-Rivero M, et al. (2025) A meta-analysis of genome-wide studies of resilience in the German population. Molecular psychiatry, 30(2), 497.

Jiang Z, et al. (2025) The X chromosome's influences on the human brain. Science advances, 11(4), eadq5360.

Wang L, et al. (2025) A cross-tissue transcriptome-wide association study identifies new susceptibility genes for benign prostatic hyperplasia. Scientific reports, 15(1), 3186.

Guo X, et al. (2025) Shared genetic architecture and bidirectional clinical risks within the psycho-metabolic nexus. EBioMedicine, 111, 105530.

Pan Q, et al. (2025) A genome-wide association study identifies genetic variants associated with hip pain in the UK Biobank cohort (N?=?221,127). Scientific reports, 15(1), 2812.

Ma Y, et al. (2025) Systematic dissection of pleiotropic loci and critical regulons in excitatory neurons and microglia relevant to neuropsychiatric and ocular diseases. Translational psychiatry, 15(1), 24.

Halligan NLN, et al. (2025) Variants in the ?-globin locus are associated with pneumonia in African American children. HGG advances, 6(1), 100374.

Zeng J, et al. (2025) Protocol for genetic analysis of population-scale ultra-low-depth sequencing data. STAR protocols, 6(1), 103579.

Shastri GG, et al. (2024) Cortico-striatal differences in the epigenome in attention-deficit/hyperactivity disorder. Translational psychiatry, 14(1), 189.

Cameron D, et al. (2024) Genetic Implication of Prenatal GABAergic and Cholinergic Neuron Development in Susceptibility to Schizophrenia. Schizophrenia bulletin, 50(5), 1171.