

Resource Summary Report

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Genomic Association Tester

RRID:SCR_020949

Type: Tool

Proper Citation

Genomic Association Tester (RRID:SCR_020949)

Resource Information

URL: <https://gat.readthedocs.io/en/latest/>

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Description: Software tool as simulation framework for testing association of genomic intervals. Used for estimating significance of overlap between multiple sets of genomic intervals. Estimates statistical significance based on simulation and controls for multiple tests using false discovery rate.

Abbreviations: GAT

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

Defining Citation: [PMID:23782611](#)

Keywords: Genomic intervals, genomic intervals association testing, overlap significance estimation, genomic intervals sets, segment length distribution, chromosomal location, isochores

Funding: UK Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: Genomic Association Tester

Resource ID: SCR_020949

Alternate URLs: <https://github.com/AndreasHeger/gat>

Old URLs: <http://code.google.com/p/genomic-association-tester>

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260812T044358+0000

Ratings and Alerts

No rating or validation information has been found for Genomic Association Tester.

No alerts have been found for Genomic Association Tester.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Fulmer D, et al. (2025) Reorganization of H3K9me2-modified chromatin regions during mouse embryonic development. *Developmental biology*, 528, 188.

Bloor S, et al. (2025) RNA binding by Periphilin plays an essential role in initiating silencing by the HUSH complex. *Nucleic acids research*, 53(2).

Chen S, et al. (2024) Cross-Species Comparative DNA Methylation Reveals Novel Insights into Complex Trait Genetics among Cattle, Sheep, and Goats. *Molecular biology and evolution*, 41(2).

Wong KG, et al. (2024) Growth factor-induced activation of MSK2 leads to phosphorylation of H3K9me2S10 and corresponding changes in gene expression. *Science advances*, 10(11), eadm9518.

St Germain CP, et al. (2022) Genomic patterns of transcription-replication interactions in mouse primary B cells. *Nucleic acids research*, 50(4), 2051.

Liu S, et al. (2022) A multi-tissue atlas of regulatory variants in cattle. *Nature genetics*, 54(9), 1438.

Lizamore D, et al. (2021) Elevated transcription of transposable elements is accompanied by het-siRNA-driven de novo DNA methylation in grapevine embryogenic callus. *BMC genomics*, 22(1), 676.

Borg M, et al. (2021) Epigenetic reprogramming rewires transcription during the alternation of generations in Arabidopsis. *eLife*, 10.

Creamer KM, et al. (2021) Nascent RNA scaffolds contribute to chromosome territory architecture and counter chromatin compaction. *Molecular cell*, 81(17), 3509.

Smith CL, et al. (2021) Global chromatin relabeling accompanies spatial inversion of chromatin in rod photoreceptors. *Science advances*, 7(39), eabj3035.

Smith CL, et al. (2021) The nuclear periphery is a scaffold for tissue-specific enhancers. *Nucleic acids research*, 49(11), 6181.

Morin A, et al. (2020) TET-Mediated Hypermethylation Primes SDH-Deficient Cells for HIF2 α -Driven Mesenchymal Transition. *Cell reports*, 30(13), 4551.

Liu S, et al. (2020) Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. *BMC biology*, 18(1), 80.

Siddique MI, et al. (2019) Identifying candidate genes for *Phytophthora capsici* resistance in pepper (*Capsicum annuum*) via genotyping-by-sequencing-based QTL mapping and genome-wide association study. *Scientific reports*, 9(1), 9962.

Benton ML, et al. (2019) Genome-wide enhancer annotations differ significantly in genomic distribution, evolution, and function. *BMC genomics*, 20(1), 511.

Abida W, et al. (2019) Genomic correlates of clinical outcome in advanced prostate cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 116(23), 11428.

Benton MC, et al. (2019) Genome-wide allele-specific methylation is enriched at gene regulatory regions in a multi-generation pedigree from the Norfolk Island isolate. *Epigenetics & chromatin*, 12(1), 60.

Handel AE, et al. (2018) Comprehensively Profiling the Chromatin Architecture of Tissue Restricted Antigen Expression in Thymic Epithelial Cells Over Development. *Frontiers in immunology*, 9, 2120.

Coulson RL, et al. (2018) Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. *Nature communications*, 9(1), 1616.

Stadlmeier M, et al. (2018) Usefulness of a Multiparent Advanced Generation Intercross Population With a Greatly Reduced Mating Design for Genetic Studies in Winter Wheat. *Frontiers in plant science*, 9, 1825.