Resource Summary Report

Generated by RRID on Aug 5, 2026

GENIE

RRID:SCR_009197
Type: Tool

Proper Citation

GENIE (RRID:SCR_009197)

Resource Information

URL: http://www-genepi.med.utah.edu/Genie/

Proper Citation: GENIE (RRID:SCR_009197)

Description: Software application that performs tests of association and transmission disequilibrium (TDT) between genetic markers and traits in studies of arbitrarily-sized families and/or independent individuals using Monte Carlo testing. For dichotomous traits, basic genotype-based or allele-based Chi-square statistics, OR, and a Chi-square trend statistic with user-defined weights, TDT, sib-TDT, combined-TDT are included. For quantitative outcomes, a difference in means test, ANOVA and QTDT are offered. Flexible haplotype testing and meta analysis across multiple centers are available. An automated haplotype building module, hapConstructor, is also offered that data mines multi-locus data for association signals. The Monte Carlo empirical significance assessment accounts for all relatedness between individuals for all tests. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GENIE

Synonyms: PEDGENIE, HAPMC

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, java 1.6, web-based

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GENIE

Resource ID: SCR_009197

Alternate IDs: nlx_154344

Old URLs: http://bioinformatics.med.utah.edu/Genie/index.html

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044219+0000

Ratings and Alerts

No rating or validation information has been found for GENIE.

No alerts have been found for GENIE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 361 mentions in open access literature.

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

Kaminska K, et al. (2025) Bi-allelic variants in three genes encoding distinct subunits of the vesicular AP-5 complex cause hereditary macular dystrophy. American journal of human genetics, 112(4), 808.

Arango-Argoty G, et al. (2025) Pretrained transformers applied to clinical studies improve predictions of treatment efficacy and associated biomarkers. Nature communications, 16(1), 2101.

Lock IC, et al. (2025) Mis-splicing drives loss of function of p53E224D point mutation. PloS one, 20(3), e0318856.

Demewoz NM, et al. (2025) Assessment of radioactivity in soil samples from Wolaita Sodo town, Ethiopia: implications for environmental and public health. Radiation protection dosimetry, 201(3), 160.

Azimi R, et al. (2025) Sensitivity analysis of unsafe behaviors in the spinning and weaving factories: Exploring the association with burnout and resilience using Bayesian networks. PloS one, 20(7), e0326883.

Mat Salleh F, et al. (2025) Safety and outcomes of bikini-incision DAA for hip arthroplasty with large acetabular cups (?56 mm): A single-surgeon series of 215 cases. SICOT-J, 11, 25.

Jürgens T, et al. (2025) Closedness of Acoustic Coupling and Audiological Measures Are Associated with Individual Speech-in-Noise Benefit From Noise Reduction in Hearing Aids. Trends in hearing, 29, 23312165251325983.

Arter ZL, et al. (2025) Tumor Mutation Burden Survey of AACR GENIE Database Revealed NTRK (NTRK+) and RET (RET+) Fusions Positive Colorectal Carcinoma (CRC) as Distinct Subsets. Cancer medicine, 14(4), e70665.

Yung KKY, et al. (2025) Using a Bayesian network to classify time to return to sport based on football injury epidemiological data. PloS one, 20(3), e0314184.

Lee J, et al. (2025) Association of clonal hematopoiesis of indeterminate potential with myocardial characteristic differences in non-ischemic heart failure. Heliyon, 11(4), e42858.

Brose MS, et al. (2025) Larotrectinib Compared With Real-World Non-Tropomyosin Receptor Kinase Inhibitor Therapies in Patients With Tropomyosin Receptor Kinase Fusion Cancer. JCO precision oncology, 9, e2400500.

Perfetto C, et al. (2025) Unraveling BRAF alterations: molecular insights to circumvent therapeutic resistance across cancer types. Cancer drug resistance (Alhambra, Calif.), 8, 14.

Sun L, et al. (2025) The global prevalence and genetic spectrum of primary carnitine deficiency. BMC genomic data, 26(1), 44.

Hwang SY, et al. (2025) Influence of lifestyle risk factors and genetic predisposition on metabolic syndrome risk in Korean adults. Scientific reports, 15(1), 24060.

Monge C, et al. (2025) Detecting PI3K and TP53 Pathway Disruptions in Early-Onset Colorectal Cancer Among Hispanic/Latino Patients. Cancer medicine, 14(7), e70791.

Chen L, et al. (2025) Molecular characterization of gliosarcoma reveals prognostic biomarkers and clinical parallels with glioblastoma. Journal of neuro-oncology, 171(2), 403.

Ghosh HS, et al. (2025) Contemporary prognostic signatures and refined risk stratification of gliomas: An analysis of 4400 tumors. Neuro-oncology, 27(1), 195.

Zhang Y, et al. (2025) Crash injury severity for ride-hailing drivers: a questionnaire study in China. Scientific reports, 15(1), 17203.

Jeong CU, et al. (2025) Artificial Intelligence-Driven Biological Age Prediction Model Using Comprehensive Health Checkup Data: Development and Validation Study. JMIR aging, 8, e64473.

Dong K, et al. (2025) Computational modeling of human genetic variants in mice. bioRxiv : the preprint server for biology.