Resource Summary Report

Generated by dkNET on Apr 17, 2025

GENIE

RRID:SCR_009197
Type: Tool

Proper Citation

GENIE (RRID:SCR_009197)

Resource Information

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

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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)

Abbreviations: GENIE

Synonyms: PEDGENIE, HAPMC

Resource Type: software resource, software application

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

Funding:

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: 20250416T063539+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 322 mentions in open access literature.

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

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.

Dankner M, et al. (2025) Clinical Activity of Mitogen-Activated Protein Kinase Inhibitors in Patients With MAP2K1 (MEK1)-Mutated Metastatic Cancers. JCO precision oncology, 9, e2400199.

Woo KA, et al. (2024) Parkinson's disease is associated with clonal hematopoiesis with TET2 mutation. NPJ Parkinson's disease, 10(1), 168.

Anaya J, et al. (2024) Characterization of Non-Monotonic Relationships between Tumor Mutational Burden and Clinical Outcomes. Cancer research communications, 4(7), 1667.

Khoshakhlagh AH, et al. (2024) Relationships between job stress, post-traumatic stress and musculoskeletal symptoms in firefighters and the role of job burnout and depression mediators: a bayesian network model. BMC public health, 24(1), 468.

Zheng S, et al. (2024) GlioPredictor: a deep learning model for identification of high-risk adult IDH-mutant glioma towards adjuvant treatment planning. Scientific reports, 14(1), 2126.

Lemieux M, et al. (2024) Functional plasticity of glutamatergic neurons of medullary reticular nuclei after spinal cord injury in mice. Nature communications, 15(1), 1542.

Pratt HG, et al. (2024) Analysis of single nuclear chromatin accessibility reveals unique myeloid populations in human pancreatic ductal adenocarcinoma. Clinical and translational medicine, 14(3), e1595.

El Zarif T, et al. (2024) TERT Promoter Mutations Frequency Across Race, Sex, and Cancer Type. The oncologist, 29(1), 8.

Lin S, et al. (2024) Immune cell senescence and exhaustion promote the occurrence of liver metastasis in colorectal cancer by regulating epithelial-mesenchymal transition. Aging, 16(9), 7704.

Yazdanirad S, et al. (2024) Unveiling the impact of siren noise exposure on cognitive function and mental health among firefighters. Scientific reports, 14(1), 25602.

Rafiee M, et al. (2024) The effect of COVID-19 anxiety on nurses' productivity determinants through perceived workload and individual job performance: A Bayesian mediation analysis. Heliyon, 10(14), e34099.

Yaacov A, et al. (2024) Cancer associated variant enrichment CAVE, a gene agnostic approach to identify low burden variants in chronic lymphocytic leukemia. Scientific reports, 14(1), 21962.

Begashaw GB, et al. (2024) Dynamic Bayesian network modeling for longitudinal data on child undernutrition in Ethiopia (2002-2016). Frontiers in public health, 12, 1399094.

Shirai Y, et al. (2024) The development of a custom RNA-sequencing panel for the identification of predictive and diagnostic biomarkers in glioma. Journal of neuro-oncology, 167(1), 75.

Nangeelil KD, et al. (2024) Using neutron activation to assess heavy metal pollution in water and sediment along Savannah River. Environmental analysis, health and toxicology, 39(1), e2024006.

Cui Y, et al. (2024) SLC7A11 protects luminal A breast cancer cells against ferroptosis induced by CDK4/6 inhibitors. Redox biology, 76, 103304.

Tripathi A, et al. (2024) Building Flexible, Scalable, and Machine Learning-Ready Multimodal Oncology Datasets. Sensors (Basel, Switzerland), 24(5).

Sanz-Garcia E, et al. (2024) Genomic Characterization and Clinical Outcomes of Patients with Peritoneal Metastases from the AACR GENIE Biopharma Collaborative Colorectal Cancer Registry. Cancer research communications, 4(2), 475.