Resource Summary Report

Generated by NIF on Apr 20, 2025

SIMULATE

RRID:SCR_009391
Type: Tool

Proper Citation

SIMULATE (RRID:SCR_009391)

Resource Information

URL: http://www.jurgott.org/linkage/simulate.html

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Description: Software program to simulate genotypes in family members for a map of linked markers unlinked to a given affection status locus. the output is ready for analysis with UNKNOWN, ISIM, LSIM, or MSIM of the SLINK package. (entry from Genetic Analysis Software)

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, pascal, ms-dos, vms, unix, bio.tools

Funding:

Resource Name: SIMULATE

Resource ID: SCR_009391

Alternate IDs: nlx_154630, biotools:simulate

Alternate URLs: https://bio.tools/simulate

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250420T015804+0000

Ratings and Alerts

No rating or validation information has been found for SIMULATE.

No alerts have been found for SIMULATE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Pianezza R, et al. (2024) GenomeDelta: detecting recent transposable element invasions without repeat library. Genome biology, 25(1), 315.

Au EH, et al. (2023) Gonomics: uniting high performance and readability for genomics with Go. Bioinformatics (Oxford, England), 39(8).

Yan H, et al. (2023) PhyloAcc-GT: A Bayesian Method for Inferring Patterns of Substitution Rate Shifts on Targeted Lineages Accounting for Gene Tree Discordance. Molecular biology and evolution, 40(9).

Nichols RH, et al. (2021) Reactivation of organophosphate-inhibited serum butyrylcholinesterase by novel substituted phenoxyalkyl pyridinium oximes and traditional oximes. Toxicology, 452, 152719.

Ayd?n A, et al. (2021) Non-technical skills for urological surgeons (NoTSUS): development and evaluation of curriculum and assessment scale. World journal of urology, 39(6), 2231.

Edrees A, et al. (2020) An Edwardsiella piscicida esaS mutant reveals contribution to virulence and vaccine potential. Microbial pathogenesis, 143, 104108.

David PHC, et al. (2019) Using SimulATe to model the effects of antibiotic selective pressure on the dynamics of pathogenic bacterial populations. Biology methods & protocols, 4(1), bpz004.

Khan SA, et al. (2017) Rules for resolving Mendelian inconsistencies in nuclear pedigrees typed for two-allele markers. PloS one, 12(3), e0172807.

Kofler R, et al. (2016) Suitability of Different Mapping Algorithms for Genome-Wide Polymorphism Scans with Pool-Seq Data. G3 (Bethesda, Md.), 6(11), 3507.

Deo AJ, et al. (2010) A novel analytical framework for dissecting the genetic architecture of behavioral symptoms in neuropsychiatric disorders. PloS one, 5(3), e9714.

Reck BH, et al. (2005) Analysis of alcohol dependence phenotype in the COGA families

using covariates to detect linkage. BMC genetics, 6 Suppl 1(Suppl 1), S143.