

# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

## SIMULATE

RRID:SCR\_009391

Type: Tool

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### Proper Citation

SIMULATE (RRID:SCR\_009391)

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### Resource Information

**URL:** <http://www.jurgott.org/linkage/simulate.html>

**Proper Citation:** SIMULATE (RRID:SCR\_009391)

**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

**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:** 20260905T133251+0000

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### Ratings and Alerts

No rating or validation information has been found for SIMULATE.

No alerts have been found for SIMULATE.

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### Data and Source Information

## Usage and Citation Metrics

We found 12 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

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

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).

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

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.

McBride KL, et al. (2009) Linkage analysis of left ventricular outflow tract malformations (aortic valve stenosis, coarctation of the aorta, and hypoplastic left heart syndrome). *European journal of human genetics : EJHG*, 17(6), 811.

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.