

# Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

## SIMWALK

RRID:SCR\_009393

Type: Tool

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### Proper Citation

SIMWALK (RRID:SCR\_009393)

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### Resource Information

**URL:** <http://www.genetics.ucla.edu/software/simwalk>

**Proper Citation:** SIMWALK (RRID:SCR\_009393)

**Description:** Software programs for generating optimal haplotype configurations on general pedigrees using a likelihood-based approach to correctly take intermarker recombination fractions into account. simcross ignores untyped parts of the pedigree, and it uses simulated annealing. simwalk combines simulated annealing with random walk method. (entry from Genetic Analysis Software)

**Synonyms:** SIMWALK/SIMCROSS

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, fortran77, unix, sunos, solaris

**Resource Name:** SIMWALK

**Resource ID:** SCR\_009393

**Alternate IDs:** nlx\_154632

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260919T195806+0000

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### Ratings and Alerts

No rating or validation information has been found for SIMWALK.

No alerts have been found for SIMWALK.

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### Data and Source Information

## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Ghaleb Y, et al. (2022) Whole Exome/Genome Sequencing Joint Analysis of a Family with Oligogenic Familial Hypercholesterolemia. *Metabolites*, 12(3).

Mahmood T, et al. (2021) A Recessively Inherited Risk Locus on Chromosome 13q22-31 Conferring Susceptibility to Schizophrenia. *Schizophrenia bulletin*, 47(3), 796.

Webster J, et al. (2020) A Turing test for crowds. *Royal Society open science*, 7(7), 200307.

Connor TM, et al. (2017) Mutations in mitochondrial DNA causing tubulointerstitial kidney disease. *PLoS genetics*, 13(3), e1006620.

Wight JE, et al. (2016) Chromosome loci vary by juvenile myoclonic epilepsy subsyndromes: linkage and haplotype analysis applied to epilepsy and EEG 3.5-6.0??Hz polyspike waves. *Molecular genetics & genomic medicine*, 4(2), 197.

Mencacci NE, et al. (2015) A missense mutation in KCTD17 causes autosomal dominant myoclonus-dystonia. *American journal of human genetics*, 96(6), 938.

Laston SL, et al. (2015) Genetics of kidney disease and related cardiometabolic phenotypes in Zuni Indians: the Zuni Kidney Project. *Frontiers in genetics*, 6, 6.

Siddiqi S, et al. (2014) A novel splice-site mutation in ALS2 establishes the diagnosis of juvenile amyotrophic lateral sclerosis in a family with early onset anarthria and generalized dystonias. *PloS one*, 9(12), e113258.

Michou L, et al. (2012) Genetic association study of UCMA/GRP and OPTN genes (PDB6 locus) with Paget's disease of bone. *Bone*, 51(4), 720.

Rogers J, et al. (2006) An initial genetic linkage map of the rhesus macaque (*Macaca mulatta*) genome using human microsatellite loci. *Genomics*, 87(1), 30.