Resource Summary Report

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SIMPED

RRID:SCR_009388
Type: Tool

Proper Citation

SIMPED (RRID:SCR_009388)

Resource Information

URL: http://bioinformatics.org/simped/

Proper Citation: SIMPED (RRID:SCR_009388)

Description: Software program that quickly generates haplotypes and/or genotype data for a large number of marker loci (>20,000) for pedigrees of virtually any size and complexity. Haplotypes and/or genotypes are generated using user specified genetic map distances and haplotypes and/or allele frequencies. (entry from Genetic Analysis Software)

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, ms-window, linux, bio.tools

Funding:

Resource Name: SIMPED

Resource ID: SCR_009388

Alternate IDs: biotools:simped, nlx_154627

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

Old URLs: http://www.hgsc.bcm.tmc.edu/genemapping

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063546+0000

Ratings and Alerts

No rating or validation information has been found for SIMPED.

No alerts have been found for SIMPED.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hunter DC, et al. (2022) Using genomic prediction to detect microevolutionary change of a quantitative trait. Proceedings. Biological sciences, 289(1974), 20220330.