

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

[ped-sim](#)

RRID:SCR_026957

Type: Tool

Proper Citation

ped-sim (RRID:SCR_026957)

Resource Information

URL: <https://github.com/williamslab/ped-sim>

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Description: Software tool to simulate pedigree structures. Used for simulating relatives that can utilize either sex-specific or sex averaged genetic maps and also either model of crossover interference or traditional Poisson model for inter-crossover distances.

Synonyms: Ped-sim

Resource Type: simulation software, software application, software resource, source code

Defining Citation: [PMID:31860654](#)

Keywords: Pedigree simulator, simulate pedigree structures, simulating relatives, sex-specific, sex averaged, genetic maps,

Funding: NIGMS R35 GM133805;
Alfred P. Sloan Research Fellowship ;
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NHLBI R01 HL0113323;
NHLBI P01 HL045222;
NIDDK R01 DK047482;
NIDDK R01 DK053889;
NIGMS T32 GM007617;
NIGMS T32 GM083937;
Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: ped-sim

Resource ID: SCR_026957

License: GNU GPL v3

Record Creation Time: 20250517T055756+0000

Record Last Update: 20260805T044606+0000

Ratings and Alerts

No rating or validation information has been found for ped-sim.

No alerts have been found for ped-sim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Avadhanam S, et al. (2025) Phase-free local ancestry inference mitigates the impact of switch errors on phase-based methods. G3 (Bethesda, Md.), 15(8).

Caballero M, et al. (2019) Crossover interference and sex-specific genetic maps shape identical by descent sharing in close relatives. PLoS genetics, 15(12), e1007979.