

Resource Summary Report

Generated by T1D on Aug 1, 2026

SIMUPOP

RRID:SCR_009392

Type: Tool

Proper Citation

SIMUPOP (RRID:SCR_009392)

Resource Information

URL: <http://simupop.sourceforge.net>

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Description: A forward-based population genetics simulation program capable of simulating very complex evolution processes on large (think of millions) populations. Major features include variable population size; many built-in and hybrid (write in python) mutation, migration, selection models. simuPOP can be extended in Python so there is no limit on what you can do with it. (entry from Genetic Analysis Software)

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, (provided as python libraries)

Resource Name: SIMUPOP

Resource ID: SCR_009392

Alternate IDs: nlx_154631

Alternate URLs: <https://pypi.python.org/pypi/simuPOP>

Old URLs: <http://bp6.stat.rice.edu:8080/simuPOP/>

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260731T042822+0000

Ratings and Alerts

No rating or validation information has been found for SIMUPOP.

No alerts have been found for SIMUPOP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

O'Reilly GD, et al. (2024) A new method for ecologists to estimate heterozygote excess and deficit for multi-locus gene families. *Ecology and evolution*, 14(7), e11561.

Lin J, et al. (2023) Simulations of rate of genetic gain in dry bean breeding programs. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 136(1), 14.

Sovic M, et al. (2019) Genetic signatures of small effective population sizes and demographic declines in an endangered rattlesnake, *Sistrurus catenatus*. *Evolutionary applications*, 12(4), 664.

Joiret M, et al. (2019) Confounding of linkage disequilibrium patterns in large scale DNA based gene-gene interaction studies. *BioData mining*, 12, 11.

Comeault AA, et al. (2018) The genomic and ecological context of hybridization affects the probability that symmetrical incompatibilities drive hybrid speciation. *Ecology and evolution*, 8(5), 2926.

Szpak M, et al. (2018) FineMAV: prioritizing candidate genetic variants driving local adaptations in human populations. *Genome biology*, 19(1), 5.

Bailleul D, et al. (2018) Large-scale genetic panmixia in the blue shark (*Prionace glauca*): A single worldwide population, or a genetic lag-time effect of the "grey zone" of differentiation? *Evolutionary applications*, 11(5), 614.

Palamara PF, et al. (2018) High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. *Nature genetics*, 50(9), 1311.

Paterno M, et al. (2017) Population genomics meet Lagrangian simulations: Oceanographic patterns and long larval duration ensure connectivity among *Paracentrotus lividus* populations in the Adriatic and Ionian seas. *Ecology and evolution*, 7(8), 2463.

Iranmehr A, et al. (2017) Clear: Composition of Likelihoods for Evolve and Resequencing Experiments. *Genetics*, 206(2), 1011.

Gussow AB, et al. (2017) Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. *PloS one*, 12(8), e0181604.

Pritchard VL, et al. (2016) Single nucleotide polymorphisms to discriminate different classes of hybrid between wild Atlantic salmon and aquaculture escapees. *Evolutionary*

applications, 9(8), 1017.

Ogbunugafor CB, et al. (2016) Adaptive Landscape by Environment Interactions Dictate Evolutionary Dynamics in Models of Drug Resistance. PLoS computational biology, 12(1), e1004710.

Picq S, et al. (2016) Population genomics of local adaptation versus speciation in coral reef fishes (*Hypoplectrus* spp, Serranidae). Ecology and evolution, 6(7), 2109.

Hackinger S, et al. (2016) Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. Human genetics, 135(4), 393.

Ogbunugafor CB, et al. (2016) A pivot mutation impedes reverse evolution across an adaptive landscape for drug resistance in *Plasmodium vivax*. Malaria journal, 15, 40.

Calboli FC, et al. (2016) A test for within-lake niche differentiation in the nine-spined sticklebacks (*Pungitius pungitius*). Ecology and evolution, 6(14), 4753.

Risso DS, et al. (2016) Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Scientific reports, 6, 25506.

Brousseau L, et al. (2016) Local Adaptation in European Firs Assessed through Extensive Sampling across Altitudinal Gradients in Southern Europe. PloS one, 11(7), e0158216.

Haber M, et al. (2016) Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. American journal of human genetics, 99(6), 1316.