

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SIMCOAL

RRID:SCR_008450

Type: Tool

Proper Citation

SIMCOAL (RRID:SCR_008450)

Resource Information

URL: <http://cmpg.unibe.ch/software/simcoal/>

Proper Citation: SIMCOAL (RRID:SCR_008450)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: SIMCOAL

Synonyms: SIMulate COAlescence

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, ms-windows, (9x/nt)

Resource Name: SIMCOAL

Resource ID: SCR_008450

Alternate IDs: nlx_154620

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260905T133240+0000

Ratings and Alerts

No rating or validation information has been found for SIMCOAL.

No alerts have been found for SIMCOAL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Flom LT, et al. (2026) Characterization of Neuronal Ensembles in a Model of Dual-Reward Conditioned Place Preference. *eNeuro*, 13(6).

Criscuolo D, et al. (2026) KRAS-mediated CCDC6 degradation drives xCT upregulation and ferroptosis evasion. *Apoptosis : an international journal on programmed cell death*, 31(8).

Schreiber D, et al. (2021) Genomic divergence landscape in recurrently hybridizing *Chironomus* sister taxa suggests stable steady state between mutual gene flow and isolation. *Evolution letters*, 5(1), 86.

Victoriano PF, et al. (2020) Contrasting evolutionary responses in two co-distributed species of *Galaxias* (Pisces, Galaxiidae) in a river from the glaciated range in Southern Chile. *Royal Society open science*, 7(7), 200632.

Perez-Pardal L, et al. (2018) Legacies of domestication, trade and herder mobility shape extant male zebu cattle diversity in South Asia and Africa. *Scientific reports*, 8(1), 18027.

Barbieri C, et al. (2017) Enclaves of genetic diversity resisted Inca impacts on population history. *Scientific reports*, 7(1), 17411.

Fujisawa T, et al. (2016) A Rapid and Scalable Method for Multilocus Species Delimitation Using Bayesian Model Comparison and Rooted Triplets. *Systematic biology*, 65(5), 759.

Nikolic N, et al. (2015) Discovery of Genome-Wide Microsatellite Markers in Scombridae: A Pilot Study on Albacore Tuna. *PloS one*, 10(11), e0141830.

Quach H, et al. (2009) Signatures of purifying and local positive selection in human miRNAs. *American journal of human genetics*, 84(3), 316.

Liu Y, et al. (2008) A survey of genetic simulation software for population and epidemiological studies. *Human genomics*, 3(1), 79.