

# Resource Summary Report

Generated by [NIF](#) on Sep 4, 2026

## SIMCOAL

RRID:SCR\_008450

Type: Tool

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### Proper Citation

SIMCOAL (RRID:SCR\_008450)

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### 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:** 20260904T000420+0000

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### Ratings and Alerts

No rating or validation information has been found for SIMCOAL.

No alerts have been found for SIMCOAL.

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### 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 [NIF](#) .

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.