Resource Summary Report

Generated by dkNET on Apr 16, 2025

SIMCOAL

RRID:SCR_008450
Type: Tool

Proper Citation

SIMCOAL (RRID:SCR_008450)

Resource Information

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

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Description: Software application (entry from Genetic Analysis Software)

Abbreviations: SIMCOAL

Synonyms: SIMulate COAlescence

Resource Type: software resource, software application

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

Funding:

Resource Name: SIMCOAL

Resource ID: SCR_008450

Alternate IDs: nlx_154620

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250416T063520+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 8 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

Pérez-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.