

Resource Summary Report

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PSMC

RRID:SCR_017229

Type: Tool

Proper Citation

PSMC (RRID:SCR_017229)

Resource Information

URL: <https://github.com/lh3/psmc.git>

Proper Citation: PSMC (RRID:SCR_017229)

Description: Software package for implementation of Pairwise Sequentially Markovian Coalescent model. Infers population size history from diploid sequence.

Synonyms: Pairwise Sequentially Markovian Coalescent

Resource Type: data processing software, data analysis software, software application, software resource

Keywords: pairwise, sequentially, Markovian, coalescent, model, infer, population, size, history, diploid, sequence

Availability: Free, Available for download, Freely available

Resource Name: PSMC

Resource ID: SCR_017229

License: MIT License

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T042813+0000

Ratings and Alerts

No rating or validation information has been found for PSMC.

No alerts have been found for PSMC.

Data and Source Information

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. *GigaScience*, 14.

Sozzoni M, et al. (2025) Quaternary Habitat Fluctuations and Demographic Dynamics in Turtles Inferred From Environmental Niche Modelling and Whole Genome Data. *Molecular ecology resources*, 25(8), e70040.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Yang YX, et al. (2024) The chromosome-level genome assembly of an endangered herb *Bergenia scopulosa* provides insights into local adaptation and genomic vulnerability under climate change. *GigaScience*, 13.

Nebenführ M, et al. (2024) Whole-genome re-sequencing of the Baikal seal and other phocid seals for a glimpse into their genetic diversity, demographic history, and phylogeny. *GigaByte (Hong Kong, China)*, 2024, gigabyte142.

Hu Y, et al. (2022) A high-resolution genome of an euryhaline and eurythermal rhinogoby (*Rhinogobius similis* Gill 1895). *G3 (Bethesda, Md.)*, 12(2).

Zhang H, et al. (2022) Genomes and demographic histories of the endangered *Bretschneidera sinensis* (Akaniaceae). *GigaScience*, 11.

Luo F, et al. (2022) A chromosome-level genome of the human blood fluke *Schistosoma japonicum* identifies the genomic basis of host-switching. *Cell reports*, 39(1), 110638.

Winter S, et al. (2022) A Chromosome-Scale Genome Assembly of the Okapi (*Okapia johnstoni*). *The Journal of heredity*, 113(5), 568.

Robledo-Ruiz DA, et al. (2022) Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. *GigaScience*, 11.

Machado AM, et al. (2022) A genome assembly of the Atlantic chub mackerel (*Scomber colias*): a valuable teleost fishing resource. *GigaByte (Hong Kong, China)*, 2022, gigabyte40.

Coimbra RTF, et al. (2021) Whole-genome analysis of giraffe supports four distinct species. *Current biology : CB*, 31(13), 2929.

Lamb S, et al. (2021) De novo chromosome-length assembly of the mule deer (*Odocoileus hemionus*) genome. GigaByte (Hong Kong, China), 2021, gigabyte34.

Zeng X, et al. (2020) Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. GigaScience, 9(12).

Lu S, et al. (2019) Chromosomal-level reference genome of Chinese peacock butterfly (*Papilio bianor*) based on third-generation DNA sequencing and Hi-C analysis. GigaScience, 8(11).