

# 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 analysis software, data processing 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:** 20260829T182531+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 17 mentions in open access literature.

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

Kylmänen A, et al. (2026) SwarmGenomics: A Unified Pipeline for Individual-Based Whole-Genome Analyses. *Molecular ecology resources*, 26(3), e70119.

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.

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

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

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.

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

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

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.

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

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

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).