

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, software application, data processing software, software resource

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

Funding:

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: 20250508T065748+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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).

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.

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

adaptions 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).