

Resource Summary Report

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LAMARC

RRID:SCR_009252

Type: Tool

Proper Citation

LAMARC (RRID:SCR_009252)

Resource Information

URL: http://evolution.genetics.washington.edu/lamarc/lamarc_prog.html

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Description: Software application that estimates effective population sizes, exponential population growth rates, and past migration rates between two or n populations, and simultaneously estimates the per-nucleotide recombination rate. Currently Lamarc can use DNA or RNA sequence data, SNP data, and microsatellite data. (entry from Genetic Analysis Software)

Abbreviations: LAMARC

Synonyms: Likelihood Analysis with Metropolis Algorithm using Random Coalescence

Resource Type: software application, software resource

Defining Citation: [DOI:10.1016/j.tree.2008.09.007](https://doi.org/10.1016/j.tree.2008.09.007)

Keywords: gene, genetic, genomic, c++, linux, ms-windows, macos

Resource Name: LAMARC

Resource ID: SCR_009252

Alternate IDs: OMICS_28408, nlx_154420

Alternate URLs: <https://sources.debian.org/src/lamarc/>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044220+0000

Ratings and Alerts

No rating or validation information has been found for LAMARC.

No alerts have been found for LAMARC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Bender AN, et al. (2023) Genetic diversity and demographic history of the leopard seal: A Southern Ocean top predator. PloS one, 18(8), e0284640.

Lima T, et al. (2023) Insights into the evolutionary history of the most skilled tool-handling platyrrhini monkey: *Sapajus libidinosus* from the Serra da Capivara National Park. Genetics and molecular biology, 46(3 Suppl 1), e20230165.

Rajora OP, et al. (2021) Genetic Diversity, Structure and Effective Population Size of Old-Growth vs. Second-Growth Populations of Keystone and Long-Lived Conifer, Eastern White Pine (*Pinus strobus*): Conservation Value and Climate Adaptation Potential. Frontiers in genetics, 12, 650299.

Schwob G, et al. (2021) Exploring the Microdiversity Within Marine Bacterial Taxa: Toward an Integrated Biogeography in the Southern Ocean. Frontiers in microbiology, 12, 703792.

Liu Z, et al. (2019) New Insight into the Evolution of Symbiotic Genes in Black Locust-Associated Rhizobia. Genome biology and evolution, 11(7), 1736.

Gundlach S, et al. (2019) Comparison of Markov Chain Monte Carlo Software for the Evolutionary Analysis of Y-Chromosomal Microsatellite Data. Computational and structural biotechnology journal, 17, 1082.

Bennett KL, et al. (2018) Comparative phylogeography of *Aedes* mosquitoes and the role of past climatic change for evolution within Africa. Ecology and evolution, 8(5), 3019.

Zhang B, et al. (2018) Genetic diversity of common *Gasterophilus* spp. from distinct habitats in China. Parasites & vectors, 11(1), 474.

Houzet L, et al. (2018) Seminal Simian Immunodeficiency Virus in Chronically Infected *Cynomolgus* Macaques Is Dominated by Virus Originating from Multiple Genital Organs. Journal of virology, 92(14).

Arias MB, et al. (2018) Population genetics and migration pathways of the Mediterranean fruit fly *Ceratitidis capitata* inferred with coalescent methods. PeerJ, 6, e5340.

da Silva Santos A, et al. (2018) Phylogeographic analyses of the pampas cat (*Leopardus colocola*; Carnivora, Felidae) reveal a complex demographic history. *Genetics and molecular biology*, 41(1 suppl 1), 273.

Guerrero-Jimenez CJ, et al. (2017) Pattern of genetic differentiation of an incipient speciation process: The case of the high Andean killifish *Orestias*. *PloS one*, 12(2), e0170380.

Huang ZS, et al. (2017) Phylogeographical structure and demographic expansion in the endemic alpine stream salamander (*Hynobiidae*: *Batrachuperus*) of the Qinling Mountains. *Scientific reports*, 7(1), 1871.

Ramos-Fregonezi AMC, et al. (2017) Population Genetic Structure of *Cnesterodon decemmaculatus* (*Poeciliidae*): A Freshwater Look at the Pampa Biome in Southern South America. *Frontiers in genetics*, 8, 214.

Almada F, et al. (2017) Historical gene flow constraints in a northeastern Atlantic fish: phylogeography of the ballan wrasse *Labrus bergylta* across its distribution range. *Royal Society open science*, 4(2), 160773.

Miller KJ, et al. (2017) A comparison of genetic connectivity in two deep sea corals to examine whether seamounts are isolated islands or stepping stones for dispersal. *Scientific reports*, 7, 46103.

Riesgo A, et al. (2017) Genetic variation and geographic differentiation in the marine triclad *Bdelloura candida* (*Platyhelminthes*, *Tricladida*, *Maricola*), ectocommensal on the American horseshoe crab *Limulus polyphemus*. *Marine biology*, 164(5), 111.

Ely CR, et al. (2017) Genetic structure among greater white-fronted goose populations of the Pacific Flyway. *Ecology and evolution*, 7(9), 2956.

Shahzad K, et al. (2017) Effects of Mountain Uplift and Climatic Oscillations on Phylogeography and Species Divergence in Four Endangered *Notopterygium* Herbs. *Frontiers in plant science*, 8, 1929.

Dong F, et al. (2017) Ice age unfrozen: severe effect of the last interglacial, not glacial, climate change on East Asian avifauna. *BMC evolutionary biology*, 17(1), 244.