Resource Summary Report

Generated by RRID on Apr 11, 2025

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 resource, software application

Defining Citation: DOI:10.1016/j.tree.2008.09.007

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

Funding:

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: 20250411T055308+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 RRID.

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.

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.

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 Ceratitis capitata inferred with coalescent methods. PeerJ, 6, e5340.

Guerrero-Jiménez 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.

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.

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.

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.

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.

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.