Resource Summary Report

Generated by NIF on Apr 26, 2025

GARLI

RRID:SCR_016117
Type: Tool

Proper Citation

GARLI (RRID:SCR_016117)

Resource Information

URL: https://github.com/Ashod/garli

Proper Citation: GARLI (RRID:SCR_016117)

Description: Software application for inferring phylogenetic trees and analysis of molecular sequence data using the maximum-likelihood criterion. It implements nucleotide, amino acid and codon-based models of sequence evolution.

Abbreviations: GARLI

Synonyms: Genetic Algorithm for Rapid Likelihood Inference

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

Keywords: inference, phylogenetic, tree, analysis, molecular, sequence, data, maximum, likelihood, criterion, nucleotide, amino acid, codon, model, evolution

Funding:

Availability: Free, Available for download, Freely available

Resource Name: GARLI

Resource ID: SCR_016117

Alternate IDs: OMICS_04234

Alternate URLs: https://code.google.com/archive/p/garli/, https://sources.debian.org/src/garli/

License: GNU General Public License v3.0

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250426T060526+0000

Ratings and Alerts

No rating or validation information has been found for GARLI.

No alerts have been found for GARLI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 279 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Glaser K, et al. (2025) New Strains of the Deep Branching Streptophyte Streptofilum: Phylogenetic Position, Cell Biological and Ecophysiological Traits, and Description of Streptofilum arcticum sp. nov. Environmental microbiology, 27(1), e70033.

Guo N, et al. (2024) Phylogenetic analysis of mammalian SIP30 sequences indicating accelerated adaptation of functional domain in primates. Biochemistry and biophysics reports, 37, 101631.

Trzebny A, et al. (2023) Microsporidian Infection in Mosquitoes (Culicidae) Is Associated with Gut Microbiome Composition and Predicted Gut Microbiome Functional Content. Microbial ecology, 85(1), 247.

Commichaux S, et al. (2023) Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. BMC genomics, 24(1), 165.

Cao G, et al. (2023) Geography shapes the genomics and antimicrobial resistance of Salmonella enterica Serovar Enteritidis isolated from humans. Scientific reports, 13(1), 1331.

Permann C, et al. (2023) 3D-reconstructions of zygospores in Zygnema vaginatum (Charophyta) reveal details of cell wall formation, suggesting adaptations to extreme habitats. Physiologia plantarum, 175(4), e13988.

Streicher MB, et al. (2023) Effect of fuchsin fixation of pollen on DNA barcode recovery. Ecology and evolution, 13(9), e10475.

Alaria A, et al. (2022) ?Relationships among Calibrachoa, Fabiana and Petunia (Petunieae tribe, Solanaceae) and a new generic placement of Argentinean endemic Petuniapatagonica. PhytoKeys, 194, 75.

Trzebny A, et al. (2022) Metabarcoding reveals low prevalence of microsporidian infections in castor bean tick (Ixodes ricinus). Parasites & vectors, 15(1), 26.

Guayasamin JM, et al. (2022) Two new glassfrogs (Centrolenidae: Hyalinobatrachium) from Ecuador, with comments on the endangered biodiversity of the Andes. PeerJ, 10, e13109.

Campioni F, et al. (2022) Whole genome sequencing analyses revealed that Salmonella enterica serovar Dublin strains from Brazil belonged to two predominant clades. Scientific reports, 12(1), 10555.

Peterson PM, et al. (2022) ?A phylogeny of the Triraphideae including Habrochloa and Nematopoa (Poaceae, Chloridoideae). PhytoKeys, 194, 123.

Palm AA, et al. (2022) Intra-Patient Evolution of HIV-2 Molecular Properties. Viruses, 14(11).

Hauzman E, et al. (2021) Simultaneous Expression of UV and Violet SWS1 Opsins Expands the Visual Palette in a Group of Freshwater Snakes. Molecular biology and evolution, 38(12), 5225.

Majaneva S, et al. (2021) Hiding in plain sight-Euplokamis dunlapae (Ctenophora) in Norwegian waters. Journal of plankton research, 43(2), 257.

Nakashima T, et al. (2021) Spatial and Temporal Variations in Pigment and Species Compositions of Snow Algae on Mt. Tateyama in Toyama Prefecture, Japan. Frontiers in plant science, 12, 689119.

Oyarzún PA, et al. (2021) Blue mussels of the Mytilus edulis species complex from South America: The application of species delimitation models to DNA sequence variation. PloS one, 16(9), e0256961.

Jordaens K, et al. (2021) Revision of the Afrotropical species of the hover fly genus Mesembrius Rondani (Diptera, Syrphidae) using morphological and molecular data. ZooKeys, 1046, 1.

Yánez-Muñoz MH, et al. (2021) A new Andean treefrog (Amphibia: Hyloscirtus bogotensis group) from Ecuador: an example of community involvement for conservation. PeerJ, 9, e11914.

Henderson LD, et al. (2020) Diversification of Campylobacter jejuni Flagellar C-Ring Composition Impacts Its Structure and Function in Motility, Flagellar Assembly, and Cellular Processes. mBio, 11(1).