Resource Summary Report

Generated by NIF on Apr 8, 2025

PHYLIP

RRID:SCR_006244
Type: Tool

Proper Citation

PHYLIP (RRID:SCR_006244)

Resource Information

URL: http://evolution.genetics.washington.edu/phylip.html

Proper Citation: PHYLIP (RRID:SCR_006244)

Description: A free package of software programs for inferring phylogenies (evolutionary trees). The source code is distributed (in C), and executables are also distributed. In particular, already-compiled executables are available for Windows (95/98/NT/2000/me/xp/Vista), Mac OS X, and Linux systems. Older executables are also available for Mac OS 8 or 9 systems.

Abbreviations: PHYLIP

Synonyms: PHYLogeny Inference Package

Resource Type: source code, data processing software, software resource, software application

Keywords: phylogeny prediction, evolutionary tree, bio.tools

Funding: NSF ;
NIGMS ;
DOE

Availability: Free

Resource Name: PHYLIP

Resource ID: SCR_006244

Alternate IDs: nif-0000-06708, OMICS_04240, biotools:phylip

Alternate URLs: https://bio.tools/phylip, https://sources.debian.org/src/phylip/

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250407T215605+0000

Ratings and Alerts

No rating or validation information has been found for PHYLIP.

No alerts have been found for PHYLIP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3511 mentions in open access literature.

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

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Okane I, et al. (2025) Xylaria iriomotensis sp. nov. from termite nests and notes on X. angulosa. Botanical studies, 66(1), 4.

Zhong H, et al. (2025) Benchmarking cross-species single-cell RNA-seq data integration methods: towards a cell type tree of life. Nucleic acids research, 53(1).

Li J, et al. (2025) SoyOD: An Integrated Soybean Multi-omics Database for Mining Genes and Biological Research. Genomics, proteomics & bioinformatics, 22(6).

Wei F, et al. (2025) Identification of Taihang-chicken-specific genetic markers using genome-wide SNPs and machine learning: BREED-SPECIFIC SNPS OF TAIHANG CHICKEN. Poultry science, 104(1), 104585.

Dodd GK, et al. (2025) In silico functional analysis of the human, chimpanzee, and gorilla MHC-A repertoires. Immunogenetics, 77(1), 12.

Mendonça P, et al. (2025) The influence of the forest corridors to the north of the Andes on the diversification of the bright-rumped Attila, Attila spadiceus (Passeriformes, Tyrannidae), during the climatic oscillations of the middle Pleistocene. Ecology and evolution, 15(1),

e70331.

Cho MS, et al. (2024) Phylogenetic relationships and genetic diversity of the Korean endemic Phedimus latiovalifolius (Crassulaceae) and its close relatives. Scientific reports, 14(1), 16255.

Cui J, et al. (2024) Does coevolution in refugia drive mimicry in bumble bees? Insights from a South Asian mimicry group. Science advances, 10(24), eadl2286.

Chen H, et al. (2024) Deciphering the Genetic Landscape: Insights Into the Genomic Signatures of Changle Goose. Evolutionary applications, 17(8), e13768.

Hugall AF, et al. (2024) Genetic variation in the brooding brittle-star: a global hybrid polyploid complex? Royal Society open science, 11(8), 240428.

Zhu S, et al. (2024) The jacktree genome and population genomics provides insights for the mechanisms of the germination obstacle and the conservation of endangered ornamental plants. Horticulture research, 11(8), uhae166.

Knief U, et al. (2024) Evolution of Chromosomal Inversions across an Avian Radiation. Molecular biology and evolution, 41(6).

Gàlvez-Morante A, et al. (2024) Dollo Parsimony Overestimates Ancestral Gene Content Reconstructions. Genome biology and evolution, 16(4).

Harrison PM, et al. (2024) Intrinsically Disordered Compositional Bias in Proteins: Sequence Traits, Region Clustering, and Generation of Hypothetical Functional Associations. Bioinformatics and biology insights, 18, 11779322241287485.

Jácome R, et al. (2024) Structural and Evolutionary Analysis of Proteins Endowed with a Nucleotidyltransferase, or Non-canonical Palm, Catalytic Domain. Journal of molecular evolution, 92(6), 799.

Hung SW, et al. (2024) A cyclic dipeptide for salinity stress alleviation and the trophic flexibility of endophyte provide insights into saltmarsh plant-microbe interactions. ISME communications, 4(1), ycae041.

Yang FS, et al. (2024) Signatures of Adaptation and Purifying Selection in Highland Populations of Dasiphora fruticosa. Molecular biology and evolution, 41(6).

Zunino L, et al. (2024) Genomic evidence of genuine wild versus admixed olive populations evolving in the same natural environments in western Mediterranean Basin. PloS one, 19(1), e0295043.

Chu L, et al. (2024) Chromosome-level reference genome and resequencing of 322 accessions reveal evolution, genomic imprint and key agronomic traits in adzuki bean. Plant biotechnology journal, 22(8), 2173.