

Resource Summary Report

Generated by [NIF](#) on Sep 17, 2026

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

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

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 3544 mentions in open access literature.

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

Zhang G, et al. (2026) Ancient genomes provide insight into the Paleolithic-to-Neolithic transition in northern East Asia. *Current biology : CB*, 36(6), 1399.

Lin J, et al. (2026) Human-specific lncRNAs contributed critically to human evolution by distinctly regulating gene expression. *eLife*, 12.

Xu L, et al. (2025) VCF2Dis: an ultra-fast and efficient tool to calculate pairwise genetic distance and construct population phylogeny from VCF files. *GigaScience*, 14.

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.

Bai M, et al. (2025) Genome sequencing of three *Polyscias* species reveals common features in terpene synthase gene family evolution in these species. *The plant genome*, 18(1), e20563.

Zwaans A, et al. (2025) A Bayesian phylodynamic inference framework for single-cell CRISPR/Cas9 lineage tracing barcode data with dependent target sites. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1919), 20230318.

Golygina VV, et al. (2025) ?Chromosomal polymorphism in natural populations of *Chironomus borokensis* Kerkis, Filippova, Shobanov, Gunderina et Kiknadze, 1988 (Diptera, Chironomidae). *Comparative cytogenetics*, 19, 51.

Liu J, et al. (2025) East Asian Gene flow bridged by northern coastal populations over past 6000 years. *Nature communications*, 16(1), 1322.

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

Shi ZF, et al. (2025) The molecular history of IDH-mutant astrocytomas without adjuvant treatment. *Brain pathology* (Zurich, Switzerland), 35(2), e13300.

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).

Liu X, et al. (2025) A 14-bp motif in the KIT active promoter region is critical for melanin accumulation in yaks, mice, and humans. *BMC biology*, 23(1), 208.

Xia Z, et al. (2025) Decoding the genome of *Brainea insignis* reveals insights into fern evolution and conservation. *Nature communications*, 17(1), 1292.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

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.

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.

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

Harcourt R, et al. (2024) Intraspecific trait variation modulates the temperature effect on elemental quotas and stoichiometry in marine *Synechococcus*. *PloS one*, 19(3), e0292337.