

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

[adephylo](#)

RRID:SCR_024267

Type: Tool

Proper Citation

adephylo (RRID:SCR_024267)

Resource Information

URL: <https://cran.r-project.org/web/packages/adephylo/index.html>

Proper Citation: adephylo (RRID:SCR_024267)

Description: Software R package provides multivariate tools to analyze comparative data. Analysis of comparative evolutionary data. Used for investigating phylogenetic signal in biological traits.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:20525823](#)

Keywords: analyze comparative data, investigating phylogenetic signal, biological traits, investigating phylogenetic signal in biological traits, comparative evolutionary data analysis,

Availability: Free, Available for download, Freely available,

Resource Name: adephylo

Resource ID: SCR_024267

Alternate IDs: OMICS_08682

Alternate URLs: <https://sources.debian.org/src/r-cran-adephylo/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260904T000024+0000

Ratings and Alerts

No rating or validation information has been found for adephylo.

No alerts have been found for adephylo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bisht MS, et al. (2024) Genome of the most noxious weed water hyacinth (*Eichhornia crassipes*) provides insights into plant invasiveness and its translational potential. *iScience*, 27(9), 110698.

Harder CB, et al. (2024) Extreme overall mushroom genome expansion in *Mycena* s.s. irrespective of plant hosts or substrate specializations. *Cell genomics*, 4(7), 100586.

Xu ZM, et al. (2024) Joint host-pathogen genomic analysis identifies hepatitis B virus mutations associated with human NTCP and HLA class I variation. *American journal of human genetics*, 111(6), 1018.