

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 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:** 20260905T133106+0000

### Ratings and Alerts

No rating or validation information has been found for adephylo.

No alerts have been found for adephylo.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

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.