

# Resource Summary Report

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## Phangorn

RRID:SCR\_017302

Type: Tool

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### Proper Citation

Phangorn (RRID:SCR\_017302)

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### Resource Information

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

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**Description:** Software R package for phylogenetic reconstruction and analysis. Used for estimation of phylogenetic trees and networks using Maximum Likelihood, Maximum Parsimony, distance methods and Hadamard conjugation. Allows to compare trees, models selection and offers visualizations for trees and split networks.

**Synonyms:** Phangorn R package

**Resource Type:** data analysis software, data processing software, data visualization software, software application, software resource, software toolkit

**Defining Citation:** [DOI:10.1093/bioinformatics/btq706](https://doi.org/10.1093/bioinformatics/btq706)

**Keywords:** phylogenetic, tree, network, reconstruction, analysis, estimation, Maximum, Likelihood, Parsimony, distance, method, Hadamard conjugation

**Funding:** Mus??um National D Histoire Naturelle

**Availability:** Free, Available for download, Freely available

**Resource Name:** Phangorn

**Resource ID:** SCR\_017302

**Alternate IDs:** OMICS\_12497

**Alternate URLs:** <https://github.com/KlausVigo/phangorn>, <https://sources.debian.org/src/r-cran-phangorn/>

**License:** GPL v2

**Record Creation Time:** 20220129T080334+0000

**Record Last Update:** 20261017T202915+0000

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## Ratings and Alerts

No rating or validation information has been found for Phangorn.

No alerts have been found for Phangorn.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.