

Resource Summary Report

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Phangorn

RRID:SCR_017302

Type: Tool

Proper Citation

Phangorn (RRID:SCR_017302)

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: software toolkit, software resource, software application, data analysis software, data visualization software, data processing software

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: Muséum 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

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Record Last Update: 20260808T190049+0000

Ratings and Alerts

No rating or validation information has been found for Phangorn.

No alerts have been found for Phangorn.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Aranda ML, et al. (2025) Genetic tuning of retinal ganglion cell subtype identity to drive visual behavior. *Nature communications*, 16(1), 8678.

Ma H, et al. (2025) Spatially Resolved Tumor Ecosystems and Cell States in Gastric Adenocarcinoma Progression and Evolution. *Cancer discovery*, 15(4), 767.

Ross TA, et al. (2025) *Enterococcus lactis* is ecologically and genetically distinct from the major opportunistic pathogen *Enterococcus faecium*. *Microbial genomics*, 11(6).

Rathinam M, et al. (2025) A chromosome-scale reference genome assembly of pigeonpea wild relative *Cajanus platycarpus* highlights the evolutionary decline of defence genes in *Cajanus cajan*. *Journal of experimental botany*, 76(20), 6166.

Wang W, et al. (2024) Decoupling of strain- and intrastrain-level interactions of microbiomes in a sponge holobiont. *Nature communications*, 15(1), 8205.

Berentsen R, et al. (2024) A reduced vernalization requirement is a key component of the early-bolting trait in globe artichoke (*Cynara cardunculus* var. *scolymus*). *iScience*, 27(9), 110829.

Verma S, et al. (2024) Antigen-level resolution of commensal-specific B cell responses can be enabled by phage display screening coupled with B cell tetramers. *Immunity*, 57(6), 1428.

Sorbie A, et al. (2023) Protocol for microbiota analysis of a murine stroke model. STAR protocols, 4(1), 101969.

Huang KK, et al. (2023) Spatiotemporal genomic profiling of intestinal metaplasia reveals clonal dynamics of gastric cancer progression. Cancer cell, 41(12), 2019.

Sedah P, et al. (2023) Impact of Seed Origin and Genetic Drift of Improved Rice Variety IR841 in Benin. Rice (New York, N.Y.), 16(1), 48.

Chiou KL, et al. (2023) A single-cell multi-omic atlas spanning the adult rhesus macaque brain. Science advances, 9(41), eadh1914.

Moysiuk J, et al. (2022) A three-eyed radiodont with fossilized neuroanatomy informs the origin of the arthropod head and segmentation. Current biology : CB, 32(15), 3302.

David P, et al. (2022) Extreme mitochondrial DNA divergence underlies genetic conflict over sex determination. Current biology : CB, 32(10), 2325.

Vatanen T, et al. (2022) Transcription shifts in gut bacteria shared between mothers and their infants. Scientific reports, 12(1), 1276.

Li R, et al. (2022) Mapping single-cell transcriptomes in the intra-tumoral and associated territories of kidney cancer. Cancer cell, 40(12), 1583.

McCauley KE, et al. (2022) Heritable vaginal bacteria influence immune tolerance and relate to early-life markers of allergic sensitization in infancy. Cell reports. Medicine, 3(8), 100713.

De Boeck I, et al. (2021) The nasal mutualist *Dolosigranulum pigrum* AMBR11 supports homeostasis via multiple mechanisms. iScience, 24(9), 102978.

Saeedi Saravi SS, et al. (2021) Lifelong dietary omega-3 fatty acid suppresses thrombotic potential through gut microbiota alteration in aged mice. iScience, 24(8), 102897.