Resource Summary Report

Generated by NIF on May 25, 2025

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

Defining Citation: DOI: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

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250525T031513+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 21 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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.

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.

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.

Shibu P, et al. (2021) Improved molecular characterization of the Klebsiella oxytoca complex reveals the prevalence of the kleboxymycin biosynthetic gene cluster. Microbial genomics, 7(6).

Zogopoulos VL, et al. (2021) Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. iScience, 24(8), 102848.

Filatov DA, et al. (2021) The mode of speciation during a recent radiation in open-ocean phytoplankton. Current biology : CB, 31(24), 5439.

Clemente F, et al. (2021) The genomic history of the Aegean palatial civilizations. Cell, 184(10), 2565.

Crispell J, et al. (2019) Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. eLife, 8.

Clemence MEA, et al. (2019) Neisseria meningitidis has acquired sequences within the capsule locus by horizontal genetic transfer. Wellcome open research, 4, 99.

Angelova M, et al. (2018) Evolution of Metastases in Space and Time under Immune Selection. Cell, 175(3), 751.