

Resource Summary Report

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[ggtree](#)

RRID:SCR_018560

Type: Tool

Proper Citation

ggtree (RRID:SCR_018560)

Resource Information

URL: <https://bioconductor.org/packages/ggtree/>

Proper Citation: ggtree (RRID:SCR_018560)

Description: Software R package for visualization and annotation of phylogenetic trees with their covariates and other tree like structures with their annotation data. Can import evolutionary data from different tree file formats and analysis programs as well as other associated data from experiments so that various sources and types of data can be displayed on tree for comparison and further analyses.

Resource Type: software resource, data visualization software, data processing software, software application

Defining Citation: [DOI:10.1111/2041-210X.12628](https://doi.org/10.1111/2041-210X.12628)

Keywords: Phylogenetic tree visualization, phylogenetic tree annotation, data, bio.tools

Funding: Seed Funding Programme for Basic Research

Availability: Free, Available for download, Freely available

Resource Name: ggtree

Resource ID: SCR_018560

Alternate IDs: biotools:ggtree

Alternate URLs: <https://bio.tools/ggtree>

License: Artistic-2.0

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260803T040758+0000

Ratings and Alerts

No rating or validation information has been found for ggtree.

No alerts have been found for ggtree.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Serna C, et al. (2025) Global dissemination of npmA mediated pan-aminoglycoside resistance via a mobile genetic element in Gram-positive bacteria. *Nature communications*, 16(1), 6360.

Newstead L, et al. (2025) Genomic characterization of *Pseudomonas aeruginosa* from canine otitis highlights the need for a One Health approach to this opportunistic pathogen. *Microbial genomics*, 11(5).

Webb J, et al. (2025) Multi-strain carriage and intrahost diversity of *Staphylococcus aureus* among Indigenous adults in the USA. *Microbial genomics*, 11(3).

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. *Cell reports*, 44(10), 116449.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Immonen TT, et al. (2024) No evidence for ongoing replication on ART in SIV-infected macaques. *Nature communications*, 15(1), 5093.

Ding X, et al. (2024) Transmission restriction and genomic evolution co-shape the genetic diversity patterns of influenza A virus. *Virologica Sinica*, 39(4), 525.

Kennedy SJ, et al. (2024) Culture-dependent identification of rare marine sediment bacteria from the Gulf of Mexico and Antarctica. *bioRxiv : the preprint server for biology*.

Joseph R, et al. (2024) Isolation of a Novel *Pythium* Species, *P. thermoculicivorax*, and *Trichoderma* sp. from Natural Enzootic Mosquito Larval Infections. *Journal of fungi (Basel, Switzerland)*, 10(3).

Tamura T, et al. (2024) Virological characteristics of the SARS-CoV-2 Omicron XBB.1.5 variant. *Nature communications*, 15(1), 1176.

Atre M, et al. (2024) Origin, evolution, and maintenance of gene-strand bias in bacteria. *Nucleic acids research*, 52(7), 3493.

Kyriacou RG, et al. (2024) GC Content Across Insect Genomes: Phylogenetic Patterns, Causes and Consequences. *Journal of molecular evolution*, 92(2), 138.

Ahlstrom CA, et al. (2024) Genomic characterization of highly pathogenic H5 avian influenza viruses from Alaska during 2022 provides evidence for genotype-specific trends of spatiotemporal and interspecies dissemination. *Emerging microbes & infections*, 13(1), 2406291.

Yajima H, et al. (2024) Structural basis for receptor-binding domain mobility of the spike in SARS-CoV-2 BA.2.86 and JN.1. *Nature communications*, 15(1), 8574.

Xu Y, et al. (2024) Chromosome-level genome of the poultry shaft louse *Menopon gallinae* provides insight into the host-switching and adaptive evolution of parasitic lice. *GigaScience*, 13(1).

Beckman RL, et al. (2024) Diverse polysaccharide production and biofilm formation abilities of clinical *Klebsiella pneumoniae*. *NPJ biofilms and microbiomes*, 10(1), 151.

Fleeman R, et al. (2024) Diverse polysaccharide production and biofilm formation abilities of clinical *Klebsiella pneumoniae*. *Research square*.

Li M, et al. (2024) Spatiotemporal and Species-Crossing Transmission Dynamics of Subclade 2.3.4.4b H5Nx HPAIVs. *Transboundary and emerging diseases*, 2024, 2862053.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. *Cancer cell*, 42(1), 135.

Panzera Y, et al. (2023) Detection and genome characterisation of SARS-CoV-2 P.6 lineage in dogs and cats living with Uruguayan COVID-19 patients. *Memorias do Instituto Oswaldo Cruz*, 117, e220177.