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

Defining Citation: DOI: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: 20250426T060722+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 47 mentions in open access literature.

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

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.

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).

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

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

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.

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.

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.

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.

Lobb B, et al. (2023) Genomic classification and antimicrobial resistance profiling of Streptococcus pneumoniae and Haemophilus influenza isolates associated with paediatric otitis media and upper respiratory infection. BMC infectious diseases, 23(1), 596.

Ahart L, et al. (2023) Retrospective evaluation of an integrated molecular-epidemiological approach to cyclosporiasis outbreak investigations - United States, 2021. Epidemiology and infection, 151, e131.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. G3 (Bethesda, Md.), 13(11).

Chung The H, et al. (2023) Multidrug resistance plasmids underlie clonal expansions and international spread of Salmonella enterica serotype 1,4,[5],12:i:- ST34 in Southeast Asia. Communications biology, 6(1), 1007.

Ni XB, et al. (2023) Metavirome of 31 tick species provides a compendium of 1,801 RNA virus genomes. Nature microbiology, 8(1), 162.

Turk Dermastia T, et al. (2023) Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. Frontiers in microbiology, 14, 1071379.