Resource Summary Report

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IQ-TREE

RRID:SCR_017254
Type: Tool

Proper Citation

IQ-TREE (RRID:SCR_017254)

Resource Information

URL: http://www.iqtree.org/

Proper Citation: IQ-TREE (RRID:SCR_017254)

Description: Software tool as stochastic algorithm for estimating maximum likelihood phylogenies. Used for phylogenomic inference.

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

Defining Citation: PMID:25371430

Keywords: stochastic, algorithm, estimate, maximum, likelihood, phylogeny, phylogenomic, inference, data, dataset, bio.tools

Funding: Austrian Science Fund ;
University of Vienna

Availability: Free, Available for download, Freely available

Resource Name: IQ-TREE

Resource ID: SCR_017254

Alternate IDs: biotools:ufboot2

Alternate URLs: https://bio.tools/ufboot2/

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250417T065615+0000

Ratings and Alerts

No rating or validation information has been found for IQ-TREE.

No alerts have been found for IQ-TREE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 576 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Vernié T, et al. (2025) Conservation of symbiotic signaling since the most recent common ancestor of land plants. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2408539121.

Osemeke OH, et al. (2025) Optimizing Tongue Fluid Sampling and Testing Protocols for Enhanced PRRSV Isolation from Perinatal Swine Mortalities. Viruses, 17(1).

Dagba Gbessin EH, et al. (2025) HIV-1 resistance mutations and genetic diversity among children failing antiretroviral treatment in five healthcare facilities in Benin, West Africa. PloS one, 20(1), e0317882.

Sawaswong V, et al. (2025) Diversity and antimicrobial resistance profiles of Mycobacterium avium complex clinical isolates in Thailand based on whole genome comparative analysis. Scientific reports, 15(1), 772.

Hamilton R, et al. (2025) Microbial hauberks: composition and function of surface layer proteins in gammaproteobacterial methanotrophs. Applied and environmental microbiology, 91(1), e0136424.

Shi C, et al. (2025) Development of a mitochondrial mini-barcode and its application in metabarcoding for identification of leech in traditional Chinese medicine. Scientific reports, 15(1), 1698.

Morita D, et al. (2025) Genomic epidemiology and genetic characteristics of clinical Campylobacter species cocirculating in West Bengal, India, 2019, using whole genome analysis. Antimicrobial agents and chemotherapy, 69(1), e0110824.

Na EJ, et al. (2025) Investigating the reassortment potential and pathogenicity of the S

segment in Akabane virus using a reverse genetics system. BMC veterinary research, 21(1), 20.

Yang K, et al. (2025) Genetic diversity of highly pathogenic avian influenza H5N6 and H5N8 viruses in poultry markets in Guangdong, China, 2020-2022. Journal of virology, 99(1), e0114524.

Facimoto CT, et al. (2025) Hindguts of Kyphosus sydneyanus harbor phylogenetically and genomically distinct Alistipes capable of degrading algal polysaccharides and diazotrophy. mSystems, 10(1), e0100724.

Mangin CC, et al. (2025) Magnetotactic bacteria affiliated with diverse Pseudomonadota families biomineralize intracellular Ca-carbonate. The ISME journal, 19(1).

Yang Y, et al. (2025) Systematic identification of secondary bile acid production genes in global microbiome. mSystems, 10(1), e0081724.

Bbosa N, et al. (2025) Case Reports of Human Monkeypox Virus Infections, Uganda, 2024. Emerging infectious diseases, 31(1), 144.

Wu F, et al. (2025) Comparative genomic analysis of ten Elizabethkingia anophelis isolated from clinical patients in China. Microbiology spectrum, 13(1), e0178024.

Baker AL, et al. (2025) Dairy cows inoculated with highly pathogenic avian influenza virus H5N1. Nature, 637(8047), 913.

van Elst T, et al. (2025) Integrative taxonomy clarifies the evolution of a cryptic primate clade. Nature ecology & evolution, 9(1), 57.

Levy S, et al. (2025) Convergent evolution of oxidized sugar metabolism in commensal and pathogenic microbes in the inflamed gut. Nature communications, 16(1), 1121.

Felipe Benites L, et al. (2024) Hot springs viruses at Yellowstone National Park have ancient origins and are adapted to thermophilic hosts. Communications biology, 7(1), 312.

Campbell AM, et al. (2024) Evolutionary dynamics of the successful expansion of pandemic Vibrio parahaemolyticus ST3 in Latin America. Nature communications, 15(1), 7828.

Kamali K, et al. (2024) Integrating phylogenetic, phylogeographic, and morphometric analyses to reveal cryptic lineages within the genus Asaccus (Reptilia: Squamata: Phyllodactylidae) in Iran. BMC zoology, 9(1), 12.