## **Resource Summary Report**

Generated by NIF on May 7, 2025

# **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, software resource, software application, data

analysis software

**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:** 20250507T061231+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 NIF.

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.

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.

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

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.

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.

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.

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

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

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

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.

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.

Kennard AS, et al. (2024) An internally controlled system to study microtubule network diversification links tubulin evolution to the use of distinct microtubule regulators. bioRxiv: the preprint server for biology.

Abolnik C, et al. (2024) Spillover of an endemic avian Influenza H6N2 chicken lineage to ostriches and reassortment with clade 2.3.4.4b H5N1 high pathogenicity viruses in chickens. Veterinary research communications, 48(2), 1233.

Ward CM, et al. (2024) Recombination, admixture and genome instability shape the genomic landscape of Saccharomyces cerevisiae derived from spontaneous grape ferments. PLoS genetics, 20(3), e1011223.