Resource Summary Report

Generated by dkNET on Apr 28, 2025

FastTree

RRID:SCR_015501
Type: Tool

Proper Citation

FastTree (RRID:SCR_015501)

Resource Information

URL: http://www.microbesonline.org/fasttree/

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Description: Source code that infers approximately-maximum-likelihood phylogenetic trees from alignments of nucleotide or protein sequences. It uses the Jukes-Cantor or generalized time-reversible (GTR) models of nucleotide evolution and the JTT, WAG, or LG models of amino acid evolution.

Resource Type: source code, software resource

Defining Citation: PMID:19377059, DOI:10.1371/journal.pone.0009490

Keywords: phylogenetic tree, phylogenetic tree creation, bio.tools

Funding:

Availability: Open source, Available for download

Resource Name: FastTree

Resource ID: SCR_015501

Alternate IDs: biotools:fasttree, OMICS_14703

Alternate URLs: https://bio.tools/fasttree, https://sources.debian.org/src/fasttree/

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250428T053924+0000

Ratings and Alerts

No rating or validation information has been found for FastTree.

No alerts have been found for FastTree.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5069 mentions in open access literature.

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

Hameed A, et al. (2025) Neobacillus driksii sp. nov. isolated from a Mars 2020 spacecraft assembly facility and genomic potential for lasso peptide production in Neobacillus. Microbiology spectrum, 13(1), e0137624.

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.

Gray HA, et al. (2025) Genomic epidemiology of extended-spectrum beta-lactamase-producing Escherichia coli from humans and a river in Aotearoa New Zealand. Microbial genomics, 11(1).

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.

Stenger PL, et al. (2025) A Multimarker Approach to Identify Microbial Bioindicators for Coral Reef Health Monitoring-Case Study in La Réunion Island. Microbial ecology, 87(1), 179.

Graça AP, et al. (2025) MftG is crucial for ethanol metabolism of mycobacteria by linking mycofactocin oxidation to respiration. eLife, 13.

O'Brien B, et al. (2025) Subtle genomic differences in Klebsiella pneumoniae sensu stricto isolates indicate host adaptation. One health (Amsterdam, Netherlands), 20, 100970.

Pilmer L, et al. (2025) Exploring single cell microbial protein as a sustainable fishmeal alternative in yellowtail kingfish (Seriola lalandi) diets: impacts on health and gut microbiome. Journal of animal science and biotechnology, 16(1), 16.

Tsukahara S, et al. (2025) Centrophilic retrotransposon integration via CENH3 chromatin in Arabidopsis. Nature, 637(8046), 744.

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable Lindaspio polybranchiata to thrive in deep-sea cold seeps. BMC biology, 23(1), 13.

Záhonová K, et al. (2025) Comparative Analysis of Protist Communities in Oilsands Tailings Using Amplicon Sequencing and Metagenomics. Environmental microbiology, 27(1), e70029.

Vignale FA, et al. (2025) Yerba mate (Ilex paraguariensis) genome provides new insights into convergent evolution of caffeine biosynthesis. eLife, 14.

Battistolli M, et al. (2025) The circadian clock gene period regulates the composition and daily bacterial load of the gut microbiome in Drosophila melanogaster. Scientific reports, 15(1), 1016.

Castelo-Branco R, et al. (2025) Genome-informed Discovery of Monchicamides A-K: Cyanobactins from the Microcoleaceae Cyanobacterium LEGE 16532. Journal of natural products, 88(1), 86.

Rocha ST, et al. (2025) The prevalence of motility-related genes within the human oral microbiota. Microbiology spectrum, 13(1), e0126424.

Manzano C, et al. (2025) Regulation and function of a polarly localized lignin barrier in the exodermis. Nature plants, 11(1), 118.

Debat H, et al. (2025) RNA Virus Discovery Sheds Light on the Virome of a Major Vineyard Pest, the European Grapevine Moth (Lobesia botrana). Viruses, 17(1).

Schechter MS, et al. (2025) Ribosomal protein phylogeography offers quantitative insights into the efficacy of genome-resolved surveys of microbial communities. bioRxiv : the preprint server for biology.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.

Li B, et al. (2025) Characteristics and phylogenetic analysis of the complete chloroplast genome of Rubus swinhoei Hance 1866 from the family Rosaceae. Mitochondrial DNA. Part B, Resources, 10(2), 119.