FastTree
RRID:SCR_015501
Type: Tool

Proper Citation
FastTree (RRID:SCR_015501)

Resource Information

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

Proper Citation: FastTree (RRID:SCR_015501)

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

Availability: Open source, Available for download

Resource Name: FastTree

Resource ID: SCR_015501

Alternate IDs: biotools:fasttree, OMICS_14703


Record Creation Time: 20220129T080326+0000

Record Last Update: 20240630T054142+0000

Ratings and Alerts
No rating or validation information has been found for FastTree.

No alerts have been found for FastTree.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 4400 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://SciCrunch.org).


Kim J, et al. (2024) MiMultiCat: A Unified Cloud Platform for the Analysis of Microbiome Data with Multi-Categorical Responses. Bioengineering (Basel, Switzerland), 11(1).

Jitsuno K, et al. (2024) Comparative single-cell genomics of Atribacterota JS1 in the Japan Trench hadal sedimentary biosphere. mSphere, 9(1), e0033723.

Javaid N, et al. (2024) Strain features of pneumococcal isolates in the pre- and post-PCV10 era in Pakistan. Microbial genomics, 10(1).


Qing W, et al. (2024) Species-level resolution for the vaginal microbiota with short amplicons. mSystems, 9(2), e0103923.


Wang FQ, et al. (2024) Particle-attached bacteria act as gatekeepers in the decomposition of complex phytoplankton polysaccharides. Microbiome, 12(1), 32.


Fan L, et al. (2024) Gene inversion led to the emergence of brackish archaeal heterotrophs in the aftermath of the Cryogenian Snowball Earth. PNAS nexus, 3(2), pgae057.

