FastTree
RRID:SCR_015501
Type: Tool

Proper Citation

FastTree (RRID:SCR_015501)

Resource Information

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

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 Name: FastTree

Proper Citation: FastTree (RRID:SCR_015501)

Resource Type: Resource, software resource, source code

Keywords: phylogenetic tree, phylogenetic tree creation

Resource ID: SCR_015501

References: PMID:19377059

Availability: Open source, Available for download

Website Status: Last checked up

Mentions Count: 1935

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 1935 mentions in open access literature.

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


Subramaniam K, et al. (2020) A New Family of DNA Viruses Causing Disease in Crustaceans from Diverse Aquatic Biomes. mBio, 11(1).


Rambo-Martin BL, et al. (2020) Influenza A Virus Field Surveillance at a Swine-Human Interface. mSphere, 5(1).


