Resource Summary Report

Generated by NIF on Apr 22, 2025

FastMulRFS

RRID:SCR_024505
Type: Tool

Proper Citation

FastMulRFS (RRID:SCR_024505)

Resource Information

URL: https://github.com/ekmolloy/fastmulrfs

Proper Citation: FastMulRFS (RRID:SCR_024505)

Description: Software pipeline for estimating species trees from multi copy gene trees.

Resource Type: software resource, software toolkit

Defining Citation: PMID:32657396

Keywords: estimating species trees, multi copy gene trees,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: FastMulRFS

Resource ID: SCR_024505

License: 3-Clause BSD

Record Creation Time: 20231002T161336+0000

Record Last Update: 20250421T054541+0000

Ratings and Alerts

No rating or validation information has been found for FastMulRFS.

No alerts have been found for FastMulRFS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Morel B, et al. (2022) SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular biology and evolution, 39(2).