Resource Summary Report

Generated by NIF on Apr 20, 2025

NOTUNG

RRID:SCR_024484
Type: Tool

Proper Citation

NOTUNG (RRID:SCR_024484)

Resource Information

URL: http://www.cs.cmu.edu/~durand/Notung/

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Description: Software package to facilitate large scale analysis, using both rooted and unrooted trees.Used for dating gene duplications and optimizing gene family trees.Used for inferring duplication dates from gene trees automatically and can also be used as exploratory analysis tool for evaluating alternative hypotheses.

Synonyms: Notung 2.9

Resource Type: software toolkit, software resource

Defining Citation: PMID:11108472

Keywords: inferring duplication dates, large scale analysis, dating gene duplications, optimizing gene family trees,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: NOTUNG

Resource ID: SCR_024484

Record Creation Time: 20231002T161336+0000

Record Last Update: 20250420T015433+0000

Ratings and Alerts

No rating or validation information has been found for NOTUNG.

No alerts have been found for NOTUNG.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Földi C, et al. (2024) Snowball: a novel gene family required for developmental patterning of fruiting bodies of mushroom-forming fungi (Agaricomycetes). mSystems, 9(3), e0120823.

Hoshino Y, et al. (2023) Genetics re-establish the utility of 2-methylhopanes as cyanobacterial biomarkers before 750 million years ago. Nature ecology & evolution, 7(12), 2045.

Merényi Z, et al. (2023) Genomes of fungi and relatives reveal delayed loss of ancestral gene families and evolution of key fungal traits. Nature ecology & evolution, 7(8), 1221.

Merényi Z, et al. (2022) Gene age shapes the transcriptional landscape of sexual morphogenesis in mushroom-forming fungi (Agaricomycetes). eLife, 11.

Villacastin AJ, et al. (2021) Dynamic differential evolution schemes of WRKY transcription factors in domesticated and wild rice. Scientific reports, 11(1), 14887.

Gauthier J, et al. (2021) Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. Communications biology, 4(1), 104.

Legan AW, et al. (2021) Expansion and Accelerated Evolution of 9-Exon Odorant Receptors in Polistes Paper Wasps. Molecular biology and evolution, 38(9), 3832.

Hickner PV, et al. (2016) The making of a pest: Insights from the evolution of chemosensory receptor families in a pestiferous and invasive fly, Drosophila suzukii. BMC genomics, 17, 648.

Pires IS, et al. (2013) Different evolutionary histories of two cation/proton exchanger gene families in plants. BMC plant biology, 13, 97.