

Resource Summary Report

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Clearcut

RRID:SCR_016059

Type: Tool

Proper Citation

Clearcut (RRID:SCR_016059)

Resource Information

URL: <http://bioinformatics.hungry.com/clearcut/>

Proper Citation: Clearcut (RRID:SCR_016059)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023.Software as a stand-alone reference implementation for the Relaxed Neighbor Joining (RNJ) algorithm. Used in distance-based phylogenetic tree reconstruction method to process large sequence datasets., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data visualization software, software resource, software application, data processing software, standalone software

Defining Citation: [PMID:16752216](#), [DOI:10.1007/s00239-005-0176-2](#)

Keywords: rnj, phylogenetic, tree, construction, neighbor, joining, distance, method, reference, standalone, implemetation, relaxed, algorithm, phylogenetic, tree, reconstruction, sequence

Funding: NIH P20 RR16448;
INBRE Program of the National Center for Research Resources ;
NSF EPS 00809035;
NIH P20 RR16454

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Clearcut

Resource ID: SCR_016059

Alternate IDs: OMICS_15083

Alternate URLs: <https://github.com/ibest/clearcut>, <https://sources.debian.org/src/clearcut/>

License: BSD license

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260728T043514+0000

Ratings and Alerts

No rating or validation information has been found for Clearcut.

No alerts have been found for Clearcut.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Gong EJ, et al. (2023) Efficacy and Safety of ClearCut™ Knife H-type in Endoscopic Submucosal Dissection for Gastric Neoplasms: A Multicenter, Randomized Trial. Journal of gastric cancer, 23(3), 451.

Yoon YC, et al. (2021) Comparison of surgically induced astigmatism between anterior and total cornea in 2.2 mm steep meridian incision cataract surgery. BMC ophthalmology, 21(1), 373.

Park S, et al. (2020) Ketone production by ketogenic diet and by intermittent fasting has different effects on the gut microbiota and disease progression in an Alzheimer's disease rat model. Journal of clinical biochemistry and nutrition, 67(2), 188.

García-Vega ÁS, et al. (2020) Diet Quality, Food Groups and Nutrients Associated with the Gut Microbiota in a Nonwestern Population. Nutrients, 12(10).

Kim DS, et al. (2020) Tetragonia tetragonioides Protected against Memory Dysfunction by Elevating Hippocampal Amyloid-? Deposition through Potentiating Insulin Signaling and Altering Gut Microbiome Composition. International journal of molecular sciences, 21(8).

Zhu Q, et al. (2019) Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature communications, 10(1), 5477.

Ou Y, et al. (2019) Deciphering Underlying Drivers of Disease Suppressiveness Against Pathogenic Fusarium oxysporum. Frontiers in microbiology, 10, 2535.

Wang R, et al. (2018) Gut Microbiota Play an Essential Role in the Antidiabetic Effects of Rhein. Evidence-based complementary and alternative medicine : eCAM, 2018, 6093282.

Waite DW, et al. (2017) Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). *Frontiers in microbiology*, 8, 682.

Rougeron V, et al. (2017) Evolutionary structure of *Plasmodium falciparum* major variant surface antigen genes in South America: Implications for epidemic transmission and surveillance. *Ecology and evolution*, 7(22), 9376.

Groendahl S, et al. (2017) The best of both worlds: A combined approach for analyzing microalgal diversity via metabarcoding and morphology-based methods. *PloS one*, 12(2), e0172808.

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Durães-Carvalho R, et al. (2015) Phylogenetic and phylogeographic mapping of the avian coronavirus spike protein-encoding gene in wild and synanthropic birds. *Virus research*, 201, 101.

Chiu HC, et al. (2014) Emergent biosynthetic capacity in simple microbial communities. *PLoS computational biology*, 10(7), e1003695.

Asarnow D, et al. (2014) Automatic classification of protein structures using low-dimensional structure space mappings. *BMC bioinformatics*, 15 Suppl 2(Suppl 2), S1.

Karwautz C, et al. (2014) Impact of hydraulic well restoration on native bacterial communities in drinking water wells. *Microbes and environments*, 29(4), 363.

Anderson KE, et al. (2013) Microbial ecology of the hive and pollination landscape: bacterial associates from floral nectar, the alimentary tract and stored food of honey bees (*Apis mellifera*). *PloS one*, 8(12), e83125.

Kistler JO, et al. (2013) Bacterial community development in experimental gingivitis. *PloS one*, 8(8), e71227.

Sangwan N, et al. (2012) Comparative metagenomic analysis of soil microbial communities across three hexachlorocyclohexane contamination levels. *PloS one*, 7(9), e46219.