Resource Summary Report

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BEAST

RRID:SCR_010228

Type: Tool

Proper Citation

BEAST (RRID:SCR_010228)

Resource Information

URL: http://beast.bio.ed.ac.uk/

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Description: A cross-platform software program for Bayesian MCMC analysis of molecular sequences. It is entirely orientated towards rooted, time-measured phylogenies inferred using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology. BEAST uses MCMC to average over tree space, so that each tree is weighted proportional to its posterior probability. We include a simple to use user-interface program for setting up standard analyses and a suit of programs for analysing the results.

Synonyms: BEaST Segmentation Library, Beast Software

Resource Type: software resource, software repository, sequence analysis software,

software application, data analysis software, data processing software

Defining Citation: DOI:10.1186/1471-2148-7-214

Keywords: bio.tools

Resource Name: BEAST

Resource ID: SCR 010228

Alternate IDs: nlx_156859, OMICS_04233, biotools:beast, SCR_015988

Alternate URLs: http://www.nitrc.org/projects/beast-library, https://bio.tools/beast,

https://sources.debian.org/src/beast-mcmc/

Old URLs: http://beast.bio.ed.ac.uk/Main_Page

Ratings and Alerts

No rating or validation information has been found for BEAST.

No alerts have been found for BEAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5512 mentions in open access literature.

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

Marquine S, et al. (2024) Sequence Data From a Travel-Associated Case of Microcephaly Highlight a Persisting Risk due to Zika Virus Circulation in Thailand. The Journal of infectious diseases, 229(2), 443.

Xing X, et al. (2024) Evolution and biological characterization of H5N1 influenza viruses bearing the clade 2.3.2.1 hemagglutinin gene. Emerging microbes & infections, 13(1), 2284294.

Onoja BA, et al. (2024) Whole genome sequencing unravels cryptic circulation of divergent dengue virus lineages in the rainforest region of Nigeria. Emerging microbes & infections, 13(1), 2307511.

Nduva GM, et al. (2024) Temporal trends and transmission dynamics of pre-treatment HIV-1 drug resistance within and between risk groups in Kenya, 1986-2020. The Journal of antimicrobial chemotherapy, 79(2), 287.

Ghafari M, et al. (2024) Revisiting the origins of the Sobemovirus genus: A case for ancient origins of plant viruses. PLoS pathogens, 20(1), e1011911.

Vázquez-López M, et al. (2024) ?Biogeographic factors contributing to the diversification of Euphoniinae (Aves, Passeriformes, Fringillidae): a phylogenetic and ancestral areas analysis. ZooKeys, 1188, 169.

Ye Y, et al. (2024) Robust expansion of phylogeny for fast-growing genome sequence data. PLoS computational biology, 20(2), e1011871.

Lizano AMD, et al. (2024) Pseudocryptic diversity and species boundaries in the sea cucumber Stichopus cf. horrens (Echinodermata: Stichopodidae) revealed by mitochondrial

and microsatellite markers. Scientific reports, 14(1), 4886.

Han Z, et al. (2024) Synergetic association between coxsackievirus A16 genotype evolution and recombinant form shifts. Virus evolution, 10(1), vead080.

Featherstone LA, et al. (2024) The effect of missing data on evolutionary analysis of sequence capture bycatch, with application to an agricultural pest. Molecular genetics and genomics: MGG, 299(1), 11.

Gojobori J, et al. (2024) Japanese wolves are most closely related to dogs and share DNA with East Eurasian dogs. Nature communications, 15(1), 1680.

Li B, et al. (2024) Genetic and Evolutionary Analysis of Porcine Deltacoronavirus in Guangxi Province, Southern China, from 2020 to 2023. Microorganisms, 12(2).

de Campos GM, et al. (2024) Updated Insights into the Phylogenetics, Phylodynamics, and Genetic Diversity of Nipah Virus (NiV). Viruses, 16(2).

Rojas A, et al. (2024) Characterization of Dengue Virus 4 Cases in Paraguay, 2019-2020. Viruses, 16(2).

Douglas J, et al. (2024) Enzymic recognition of amino acids drove the evolution of primordial genetic codes. Nucleic acids research, 52(2), 558.

Seesamut T, et al. (2024) Global species delimitation of the cosmopolitan marine littoral earthworm Pontodrilus litoralis (Grube, 1855). Scientific reports, 14(1), 1753.

Ualiyeva D, et al. (2024) Genetic Structure and Population History of the Zaisan Toad-Headed Agama (Phrynocephalus melanurus) Inferred from Mitochondrial DNA. Animals: an open access journal from MDPI, 14(2).

Mirzaee Z, et al. (2024) Biology, ecology, and biogeography of eremic praying mantis Blepharopsis mendica (Insecta: Mantodea). PeerJ, 12, e16814.

Kinganda-Lusamaki E, et al. (2024) 2020 Ebola virus disease outbreak in Équateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. The Lancet. Microbe, 5(2), e109.

Soares LS, et al. (2024) The phylogeographic journey of a plant species from lowland to highlands during the Pleistocene. Scientific reports, 14(1), 3825.