Resource Summary Report

Generated by NIF on Apr 26, 2025

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: data processing software, data analysis software, sequence analysis software, software repository, software resource, software application

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

Keywords: bio.tools

Funding:

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

Record Creation Time: 20220129T080257+0000

Record Last Update: 20250426T060151+0000

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 6030 mentions in open access literature.

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

Zhu W, et al. (2025) Origin, pathogenicity, and transmissibility of a human isolated influenza A(H10N3) virus from China. Emerging microbes & infections, 14(1), 2432364.

Foerster SÍA, et al. (2025) Body size prediction in scorpions: a phylogenetic comparative examination of linear measurements of individual body parts. PeerJ, 13, e18621.

Nicholls JA, et al. (2025) Continuous colonization of the Atlantic coastal rain forests of South America from Amazônia. Proceedings. Biological sciences, 292(2039), 20241559.

Mendonça P, et al. (2025) The influence of the forest corridors to the north of the Andes on the diversification of the bright-rumped Attila, Attila spadiceus (Passeriformes, Tyrannidae), during the climatic oscillations of the middle Pleistocene. Ecology and evolution, 15(1), e70331.

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (Duttaphrynus melanostictus). Nature communications, 16(1), 298.

Morey-León G, et al. (2025) Global epidemiology of Mycobacterium tuberculosis lineage 4 insights from Ecuadorian genomic data. Scientific reports, 15(1), 3823.

Lou Y, et al. (2025) Detection and Whole Genome Amplification of the 4d Type of Porcine Hepatitis E Virus in Eastern Tibet, China. Veterinary medicine and science, 11(1), e70194.

Witharana EP, et al. (2025) Subfamily evolution analysis using nuclear and chloroplast data from the same reads. Scientific reports, 15(1), 687.

de Sousa LLF, et al. (2025) Phylogenetic inferences reveal multiple intra- and interhost genetic diversity among bat rabies viruses circulating in northeastern Brazil. One health outlook, 7(1), 1.

Schenk JJ, et al. (2025) Comparative diversification analyses of Hydrangeaceae and Loasaceae reveal complex evolutionary history as species disperse out of Mesoamerica. American journal of botany, 112(1), e16455.

Veytsel G, et al. (2025) Molecular epidemiology, evolution, and transmission dynamics of raccoon rabies virus in Connecticut. Virus evolution, 11(1), veae114.

Zamunér CFC, et al. (2025) Evolution and spread of Xanthomonas citri subsp. citri in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. Microbial genomics, 11(1).

Zang G, et al. (2025) Identifications of Common Species and Descriptions of Two New Species of Siphonaria (Mollusca: Gastropoda) in China. Biology, 14(1).

Dang Y, et al. (2025) Temperature-dependent variations in under-canopy herbaceous foliar diseases following shrub encroachment in grasslands. Nature communications, 16(1), 1131.

Simmonds P, et al. (2025) Integrated analysis of protein sequence and structure redefines viral diversity and the taxonomy of the Flaviviridae. bioRxiv : the preprint server for biology.

Ne?as T, et al. (2025) ?An eastern Congolian endemic, or widespread but secretive? New data on the recently described Afrixaluslacustris (Anura, Hyperoliidae) from the Democratic Republic of the Congo. ZooKeys, 1224, 55.

Richard G, et al. (2025) Major change in swine influenza virus diversity in France owing to emergence and widespread dissemination of a newly introduced H1N2 1C genotype in 2020. Virus evolution, 11(1), veae112.

Maduenyane M, et al. (2025) Multifaceted taxonomy of two Dactylogyrus species on Enteromius paludinosus: Integrating light microscopy, scanning electron microscopy and molecular approaches. Parasite (Paris, France), 32, 5.

Yang K, et al. (2025) Genetic diversity of highly pathogenic avian influenza H5N6 and H5N8 viruses in poultry markets in Guangdong, China, 2020-2022. Journal of virology, 99(1), e0114524.

Keogh SM, et al. (2025) Secondary contact erodes Pleistocene diversification in a wide-ranging freshwater mussel (Quadrula). Molecular ecology, 34(1), e17572.