

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 17, 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: software repository, sequence analysis software, data analysis software, software application, data processing software, software resource

Defining Citation: [DOI:10.1186/1471-2148-7-214](https://doi.org/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: 20250417T065350+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 [FDI Lab - SciCrunch.org](#).

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.

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

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.

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

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

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

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).

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.

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

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.

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

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

Otieno JR, et al. (2025) Global genomic surveillance of monkeypox virus. *Nature medicine*, 31(1), 342.

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

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.

Hrala M, et al. (2025) Whole genome sequences of nine *Taylorella equigenitalis* strains isolated in the Czech Republic between 1982-2021: Molecular dating suggests a common ancestor at the time of Roman Empire. *PloS one*, 20(1), e0315946.

Patil A, et al. (2025) Looking back into the Hepatitis C Virus epidemic dynamics from Unnao, India through phylogenetic approach. *PloS one*, 20(1), e0317705.

Khemiri H, et al. (2025) SARS-CoV-2 excretion and genetic evolution in nasopharyngeal and stool samples from primary immunodeficiency and immunocompetent pediatric patients. *Virology journal*, 22(1), 9.