Resource Summary Report

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BEAST2

RRID:SCR_017307
Type: Tool

Proper Citation

BEAST2 (RRID:SCR_017307)

Resource Information

URL: https://www.beast2.org/

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Description: Software package for advanced Bayesian evolutionary analysis by sampling trees. Used for phylogenetics, population genetics and phylodynamics. Program for Bayesian phylogenetic analysis of molecular sequences. Estimates rooted, time measured phylogenies using strict or relaxed molecular clock models. Framework can be extended by third parties. Comprised of standalone programs including BEAUti, BEAST, MASTER, RBS, SNAPP, MultiTypeTree, BDSKY, LogAnalyser, LogCombiner, TreeAnnotator, DensiTree and package manager.

Synonyms: , Beast 2.5

Resource Type: software application, software toolkit, data analysis software, data processing software, sequence analysis software, software resource

Defining Citation: PMID:30958812

Keywords: Bayesian, evolutionary, sampling, tree, phylogenic, analysis, Markov, chain, monte carlo, phylogenetic, population, genetic, phylodynamic, sequence

Funding: Royal Society of New Zealand Marsden award ;
European Research Council ;
NIGMS U01 GM110749;
Swiss National Science foundation ;
Max Planck Society ;
EMBL

Availability: Free, Available for download, Freely available

Resource Name: BEAST2

Resource ID: SCR_017307

License: GNU GPL v2

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250519T203955+0000

Ratings and Alerts

No rating or validation information has been found for BEAST2.

No alerts have been found for BEAST2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 128 mentions in open access literature.

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

Tarr GAM, et al. (2025) Persistent cross-species transmission systems dominate Shiga toxin-producing Escherichia coli O157:H7 epidemiology in a high incidence region: A genomic epidemiology study. eLife, 13.

Coomber AL, et al. (2025) A pangenome analysis reveals the center of origin and evolutionary history of Phytophthora infestans and 1c clade species. PloS one, 20(1), e0314509.

Talavera A, et al. (2024) Genomic insights into the Montseny brook newt (Calotriton arnoldi), a Critically Endangered glacial relict. iScience, 27(1), 108665.

Waddell PJ, et al. (2024) An independent base composition of each rate class for improved likelihood-based phylogeny estimation; the 5rf model. bioRxiv : the preprint server for biology.

Lecocq de Pletincx N, et al. (2024) Ecological diversification preceded geographical expansion during the evolutionary radiation of Cataglyphis desert ants. iScience, 27(6), 109852.

White RT, et al. (2024) Rapid identification and subsequent contextualization of an outbreak of methicillin-resistant Staphylococcus aureus in a neonatal intensive care unit using nanopore sequencing. Microbial genomics, 10(7).

Bickerstaff JRM, et al. (2024) Two sympatric lineages of Australian Cnestus solidus share Ambrosiella symbionts but not Wolbachia. Heredity, 132(1), 43.

Emami-Khoyi A, et al. (2024) The complete mitogenome dataset of the Critically Endangered estuarine pipefish, Syngnathus watermeyeri. Data in brief, 52, 109864.

Schmidt LA, et al. (2024) Unveiling ophiuroid biodiversity across North Atlantic habitats via an integrative perspective. Scientific reports, 14(1), 20405.

Ndiaye N, et al. (2024) Recent Molecular Epidemiology of Echovirus 11 Throughout North and West Africa Resulted in the First Identification of a Recombinant Strain from an Acute Flaccid Paralysis Case in West Africa. Viruses, 16(11).

Liu X, et al. (2024) Introgression and disruption of migration routes have shaped the genetic integrity of wildebeest populations. Nature communications, 15(1), 2921.

Wang R, et al. (2024) Increase in antioxidant capacity associated with the successful subclone of hypervirulent carbapenem-resistant Klebsiella pneumoniae ST11-KL64. Nature communications, 15(1), 67.

White RT, et al. (2024) Genomic epidemiology reveals geographical clustering of multidrug-resistant Escherichia coli ST131 associated with bacteraemia in Wales. Nature communications, 15(1), 1371.

Majander K, et al. (2024) Redefining the treponemal history through pre-Columbian genomes from Brazil. Nature, 627(8002), 182.

Douglas J, et al. (2024) HetMM: A Michaelis-Menten model for non-homogeneous enzyme mixtures. iScience, 27(2), 108977.

Russo A, et al. (2024) Genome of the early spider-orchid Ophrys sphegodes provides insights into sexual deception and pollinator adaptation. Nature communications, 15(1), 6308.

Pereira AC, et al. (2024) Population structure and history of Mycobacterium bovis European 3 clonal complex reveal transmission across ecological corridors of unrecognized importance in Portugal. Microbiology spectrum, 12(7), e0382923.

Shahabi S, et al. (2024) Leishmania major Infection in Synanthropic Rodents: Evidence for the Urbanization of Zoonotic Cutaneous Leishmaniasis (ZCL) in Southern Iran. The

Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale, 2024, 4896873.

Daniels SR, et al. (2024) Let's get high: Cladogenesis in freshwater crabs (Decapoda: Potamonautidae: Potamonautes) supports the mountain gradient speciation hypothesis in the Cape Fold and Drakensberg Mountains, South Africa. Ecology and evolution, 14(3), e10960.

Daza JD, et al. (2024) Compound osteoderms preserved in amber reveal the oldest known skink. Scientific reports, 14(1), 15662.