

Resource Summary Report

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Tracer

RRID:SCR_019121

Type: Tool

Proper Citation

Tracer (RRID:SCR_019121)

Resource Information

URL: <https://bioweb.pasteur.fr/packages/pack@Tracer@v1.6>

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Description: Open source software tool for analysing trace files generated by Bayesian MCMC runs. Software package for visualising and analysing MCMC trace files generated through Bayesian phylogenetic inference. Provides kernel density estimation, multivariate visualisation, demographic trajectory reconstruction, conditional posterior distribution summary and more.

Synonyms: Tracer v1.7.1, Tracer v1.6

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

Defining Citation: [PMID:29718447](#)

Keywords: Analysing trace files, files generated by Bayesian MCMC runs, MCMC trace files, conditional posterior distribution summary, demographic trajectory reconstruction, Bayesian phylogenetic inference, kernel density estimation, multivariate visualisation

Funding: Wellcome Trust ;
European Union Seventh Framework Programme ;
NSF DMS 1264153;
NIAID R01 AI107034;
NIAID U19 AI135995

Availability: Free, Available for download, Freely available

Resource Name: Tracer

Resource ID: SCR_019121

Alternate URLs: <https://github.com/beast-dev/tracer>,
<http://gensoft.pasteur.fr/docs/Tracer/v1.6>, <http://beast.community/tracer>,
<https://github.com/beast-dev/tracer/releases/tag/v1.7.1>

License: GNU lesser general public license

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260729T044456+0000

Ratings and Alerts

No rating or validation information has been found for Tracer.

No alerts have been found for Tracer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1582 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Troyer EM, et al. (2025) Macroevolutionary role reversals in the earliest radiation of bony fishes. *Current biology : CB*.

Hernández C, et al. (2025) Multilocus analysis uncovers the evolution of the Rhodniini tribe, vectors of *Trypanosoma cruzi*. *Scientific reports*, 15(1), 20401.

Shin E, et al. (2025) Emergence of Distinct *Salmonella enterica* Serovar Enteritidis Lineage since 2020, South Korea. *Emerging infectious diseases*, 31(7), 1386.

Quainoo DK, et al. (2025) Genetic insights for enhancing conservation strategies in captive and wild Asian elephants through improved non-invasive DNA-based individual identification. *PloS one*, 20(5), e0320480.

Neira V, et al. (2025) Genetic Characterization of Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b, Antarctica, 2024. *Emerging infectious diseases*, 31(8), 1618.

- Hakim MS, et al. (2024) Sequence analysis of the Spike, RNA-dependent RNA polymerase, and protease genes reveals a distinct evolutionary pattern of SARS-CoV-2 variants circulating in Yogyakarta and Central Java provinces, Indonesia. *Virus genes*, 60(2), 105.
- Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.
- Wang M, et al. (2024) Genomic insights into Neolithic founding paternal lineages around the Qinghai-Xizang Plateau using integrated YanHuang resource. *iScience*, 27(12), 111456.
- Kuhar F, et al. (2024) Comprehensive Characterization of *Tuber maculatum*, New in Uruguay: Morphological, Molecular, and Aromatic Analyses. *Journal of fungi (Basel, Switzerland)*, 10(6).
- Patta C, et al. (2024) Questioning inbreeding: Could outbreeding affect productivity in the North African catfish in Thailand? *PloS one*, 19(5), e0302584.
- Liao JY, et al. (2024) Emerging and characterization of a novel fowl adenovirus 4 strain with open reading frame 19 (ORF19) in diseased chickens from China. *Poultry science*, 104(2), 104702.
- Hu X, et al. (2024) Classification of a Massive Number of Viral Genomes and Estimation of Time of Most Recent Common Ancestor (tMRCA) of SARS-CoV-2 Using Phylodynamic Analysis. *Bio-protocol*, 14(6), e4955.
- He F, et al. (2024) Genomic surveillance reveals low-level circulation of two subtypes of genogroup C coxsackievirus A10 in Nanchang, Jiangxi Province, China, 2015-2023. *Frontiers in microbiology*, 15, 1459917.
- Quijano-Barraza JM, et al. (2023) Evolution and functional role prediction of the CYP6DE and CYP6DJ subfamilies in *Dendroctonus* (Curculionidae: Scolytinae) bark beetles. *Frontiers in molecular biosciences*, 10, 1274838.
- Li YC, et al. (2023) Mitogenome evidence shows two radiation events and dispersals of matrilineal ancestry from northern coastal China to the Americas and Japan. *Cell reports*, 42(5), 112413.
- Argyriou A, et al. (2023) Single-cell profiling of muscle-infiltrating T cells in idiopathic inflammatory myopathies. *EMBO molecular medicine*, 15(10), e17240.
- Fehrer J, et al. (2022) A Multigene Phylogeny of Native American Hawkweeds (*Hieracium* Subgen. *Chionoracium*, Cichorieae, Asteraceae): Origin, Speciation Patterns, and Migration Routes. *Plants (Basel, Switzerland)*, 11(19).
- Liu S, et al. (2022) A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. *GigaScience*, 11.