

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

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

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

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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 1598 mentions in open access literature.

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

Sun X, et al. (2026) Comparative genomic and phylogenetic analyses of Crataegus chloroplast genomes: insights for evolution and identification. *Frontiers in plant science*, 17, 1767012.

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) Macroevoolutionary 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.

Motayo BO, et al. (2025) Phylodynamics of SARS-CoV-2 Lineages B.1.1.7, B.1.1.529 and B.1.617.2 in Nigeria Suggests Divergent Evolutionary Trajectories. *Pathogens (Basel, Switzerland)*, 14(11).

Winn JC, et al. (2025) Annotated Bioinformatic Pipelines for Phylogenomic Placement of Mitochondrial Genomes. *Bio-protocol*, 15(5), e5232.

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.

Hu SY, et al. (2025) Comprehensive sampling of mitochondrial genomes substantiates the Neoproterozoic origin of land plants. *Plant communications*, 6(11), 101497.

Wang Z, et al. (2025) Decoding the Mitochondrial Genome of the Tiger Shrimp: Comparative Genomics and Phylogenetic Placement Within Caridean Shrimps. *Genes*, 16(4).

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

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.

Sun Z, et al. (2025) Genomic insights into the spread of methicillin-resistant *Staphylococcus aureus* involved in ear infections. *BMC infectious diseases*, 25(1), 661.

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.

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.

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.