Resource Summary Report

Generated by RRID on Apr 28, 2025

Examl

RRID:SCR_016087

Type: Tool

Proper Citation

Examl (RRID:SCR_016087)

Resource Information

URL: https://github.com/stamatak/ExaML

Proper Citation: Examl (RRID:SCR_016087)

Description: Source code for large-scale phylogenetic analyses on whole-transcriptome and

whole-genome alignments using supercomputers.

Abbreviations: Examl

Synonyms: Examl: Exascale Maximum Likelihood

Resource Type: source code, software application, software resource

Defining Citation: PMID:25819675

Keywords: phylogenetic, analysis, database, large scale, whole genome, whole

transcriptome, alignment, efficiency, bio.tools, FASEB list

Funding: Heidelberg Institute for Theoretical Studies

Availability: Free, Available for download

Resource Name: Examl

Resource ID: SCR_016087

Alternate IDs: OMICS_08024, biotools:ExaML

Alternate URLs: https://bio.tools/ExaML, https://sources.debian.org/src/examl/

License: GNU GPL

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250428T053942+0000

Ratings and Alerts

No rating or validation information has been found for Examl.

No alerts have been found for Examl.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 60 mentions in open access literature.

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

Tang RX, et al. (2022) Genomics and morphometrics reveal the adaptive evolution of pikas. Zoological research, 43(5), 813.

Liu S, et al. (2022) Evolution and diversification of Mountain voles (Rodentia: Cricetidae). Communications biology, 5(1), 1417.

Cai D, et al. (2022) Radiocarbon and genomic evidence for the survival of Equus Sussemionus until the late Holocene. eLife, 11.

Bayless KM, et al. (2021) Beyond Drosophila: resolving the rapid radiation of schizophoran flies with phylotranscriptomics. BMC biology, 19(1), 23.

Wang W, et al. (2021) Build a better bootstrap and the RAWR shall beat a random path to your door: phylogenetic support estimation revisited. Bioinformatics (Oxford, England), 37(Suppl_1), i111.

Bennedbæk M, et al. (2021) Phylogenetic analysis of HIV-1 shows frequent cross-country transmission and local population expansions. Virus evolution, 7(2), veab055.

Booher DB, et al. (2021) Functional innovation promotes diversification of form in the evolution of an ultrafast trap-jaw mechanism in ants. PLoS biology, 19(3), e3001031.

Lamichhane B, et al. (2020) A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new sub-population of Helicobacter pylori from

Australia. Evolutionary applications, 13(2), 278.

Fischer G, et al. (2020) Socially Parasitic Ants Evolve a Mosaic of Host-Matching and Parasitic Morphological Traits. Current biology: CB, 30(18), 3639.

Katale BZ, et al. (2020) Whole genome sequencing of Mycobacterium tuberculosis isolates and clinical outcomes of patients treated for multidrug-resistant tuberculosis in Tanzania. BMC genomics, 21(1), 174.

Liu C, et al. (2020) Colonize, radiate, decline: Unraveling the dynamics of island community assembly with Fijian trap-jaw ants. Evolution; international journal of organic evolution, 74(6), 1082.

Züst T, et al. (2020) Independent evolution of ancestral and novel defenses in a genus of toxic plants (Erysimum, Brassicaceae). eLife, 9.

Peijnenburg KTCA, et al. (2020) The origin and diversification of pteropods precede past perturbations in the Earth's carbon cycle. Proceedings of the National Academy of Sciences of the United States of America, 117(41), 25609.

Feng S, et al. (2020) Dense sampling of bird diversity increases power of comparative genomics. Nature, 587(7833), 252.

Le Vu S, et al. (2019) HIV-1 Transmission Patterns in Men Who Have Sex with Men: Insights from Genetic Source Attribution Analysis. AIDS research and human retroviruses, 35(9), 805.

Folk RA, et al. (2019) Rates of niche and phenotype evolution lag behind diversification in a temperate radiation. Proceedings of the National Academy of Sciences of the United States of America, 116(22), 10874.

Oliveros CH, et al. (2019) Earth history and the passerine superradiation. Proceedings of the National Academy of Sciences of the United States of America, 116(16), 7916.

de Moya RS, et al. (2019) Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. Communications biology, 2, 445.

, et al. (2019) One thousand plant transcriptomes and the phylogenomics of green plants. Nature, 574(7780), 679.

Cloutier A, et al. (2019) Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. Systematic biology, 68(6), 937.