

Resource Summary Report

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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: software application, software resource, source code

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: 20260727T040640+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 [nidm-terms](#) .

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.

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.

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

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.

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

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.

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.

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.

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

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.

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.

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.

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.

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

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