

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, source code, 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: 20260803T040711+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 [ASWG](#) .

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

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

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.

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.

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

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.

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

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.

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.

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

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.

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.