

Resource Summary Report

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Hyphygui

RRID:SCR_016271

Type: Tool

Proper Citation

Hyphygui (RRID:SCR_016271)

Resource Information

URL: <http://hyphy.org/>

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Description: It is an open-source software package for comparative sequence analysis using stochastic evolutionary models. Used for the analysis of genetic sequence data (in particular the inference of natural selection) using techniques in phylogenetics, molecular evolution, and machine learning.

Synonyms: HyPhy:Hypothesis Testing using Phylogenies

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

Keywords: analysis, genetic, sequence, data, natural, selection, phylogenetic, molecular, evolution, machine, learning

Funding: MIDAS ;
NIGMS R01 GM093939

Availability: Free, Available for download

Resource Name: Hyphygui

Resource ID: SCR_016271

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260903T235329+0000

Ratings and Alerts

No rating or validation information has been found for Hyphygui.

No alerts have been found for Hyphygui.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

DeSalle R, et al. (2026) Natural selection and language genes in humans. Scientific reports, 16(1).

Chen W, et al. (2026) Rapid detection and genomic characterisation of feline chaphamaparvovirus in southwestern China. Journal of feline medicine and surgery, 28(1), 1098612X251407164.

Sun B, et al. (2025) Genomic variants and molecular epidemiological characteristics of dengue virus in China revealed by genome-wide analysis. Virus evolution, 11(1), veaf013.

Maclary ET, et al. (2025) Widespread Variation in EDNRB2 Is Associated With Diverse Melanin Loss Phenotypes Across Avian Species. Molecular biology and evolution, 42(11).

Maclary ET, et al. (2025) Widespread variation in EDNRB2 is associated with diverse melanin loss phenotypes across avian species. bioRxiv : the preprint server for biology.

Wülbern J, et al. (2024) Unprecedented genetic variability of PFam54 paralogs among Eurasian Lyme borreliosis-causing spirochetes. Ecology and evolution, 14(5), e11397.

Camacho J, et al. (2024) Sugar assimilation underlying dietary evolution of Neotropical bats. Nature ecology & evolution, 8(9), 1735.

Morel M, et al. (2024) Accurate Detection of Convergent Mutations in Large Protein Alignments With ConDor. Genome biology and evolution, 16(4).

Võ TC, et al. (2023) Genetic polymorphism and natural selection of the erythrocyte binding antigen 175 region II in Plasmodium falciparum populations from Myanmar and Vietnam. Scientific reports, 13(1), 20025.

Chen H, et al. (2023) Conserved chloroplast genome sequences of the genus Clerodendrum Linn. (Lamiaceae) as a super-barcode. PloS one, 18(2), e0277809.

Álvarez-Carretero S, et al. (2023) Beginner's Guide on the Use of PAML to Detect Positive Selection. Molecular biology and evolution, 40(4).

Yang Z, et al. (2023) Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in Panax. Plant communications, 4(4), 100591.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. PloS one, 18(2), e0279597.

Santos-Júnior CD, et al. (2023) Computational exploration of the global microbiome for antibiotic discovery. bioRxiv : the preprint server for biology.

Maher MC, et al. (2022) Predicting the mutational drivers of future SARS-CoV-2 variants of concern. Science translational medicine, 14(633), eabk3445.

Vakirlis N, et al. (2022) De novo birth of functional microproteins in the human lineage. Cell reports, 41(12), 111808.

Martin DP, et al. (2022) Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular biology and evolution, 39(4).

Martin DP, et al. (2022) Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. bioRxiv : the preprint server for biology.

Wang T, et al. (2022) Sympatric Recombination in Zoonotic Cryptosporidium Leads to Emergence of Populations with Modified Host Preference. Molecular biology and evolution, 39(7).

Kin K, et al. (2022) Evolution of a novel cell type in Dictyostelia required gene duplication of a cudA-like transcription factor. Current biology : CB, 32(2), 428.