

Resource Summary Report

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OBITools

RRID:SCR_024141

Type: Tool

Proper Citation

OBITools (RRID:SCR_024141)

Resource Information

URL: <https://pypi.org/project/OBITools/>

Proper Citation: OBITools (RRID:SCR_024141)

Description: Software package for analysing NGS data in DNA metabarcoding context. Used to filter and edit sequences while taking into account taxonomic annotation to set up tailor-made analysis pipelines for broad range of DNA metabarcoding applications, including biodiversity surveys or diet analyses.

Synonyms: obitools

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:25959493](#)

Keywords: analysing NGS data, DNA metabarcoding, filter and edit sequences, taxonomic annotation, analysis pipelines for DNA metabarcoding applications,

Availability: Free, Available for download, Freely available,

Resource Name: OBITools

Resource ID: SCR_024141

Alternate IDs: OMICS_32696

Alternate URLs: <https://sources.debian.org/src/obitools/>

License: CeCILL-V2

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260919T195619+0000

Ratings and Alerts

No rating or validation information has been found for OBITools.

No alerts have been found for OBITools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Gonzalez-Saldias F, et al. (2026) A Comparative Analysis of DNA Metabarcoding and Morphological Identification in Diatoms Reveals Similar Patterns of Environmental Response. *Ecology and evolution*, 16(2), e72644.

Zhang Y, et al. (2026) Integrated Reanalysis of Global Riverine Fish eDNA Datasets Shows Robustness and Congruence of Biodiversity Conclusions. *Molecular ecology*, 35(8), e70340.

Liu Y, et al. (2025) Plant interactions associated with a directional shift in the richness range size relationship during the Glacial-Holocene transition in the Arctic. *Nature communications*, 16(1), 1128.

Sharif MB, et al. (2025) Environmental DNA from peck marks shows potential for non-invasive monitoring of woodpeckers. *PloS one*, 20(8), e0328831.

Ozturk S, et al. (2025) Decoding past microbial life and antibiotic resistance in ?nonü Cave's archaeological soil. *PloS one*, 20(7), e0326358.

Kamenova S, et al. (2025) Arctic Greening Drives Changes in the Diet and Gut Microbiome of a Large Herbivore With Consequences for Body Mass. *Ecology and evolution*, 15(7), e71731.

Daraghmeh N, et al. (2025) A Long-Term Ecological Research Data Set From the Marine Genetic Monitoring Program ARMS-MBON 2018-2020. *Molecular ecology resources*, 25(4), e14073.

Walker SJ, et al. (2025) A 75,000-y-old Scandinavian Arctic cave deposit reveals past faunal diversity and paleoenvironment. *Proceedings of the National Academy of Sciences of the United States of America*, 122(32), e2415008122.

Shen W, et al. (2025) Post-Glacial Vegetation Trajectories on the Eastern Tibetan Plateau Reflect Millennial-Scale Migration Lags in Complex Mountain Terrain Based on Sedimentary Ancient DNA and Dynamic Dispersal Modeling. *Ecology and evolution*, 15(1), e70862.

Sanchez L, et al. (2025) eDNA surveys substantially expand known geographic and ecological niche boundaries of marine fishes. *PLoS biology*, 23(10), e3003432.

Garcés-Pastor S, et al. (2025) Wild and domesticated animal abundance is associated with greater late-Holocene alpine plant diversity. *Nature communications*, 16(1), 3924.

Neby M, et al. (2024) Is the diet cyclic phase-dependent in boreal vole populations? *Ecology and evolution*, 14(4), e11227.

Ficetola GF, et al. (2024) In silico assessment of 18S rDNA metabarcoding markers for the characterization of nematode communities. *PloS one*, 19(4), e0298905.

Foulquier A, et al. (2024) Unravelling large-scale patterns and drivers of biodiversity in dry rivers. *Nature communications*, 15(1), 7233.

Boilard A, et al. (2024) Ancient DNA and osteological analyses of a unique paleo-archive reveal Early Holocene faunal expansion into the Scandinavian Arctic. *Science advances*, 10(13), eadk3032.

Walker RH, et al. (2023) Mechanisms of individual variation in large herbivore diets: Roles of spatial heterogeneity and state-dependent foraging. *Ecology*, 104(2), e3921.

Mück F, et al. (2023) Complementary authentication of Chinese herbal products to treat endometriosis using DNA metabarcoding and HPTLC shows a high level of variability. *Frontiers in pharmacology*, 14, 1305410.

Raclariu-Manolic AC, et al. (2023) Authentication of milk thistle commercial products using UHPLC-QTOF-ESI + MS metabolomics and DNA metabarcoding. *BMC complementary medicine and therapies*, 23(1), 257.

Hayek S, et al. (2023) The Effects of Local Weed Species on Arbuscular Mycorrhizal Fungal Communities in an Organic Winter Wheat (*Triticum durum* L.) Field in Lebanon. *Microorganisms*, 12(1).

Walker TWN, et al. (2022) Lowland plant arrival in alpine ecosystems facilitates a decrease in soil carbon content under experimental climate warming. *eLife*, 11.