

Resource Summary Report

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MICtools

RRID:SCR_016121

Type: Tool

Proper Citation

MICtools (RRID:SCR_016121)

Resource Information

URL: <https://github.com/minepy/mictools>

Proper Citation: MICtools (RRID:SCR_016121)

Description: Software which combines the TICE and MICE measures into a two-step procedure that allows to identify relationships of various degrees of complexity in large datasets. TICE is used to perform an efficient high throughput screening of all the possible pairwise relationships and a permutation based approach is used to assess their significance.

Synonyms: Maximal Information Coefficient (MIC) Tools, MIC Tools, Maximal Information Coefficient Tools

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

Keywords: tice, mice, dataset, permutation, statistic

Availability: Open source

Resource Name: MICtools

Resource ID: SCR_016121

License: GPL v3.0

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260808T190048+0000

Ratings and Alerts

No rating or validation information has been found for MICtools.

No alerts have been found for MICtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Hill RA, et al. (2025) Eucalyptus grandis MYB-Like and RAN-Like Zinc Finger Proteins Display Dual Roles in Regulating Plant Immunity and Symbiosis Pathways. *Physiologia plantarum*, 177(4), e70454.

Auxillos J, et al. (2024) Spatially resolved analysis of microenvironmental gradient impact on cancer cell phenotypes. *Science advances*, 10(18), eadn3448.

Chelliah DS, et al. (2024) The Vestfold Hills are alive: characterising microbial and environmental dynamics in Old Wallow, eastern Antarctica. *Frontiers in microbiology*, 15, 1443491.

Nikhil KL, et al. (2024) The Functional Connectome Mediating Circadian Synchrony in the Suprachiasmatic Nucleus. *bioRxiv : the preprint server for biology*.

Coles DW, et al. (2024) Functional genomics identifies a small secreted protein that plays a role during the biotrophic to necrotrophic shift in the root rot pathogen *Phytophthora medicaginis*. *Frontiers in plant science*, 15, 1439020.

Arboleda-Baena C, et al. (2024) Microbial community and network responses across strong environmental gradients: How do they compare with macroorganisms? *FEMS microbiology ecology*, 100(3).

O'Brien L, et al. (2023) Tributary Inflows to a Regulated River Influence Bacterial Communities and Increase Bacterial Carbon Assimilation. *Microbial ecology*, 86(4), 2642.

Zhang ZF, et al. (2021) Biogeography, Assembly Patterns, Driving Factors, and Interactions of Archaeal Community in Mangrove Sediments. *mSystems*, 6(3), e0138120.

Latorre F, et al. (2021) Niche adaptation promoted the evolutionary diversification of tiny ocean predators. *Proceedings of the National Academy of Sciences of the United States of America*, 118(25).

Arroyo AS, et al. (2020) Gene Similarity Networks Unveil a Potential Novel Unicellular Group Closely Related to Animals from the Tara Oceans Expedition. *Genome biology and evolution*, 12(9), 1664.

Barelli C, et al. (2020) The Gut Microbiota Communities of Wild Arboreal and Ground-Feeding Tropical Primates Are Affected Differently by Habitat Disturbance. *mSystems*, 5(3).

Albanese D, et al. (2018) A practical tool for maximal information coefficient analysis. GigaScience, 7(4), 1.