

Resource Summary Report

Generated by [dkNET](#) on Aug 10, 2026

[mtradeR](#)

RRID:SCR_022977

Type: Tool

Proper Citation

mtradeR (RRID:SCR_022977)

Resource Information

URL: <https://github.com/qianli10000/mtradeR>

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Description: Software R package implements Joint model with Matching and Regularization and simulation pipeline. Used to test association between taxa and disease risk, and adjusted for correlated taxa screened by pre-selection procedure in abundance and prevalence, individually.

Synonyms: Metagenomic TRajjectory Analysis with Disease Endpoint and Risk factors

Resource Type: software toolkit, software resource

Defining Citation: [PMID:36123651](#)

Keywords: test association between taxa and disease risk, correlated taxa screening, taxa and disease risk

Funding: NIDDK U24DK097771;
NCI CA21765;
American Lebanese Syrian Associated Charities

Availability: Free, Available for download, Freely available

Resource Name: mtradeR

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License URLs: <https://github.com/qianli10000/mtradeR/blob/main/LICENSE>

Record Creation Time: 20221118T050202+0000

Record Last Update: 20260810T040810+0000

Ratings and Alerts

No rating or validation information has been found for mtradeR.

No alerts have been found for mtradeR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Li Q, et al. (2022) A robust and transformation-free joint model with matching and regularization for metagenomic trajectory and disease onset. BMC genomics, 23(1), 661.