Package ‘TestNet’

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Type Package

Title A Method for Inferring Microbial Networks with FDR Control

Version 1.0

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Description A testing method for inferring microbial networks. It differs from existing microbial network analyses in that it provides calibrated results by controlling the false discovery rate. The method accounts for the complex features of taxa count data. It also accommodates both independent and clustered samples, offers separate linear and nonlinear tests for each pair of taxa, and includes an omnibus test that bypasses the need to specify the type of relationship for each pair of taxa.

License GPL (>= 2)

RoxygenNote 7.3.2

Depends R (>= 3.5.0)

Imports permute, matrixStats, dcov, stats, utils

Suggests R.rsp, testthat

URL `https://github.com/yijuanhu/TestNet`

BugReports `https://github.com/yijuanhu/TestNet/issues`

Encoding UTF-8

LazyData true

NeedsCompilation no

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Repository CRAN

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Contents

`sim.otu.tab` *OTU count table of the simulated microbiome samples*

Description

This table contains read count data simulated for 100 samples and 46 OTUs and under the AR1 dependence structure

Usage

```
data("sim.otu.tab")
```

Format

A data frame with 100 observations on 46 OTUs

Examples

```
data(sim.otu.tab)
```

`TestNet` *A testing method for inferring microbial networks*

Description

This function generates a p-value and a q-value for each (linear, nonlinear, or omnibus) test of a pair of taxa.

Usage

```
TestNet(
  otu.tab,
  clustered.data = FALSE,
  cluster.id = NULL,
  fdr.nominal = 0.1,
  n.perm.max = NULL,
  seed = NULL,
  verbose = TRUE
)
```

Arguments

`otu.tab`	An `n.sam` by `n.otu` matrix of read counts.
`clustered.data`	A logical variable indicating whether the samples are clustered. The default is FALSE.
`cluster.id`	An array of `n.sam` cluster identifiers, used in the permutation procedure to shuffle the samples as a whole across clusters and simultaneously shuffle the samples within clusters when `clustered.data=TRUE`. The default is NULL.
`fdr.nominal`	The nominal FDR level. The default is 0.1.
`n.perm.max`	The maximum number of permutation replicates. The default is NULL, in which case a maximum of `n.otu` * `n.rej.stop` * (1/`fdr.nominal`) are used, where `n.rej.stop` is set to 20.
`seed`	A single-value integer seed for the random process of drawing permutation replicates. The default is NULL.
`verbose`	A logical variable indicating whether to write information messages to the console. The default is TRUE.

Value

a list consisting of

`p.linear`	An `n.otu` by `n.otu` matrix of p-values for the linear tests
`q.linear`	An `n.otu` by `n.otu` matrix of q-values for the linear tests
`p.nonlinear`	An `n.otu` by `n.otu` matrix of p-values for the nonlinear tests
`q.nonlinear`	An `n.otu` by `n.otu` matrix of q-values for the nonlinear tests
`p.omni`	An `n.otu` by `n.otu` matrix of p-values for the omnibus tests
`q.omni`	An `n.otu` by `n.otu` matrix of q-values for the omnibus tests
`which.pmin`	An `n.otu` by `n.otu` matrix of 0, 1, and 2 values, where 0 and 1 indicate that the nonlinear and linear tests, respectively, achieved the minimum p-value between the two, and 2 indicates that both tests yielded similar p-values.
`seed`	the seed used to generate the permutation replicates

Author(s)

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References

Su C, Mao Y, He M, Van Doren VE, Kelley CF, Hu YJ (2026). TestNet: a method for inferring microbial networks with false discovery rate control for clustered and unclustered samples. Genome Biology, in press.

Examples

```
data(sim.otu.tab)
TestNet.res <- TestNet(otu.tab = sim.otu.tab, n.perm.max = 100) # recommend to use n.perm.max = NULL
```

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