Package: TestNet (via r-universe)

June 3, 2026

Type Package

Title A method for inferring microbial networks with false discovery rate control for clustered and unclustered samples

Version 1.0

Description TestNet is 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. TestNet accounts for the features of compositionality, sparsity, and overdispersion in 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 pre-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

VignetteBuilder R.rsp

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

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

Encoding UTF-8

LazyData true

Repository https://yijuanhu.r-universe.dev

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RemoteUrl https://github.com/yijuanhu/testnet

RemoteRef HEAD

RemoteSha 7623747e14e72d9abda01a99aaa8e073fecd169f

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 = 123
)
```

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 123.

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.

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)
```

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