

Package ‘phyloseqGraphTest’

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Title Graph-Based Permutation Tests for Microbiome Data

Version 0.0.2

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Description Provides functions for graph-based multiple-sample testing and visualization of microbiome data, in particular data stored in 'phyloseq' objects. The tests are based on those described in Friedman and Rafsky (1979) <<http://www.jstor.org/stable/2958919>>, and the tests are described in more detail in Callahan et al. (2016) <[doi:10.12688/f1000research.8986.1](https://doi.org/10.12688/f1000research.8986.1)>.

Imports ggnetwork (>= 0.5.1), igraph (>= 1.1.2), intergraph (>= 2.0.2)

Depends R (>= 3.5.0), ggplot2 (>= 2.2.1), phyloseq (>= 1.24.0)

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LazyData true

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://github.com/jfukuyama/phyloseqGraphTest>

biocViews

RoxygenNote 6.0.1

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 phyloseqGraphTest-package

phyloseqGraphTest: Non-parametric graph-based testing for microbiome data.

Description

This package lets you test for differences between groups of samples with a graph-based permutation test.

Details

The main function in the package is [graph_perm_test](#), which takes a [phyloseq](#) object.

The graph used in the test can be visualized using [plot_test_network](#). The permutation distribution and the test statistic can be visualized with [plot_permutations](#).

graph_perm_test	<i>Performs graph-based permutation tests</i>
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Description

Performs graph-based tests for one-way designs.

Usage

```
graph_perm_test(physeq, samplotype, grouping = 1:nsamples(physeq),
  distance = "jaccard", type = c("mst", "knn", "threshold.value",
  "threshold.nedges"), max.dist = 0.4, knn = 1, nedges = nsamples(physeq),
  keep.isolates = TRUE, nperm = 499)
```

Arguments

physeq	A phyloseq object.
samplotype	A string giving the column name of the sample to be tested. This should be a factor with two or more levels.
grouping	Either a string with the name of a sample data column or a factor of length equal to the number of samples in physeq. These are the groups of samples whose labels should be permuted and are used for repeated measures designs. Default is no grouping (each group is of size 1).
distance	A distance, see distance for a list of the possible methods.
type	One of "mst", "knn", "threshold". If "mst", forms the minimum spanning tree of the sample points. If "knn", forms a directed graph with links from each node to its k nearest neighbors. If "threshold", forms a graph with edges between every pair of samples within a certain distance.

max.dist	For type "threshold", the maximum distance between two samples such that we put an edge between them.
knn	For type "knn", the number of nearest neighbors.
nedges	If using "threshold.nedges", the number of edges to use.
keep.isolates	In the returned network, keep the unconnected points?
nperm	The number of permutations to perform.

Value

A list with the observed number of pure edges, the vector containing the number of pure edges in each permutation, the permutation p-value, the graph used for testing, and a vector with the sample types used for the test.

Examples

```
library(phyloseq)
data(enterotype)
gt = graph_perm_test(enterotype, samplotype = "SeqTech", type = "mst")
gt
```

plot_permutations *Plots the permutation distribution*

Description

Plots a histogram of the permutation distribution of the number of pure edges and a mark showing the observed number of pure edges.

Usage

```
plot_permutations(graphtest, bins = 30)
```

Arguments

graphtest	The output from graph_perm_test.
bins	The number of bins to use for the histogram.

Value

A ggplot object.

Examples

```
library(phyloseq)
data(enterotype)
gt = graph_perm_test(enterotype, samplotype = "SeqTech")
plot_permutations(gt)
```

plot_test_network *Plots the graph used for testing*

Description

When using the graph_perm_test function, a graph is created. This function will plot the graph used for testing with nodes colored by sample type and edges marked as pure or mixed.

Usage

```
plot_test_network(graphtest)
```

Arguments

graphtest The output from graph_perm_test.

Value

A ggplot object created by ggnetwork.

Examples

```
library(phyloseq)
data(enterotype)
gt = graph_perm_test(enterotype, sampletype = "SeqTech")
plot_test_network(gt)
```

print.psgraphtest *Print psgraphtest objects*

Description

Print psgraphtest objects

Usage

```
## S3 method for class 'psgraphtest'
print(x, ...)
```

Arguments

x psgraphtest object.
... Not used

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