Package ‘phyloseqGraphTest’

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Title Graph-Based Permutation Tests for Microbiome Data
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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>.
Imports ggnetwork (>= 0.5.1), igraph (>= 1.1.2), intergraph (>= 2.0.2)
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graph_perm_test

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

Performs graph-based permutation tests

Description

Performs graph-based tests for one-way designs.

Usage

```
graph_perm_test(physeq, sampletype, 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.
- `sampletype`: 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.
For type "threshold", the maximum distance between two samples such that we put an edge between them.

For type "knn", the number of nearest neighbors.

If using "threshold.nedges", the number of edges to use.

In the returned network, keep the unconnected points?

The number of permutations to perform.

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.

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

A ggplot object.

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