Package 'iNEXT.UniFrac'

Type Package

Title Interpolation and Extrapolation for UniFrac based on dissimilarity measure

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Description iNEXT.UniFrac provides the function to calculate UniFrac for multiple assemblages.

Depends R (>= 4.0)

Imports tidyverse,
magrittr,
tidyr,
ggplot2,
abind,
ape,
ade4,
phytools,
phyclust,
tidytree,
colorRamps,
future.apply,
iNEXT.3D,
iNEXT.beta3D

Remotes AnneChao/iNEXT.beta3D

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

R topics documented:

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iNEXTUniFrac   *function to calculate UniFrac based on dissimilarity measure*

Description

iNEXTUniFrac: function to calculate UniFrac based on Sørensen- and Jaccard-type dissimilarity measure

Usage

```
iNEXTUniFrac(
  data,
  q = c(0, 1, 2),
  datatype = "abundance",
  level = NULL,
  nboot = 10,
  conf = 0.95,
  PDtree = NULL,
  PDreftime = NULL
)
```

Arguments

data	(a) For datatype = "abundance", data can be input as a matrix/data.frame (species by assemblages), or a list of matrices/data.frames, each matrix represents species-by-assemblages abundance matrix.
	(b) For datatype = "incidence_raw", data can be input as a list (a region) with several lists (assemblages) of matrices/data.frames, each matrix represents species-by-sampling units.
q	a numerical vector specifying the diversity orders. Default is c(0, 1, 2).
datatype	data type of input data: individual-based abundance data (datatype = "abundance") or species by sampling-units incidence matrix (datatype = "incidence_raw") with all entries being 0 (non-detection) or 1 (detection).
level	A numerical vector specifying the particular value of sample coverage (between 0 and 1). level = 1 means complete coverage (the corresponding UniFrac represents asymptotic UniFrac).
	If level = NULL, this function computes the gamma and alpha diversity estimates up to one (for q>0) or up to the coverage of double the reference sample size (for q = 0); the corresponding beta diversity and UniFrac is computed up to the same maximum coverage as the alpha diversity.
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Bootstrap replications are generally time consuming. Enter 0 to skip the bootstrap procedures. Default is 10.
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
PDtree	a phylogenetic tree in Newick format for all observed species in the pooled assemblage.
PDreftime	a numerical value specifying reference time for PD. Default is NULL (i.e., the age of the root of PDtree).

Value

a list of two data frames with two types dissimilarity measure for UniFrac.

Examples

```
data("tongue_cheek")
data("tongue_cheek_tree")
output <- iNEXTUniFrac(tongue_cheek, q=c(0,1,2), level = seq(0.5, 1, 0.05), nboot = 10, conf = 0.95, PDtree = to
```

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tongue_cheek	*tongue and cheek OTU count data*

Usage

```
data("tongue_cheek")
```

Format

A data frame with 2549 observations on the following 2 variables.

Cheek a numeric vector

Tongue a numeric vector

Examples

```
data(tongue_cheek)
```

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tongue_cheek_tree	*phylogenetic for tongue and cheek data*

Usage

```
data("tongue_cheek_tree")
```

Format

The format is: List of 4 $ edge : int [1:25400, 1:2] 12702 12703 12704 12704 12705 12706 12706 12707 12707 12705 ... $ edge.length: num [1:25400] 2.20e-03 9.91e-01 6.61e-03 7.87e-05 6.38e-03 ... $ Nnode : int 12700 $ tip.label : chr [1:12701] "OTU_97.15099" "OTU_97.13686" "OTU_97.30326" "OTU_97.26112" ... - attr(*, "class")= chr "phylo" - attr(*, "order")= chr "cladewise"

Examples

```
data(tongue_cheek_tree)
```

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