Package 'iNEXT.seq'

December 12, 2023

Type Package

Title Interpolation and Extrapolation for phylogenetic beta diversity and dissimilarity measure for genetic sequence data

Version 0.1.0

Author YaYun Teng

Maintainer YaYun Teng <jewel860911@gmail.com>

Description iNEXT.seq provides the function to calculate beta diversity and dissimilarity measure 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:

---

gghierPD   *ggplot2 extension for an hierPD object*

Description

gghierPD: the `ggplot` extension for `hierPD` object to plot order q against to hierarchical phyloge-
netic diversity decomposition and dissimilarity measure.

Usage

```
gghierPD(output, method = "A")
```

Arguments

output	the output from hierPD.
method	(method = "A") diversity(alpha, gamma); (method = "B") beta diversity; (method = "D") dissimilarity measure based on multiplicative decomposition.

Value

a figure for hierarchical phylogenetic diversity decomposition or dissimilarity measure.

Examples

```
data("antechinus")
data("antechinus_mat")
data("antechinus_tree")
hier_output <- hierPD(antechinus, mat = antechinus_mat, tree = antechinus_tree, q = seq(0, 2, 0.2))
gghierPD(hier_output, method = "A")
```

---

ggiNEXTseq   *ggplot2 extension for an iNEXT.seq object*

Description

ggiNEXTseq: the `ggplot` extension for `iNEXTseq` object to plot coverage- or sample-sized-based
rarefaction/extrapolation curves for phylogenetic diversity decomposition and dissimilarity mea-
sure.

Usage

```
ggiNEXTseq(output, type = "B", scale = "fixed", transp = 0.4)
```

Arguments

output	the output from iNEXTseq
type	(required only when base = "coverage"), selection of plot type : type = 'B' for plotting the gamma, alpha, and beta diversity ; type = 'D' for plotting 4 turnover dissimilarities.
scale	Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")?
transp	a value between 0 and 1 for controlling transparency. transp = 0 is completely transparent, default is 0.4.

Value

a figure for phylogenetic diversity decomposition or dissimilarity measure.

Examples

```
data("tongue_cheek")
data("tongue_cheek_tree")
output <- iNEXTseq(tongue_cheek, q=c(0,1,2), nboot = 0, PDtree = tongue_cheek_tree)
ggiNEXTseq(output, scale = 'free', transp = 0.4)
```

---

hierPD	*function to calculate hierarchical phylogenetic gamma, alpha, beta diversity and dissimilarity measure*

Description

hierPD: function to calculate empirical estimates for hierarchical phylogenetic gamma, alpha, beta diversity and dissimilarity measure

Usage

```
hierPD(
  data,
  mat,
  PDtree,
  q = seq(0, 2, 0.2),
  weight = "size",
  nboot = 20,
  conf = 0.95,
  type = "mle",
  decomposition = "relative"
)
```

Arguments

data	data should be input as a `matrix/data.frame` (species by assemblages).
mat	hierarchical structure of data should be input as a `matrix`.
q	a numerical vector specifying the diversity orders. Default is `seq(0, 2, 0.2)`.
weight	weight for relative decomposition. Default is `"size"`.
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 `20`.
conf	a positive number < 1 specifying the level of confidence interval. Default is `0.95`.
type	estimate type: estimate (`type = "est"`), empirical estimate (`type = "mle"`). Default is `"mle"`.
decomposition	relative decomposition: (`decomposition = "relative"`), Absolute decomposition: (`decomposition = "absolute"`).
tree	a phylogenetic tree in Newick format for all observed species in the pooled assemblage.

Value

a data frames with hierarchical phylogenetic diversity (gamma, alpha, and beta) and four types dissimilarity measure.

Examples

```
data("antechinus")
data("antechinus_mat")
data("antechinus_tree")
hier_output <- hierPD(antechinus, mat = antechinus_mat, tree = antechinus_tree, q = seq(0, 2, 0.2))
```

---

iNEXTseq	*function to calculate phylogenetic gamma, alpha, beta diversity and dissimilarity measure*

Description

iNEXTseq: function to calculate interpolation and extrapolation for phylogenetic gamma, alpha, beta diversity and dissimilarity measure

Usage

```
iNEXTseq(
  data,
  q = c(0, 1, 2),
  base = "coverage",
  level = NULL,
  nboot = 10,
  conf = 0.95,
```

```
    PDtree = NULL,
    PDreftime = NULL
)
```

Arguments

data	OTU 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.
q	a numerical vector specifying the diversity orders. Default is c(0, 1, 2).
base	sample-sized-based rarefaction and extrapolation for gamma and alpha diversity (base = "size") or coverage-based rarefaction and extrapolation for gamma, alpha and beta diversity (base = "coverage"). Default is base = "coverage".
level	A numerical vector specifying the particular value of sample coverage (between 0 and 1 when base = "coverage") or sample size (base = "size"). level = 1 (base = "coverage") means complete coverage (the corresponding diversity represents asymptotic diversity). If base = "size" and level = NULL, then this function computes the gamma and alpha diversity estimates up to double the reference sample size. If base = "coverage" and level = NULL, then this function computes the gamma and alpha diversity estimates up to one (for q = 1, 2) or up to the coverage of double the reference sample size (for q = 0); the corresponding beta diversity 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

If base = "coverage", return a list of seven data frames with three coverage-based diversity (gamma, alpha, and beta) and four types dissimilarity measure. If base = "size", return a list of two data frames with two diversity (gamma and alpha).

Examples

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

---

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)
```

---

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 "clade-wise"

Examples

```
data(tongue_cheek_tree)
```

Index