

Package ‘hiDIP’

August 30, 2022

Type Package

Title Hierarchical Decomposition Partitioning

Version 1.0.1

Author Anne Chao, Jian-You Lin

Maintainer Anne Chao <chao@stat.nthu.edu.tw>

Description Provides functions for hierarchical diversity analysis.

License GPL (>= 3)

Depends R (>= 4.0)

Suggests knitr,
rmarkdown,
ggpubr

Imports Rcpp,
dplyr,
ggplot2,
ape,
data.tree,
ade4,
phytools,
reshape2,
networkD3,
maps

LazyData true

Encoding UTF-8

RoxygenNote 7.2.1

LinkingTo Rcpp

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DataInfo

*Exhibit basic data information***Description**

DataInfo: exhibits basic data information

Usage

```
DataInfo(data, diversity = "TD", datatype = "abundance", tree = NULL)
```

Arguments

data	data.frames
diversity	selection of diversity type: 'TD' = 'Taxonomic diversity', 'PD' = 'Phylogenetic diversity', and 'FD' = 'Functional diversity'.
datatype	data type of input data: individual-based abundance data (datatype = "abundance"), sampling-unit-based incidence frequencies data (datatype = "incidence"),

Value

a data.frame of basic data information including sample size, observed species richness, sample coverage estimate, and the first ten abundance frequency counts.

Examples

```
## Taxonomic diversity
data(macro)
DataInfo(data = macro, diversity = 'TD')

## Phylogenetic diversity
data(macro)
data(macro_tree)
DataInfo(data = macro, diversity = 'PD', tree = macro_tree)

## Functional diversity
data(macro)
DataInfo(data = macro, diversity = 'FD')
```

gghier_functional

*ggplot2 extension for outcome from hier_functional***Description**

ggplot2 extension for outcome from hier_functional

Usage

```
gghier_functional(outcome, method = 1, profile = "q")
```

Arguments

outcome	a list object computed by hier_functional.
method	(method = 1) diversity(alpha, gamma) based on Tsallis entropy (1988); (method = 2) beta diversity based on additive decomposition; (method = 3) dissimilarity measure based on additive decomposition; (method = 4) diversity(alpha, gamma) based on Hill Number (1973); (method = 5) beta diversity based on multiplicative decomposition; (method = 6) dissimilarity measure based on multiplicative decomposition.
profile	a selection of profile versus to diversity.q-profile (profile = "q");tau-profile (prifile = "tau")

Examples

```
## Functional diversity
data(macro)
data(macro_mat)
data(macro_dis)
output3 = hier_functional(data = macro, mat = macro_mat, dis = macro_dis, q = c(0, 1, 2), FDtau = c(0.2, 0.4, 0.6))
gghier_functional(output3, method = 1, profile = "q")
output4 = hier_functional(data = macro, mat = macro_mat, dis = macro_dis, q = c(0, 1, 2), FDtype = "AUC")
gghier_functional(output4, method = 1, profile = "q")
```

gghier_phylogeny

*ggplot2 extension for outcome from hier_phylogeny***Description**

ggplot2 extension for outcome from hier_phylogeny

Usage

gghier_phylogeny(outcome, method = 1)

Arguments

outcome	a list object computed by hier_phylogeny.
method	(method = 1) diversity(alpha, gamma) based on Tsallis entropy (1988); (method = 2) beta diversity based on additive decomposition; (method = 3) dissimilarity measure based on additive decomposition; (method = 4) diversity(alpha, gamma) based on Hill Number (1973); (method = 5) beta diversity based on multiplicative decomposition; (method = 6) dissimilarity measure based on multiplicative decomposition.

Examples

```
## Phylogeny diversity
data(macro)
data(macro_mat)
data(macro_tree)
output2 = hier_phylogeny(data = macro, mat = macro_mat, tree = macro_tree, q = seq(0, 2, 0.2))
gghier_phylogeny(output2, method = 1)
```

gghier_taxonomy	<i>ggplot2 extension for outcome from hier_taxonomy</i>
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Description

ggplot2 extension for outcome from hier_taxonomy

Usage

```
gghier_taxonomy(outcome, method = 1)
```

Arguments

outcome	a list object computed by hier_taxonomy.
method	(method = 1) diversity(alpha, gamma) based on Tsallis entropy (1988); (method = 2) beta diversity based on additive decomposition; (method = 3) dissimilarity measure based on additive decomposition; (method = 4) diversity(alpha, gamma) based on Hill Number (1973); (method = 5) beta diversity based on multiplicative decomposition; (method = 6) dissimilarity measure based on multiplicative decomposition.

Examples

```
## Taxonomy diversity
data(macro)
data(macro_mat)
output1 = hier_taxonomy(data = macro, mat = macro_mat, q = seq(0, 2, 0.2))
gghier_taxonomy(output1, method = 1)
```

hier.functional	<i>Decomposition of functional diversity</i>
-----------------	--

Description

Decomposition of functional diversity

Usage

```
hier.functional(
  data,
  mat,
  dis,
  q = seq(0, 2, 0.2),
  FDtype = "tau_values",
  FDtau = NULL,
  weight = "size",
  nboot = 20,
  conf = 0.95,
  type = "mle",
  datatype = "abundance",
  decomposition = "relative"
)
```

Arguments

data	data.frames
mat	hierarchical structure of data.
dis	species pairwise distance matrix for all species in the pooled assemblage.
q	a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
FDtype	select FD type: (FDtype = "tau_values") for FD under specified threshold values, or (FDtype = "AUC") (area under the curve of tau-profile) for an over-all FD which integrates all threshold values between zero and one. Default is "tau_values".
FDtau	a numerical vector between 0 and 1 specifying tau values (threshold levels). If NULL (default), then threshold is set to be the mean distance between any two individuals randomly selected from the pooled assemblage (i.e., quadratic entropy).
weight	weight for relative decomposition.
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").

Examples

```
## Functional diversity
data(macro)
data(macro_mat)
data(macro_dis)
output3 = hier.functional(data = macro, mat = macro_mat, dis = macro_dis, q = seq(0, 2, 0.2))
output3
```

hier.phylogeny	<i>Decomposition of phylogeny diversity</i>
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Description

Decomposition of phylogeny diversity

Usage

```
hier.phylogeny(
  data,
  mat,
  tree,
  q = seq(0, 2, 0.2),
```

```

weight = "size",
nboot = 20,
conf = 0.95,
type = "mle",
decomposition = "relative"
)

```

Arguments

data	data.frames
mat	hierarchical structure of data.
tree	a phylogenetic tree in Newick format for all observed species in the pooled assemblage.
q	a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
weight	weight for relative decomposition.
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").

Examples

```

## Phylogeny diversity
data(macro)
data(macro_mat)
data(macro_tree)
output2 = hier.phylogeny(data = macro, mat = macro_mat, tree = macro_tree, q = seq(0, 2, 0.2))
output2

```

hier.taxonomy	<i>Decomposition of taxonomy diversity</i>
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Description

Decomposition of taxonomy diversity

Usage

```

hier.taxonomy(
  data,
  mat,
  q = seq(0, 2, 0.2),
  weight = "size",

```

```

nboot = 20,
conf = 0.95,
type = "mle",
datatype = "abundance",
decomposition = "relative"
)

```

Arguments

data	data.frames
mat	hierarchical structure of data.
q	a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
weight	weight for relative decomposition.
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".
datatype	data type of input data: individual-based abundance data (datatype = "abundance"), sampling-unit-based incidence frequencies data (datatype = "incidence").
decomposition	Relative decomposition: (decomposition = "relative"), Absolute decomposition: (decomposition = "absolute").

Examples

```

## Taxonomic diversity
data(macro)
data(macro_mat)
output1 = hier.taxonomy(data = macro, mat = macro_mat, q = seq(0, 2, 0.2))
output1

```

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