Package 'iNEXT.link'

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Type Package

Title Network diversity iNterpolation/Extrapolation Estimation

Version 1.1.1

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Description Provides functions for network diversity analysis.
(1) The iNEXT standardization for network diversity: computes and plots rarefaction and extrapolation of network diversity based on two types of standardization methods (sample size and sample coverage).
(2) The phylogenetic diversity estimation: computes and plots asymptotic phylogenetic network diversity profile as a function of diversity order (q-profile) or time (time-profile).
Provides simple functions to compute and plot two types (sample-size- and coverage-based) rarefaction and
extrapolation of species diversity (Hill numbers) for individual-based (abundance) data

License GPL (>= 3)

Depends R (>= 3.6)

Suggests knitr,
rmarkdown,
ggpubr,
ade4

Imports chaoUtility,
phytools,
Rcpp,
dplyr,
ggplot2,
tidyr,
tidytree,
tibble,
stats,
ape,
sets,
phyclust,
utils,
PhD,
iNEXT.3D,
iNEXTPD2,
iNEXT.4steps,
iNEXT.beta

LinkingTo Rcpp

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Remotes YanHanChen/PhD , chaolab2019/chaoUtility, KaiHsiangHu/iNEXT.3D, KaiH-siangHu/iNEXTPD2, KaiHsiangHu/iNEXT.4steps, crazymin2266/iNEXT.beta

R **topics documented:**

Asy.link   *Asymptotic diversity q profile*

Description

Asy.link The estimated and empirical diversity of order q

Usage

```
Asy.link(
  data,
  diversity = "TD",
  q = seq(0, 2, 0.2),
  datatype = "abundance",
  nboot = 30,
  conf = 0.95,
  row.tree = NULL,
  col.tree = NULL
)
```

Arguments

data	a matrix/data.frame of species abundances (for abundance data) or species-by-site incidence raw matrix/data.frame (for incidence data).
	Abundance data: a species-by-site matrix/data.frame of species abundances. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
	Incidence raw data: species-by-site raw incidence matrix/data.frame. When there are N assemblages and thus N matrices, users must first merge the N matrices by species identity to obtain a large merged incidence matrix, where the rows of the matrix refer to all species presented in the merged data. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold.
q	a nonnegative value or sequence specifying the diversity order. 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"`).
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Enter 0 to skip the bootstrap procedures. Default is 50
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
row.tree	phylogenetic tree of row assemblage in interaction matrix.
col.tree	phylogenetic tree of column assemblage in interaction matrix

Value

a table of Asymptotic network diversity q profile

Examples

```
## Not run:
## Ex.1
data(Norfolk)
out1 <- Asy.link(Norfolk, diversity = 'TD', datatype = "abundance", nboot = 10)
ggAsy.link(out1)
## Ex.2
data(puerto.rico)
out2 <- Asy.link(puerto.rico$data, diversity = 'PD', datatype = "abundance", nboot = 10,
row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)
ggAsy.link(out2)

## End(Not run)
```

DataInfo.link   *Exhibit basic data information*

Description

`DataInfo.link`: exhibits basic data information

Usage

```
DataInfo.link(
  data,
  diversity = "TD",
  datatype = "abundance",
  row.tree = NULL,
  col.tree = NULL
)
```

Arguments

data	a vector/matrix/list of species abundances or incidence frequencies. If datatype = "incidence", then the first entry of the input data must be total number of sampling units, followed by species incidence frequencies.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold.
datatype	data type of input data: individual-based abundance data (datatype = "abundance") or species by sampling-units incidence matrix (datatype = "incidence_raw").#' @return a data.frame of basic data information including sample size, observed species richness, sample coverage estimate, and the first ten abundance/incidence frequency counts.

Examples

```
## Not run:
data(puerto.rico)
DataInfo.link(puerto.rico$data, diversity = 'TD', datatype="abundance")
DataInfo.link(puerto.rico$data, diversity = 'PD', datatype="abundance",
row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)

## End(Not run)
```

---

estimateD.link   *Compute species diversity with a particular of sample size/coverage*

Description

estimateD.link computes species diversity (Hill numbers with q = 0, 1 and 2) with a particular user-specified level of sample size or sample coverage.

Usage

```
estimateD.link(
  data,
  diversity = "TD",
  q = c(0, 1, 2),
  datatype = "abundance",
  base = "size",
  level = NULL,
  nboot = 50,
  conf = 0.95,
```

```
    row.tree = NULL,
    col.tree = NULL
)
```

Arguments

data	a matrix, data.frame (species by assemblages), or list of species abundance/incidence raw data.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold. Besides,'AUC' is the fourth choice which integrates several threshold functional diversity to get diversity.
q	a numerical vector of the order of Hill number.
datatype	data type of input data: individual-based abundance data (datatype = "abundance") or species by sampling-units incidence matrix (datatype = "incidence_raw").
base	comparison base: sample-size-based (base="size") or coverage-based (base="coverage").
level	a sequence specifying the particular sample sizes or sample coverages(between 0 and 1). If base="size" and level=NULL, then this function computes the diversity estimates for the minimum sample size among all sites extrapolated to double reference sizes. If base="coverage" and level=NULL, then this function computes the diversity estimates for the minimum sample coverage among all sites extrapolated to double reference sizes.
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Enter 0 to skip the bootstrap procedures. Default is 50
conf	a positive number < 1 specifying the level of confidence interval, default is 0.95.
row.tree	phylogenetic tree of row assemblage in interaction matrix.
col.tree	phylogenetic tree of column assemblage in interaction matrix

Value

a data.frame of species diversity table including the sample size, sample coverage, method (rarefaction or extrapolation), and diversity estimates with q = 0, 1, and 2 for the user-specified sample size or sample coverage.

Examples

```
## Not run:
data(Norfolk)
out1 <- estimateD.link(Norfolk, diversity = 'TD',datatype="abundance",
                       base="coverage", level=0.7, nboot = 30)
out2 <- estimateD.link(Norfolk, diversity = 'TD',datatype="abundance",
                       base="size", level=0.7, nboot = 30)


## End(Not run)
```

---

ggAsy.link   *ggplot for Asymptotic Network diversity*

Description

ggAsy.link Plots q-profile based on the outcome of Asy.link using the ggplot2 package.

Usage

```
ggAsy.link(outcome, diversity = "TD", text.size = 14)
```

Arguments

outcome   the outcome of the functions Asy.link .

text.size   control the text size of the output plot.

Value

a figure of estimated sample completeness with order q

Examples

```
## Not run:
## Ex.1
data(Norfolk)
out1 <- Asy.link(Norfolk, diversity = 'TD', datatype = "abundance", nboot = 10)
ggAsy.link(out1)
## Ex.2
data(puerto.rico)
out2 <- Asy.link(puerto.rico$data, diversity = 'PD', datatype = "abundance",
              nboot = 10, row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)
ggAsy.link(out2)

## End(Not run)
```

---

ggiNEXT.link   *ggplot2 extension for outcome from* iNEXT.link

---

Description

ggiNEXT.link: the ggplot extension for iNEXT.link Object to plot sample-size- and coverage-based rarefaction/extrapolation curves along with a bridging sample completeness curve

Usage

```
ggiNEXT.link(
  outcome,
  diversity = "TD",
  type = 1,
  se = TRUE,
  facet.var = "Order.q",
  color.var = "Assemblage",
  text.size = 12,
  stript.size = 12
)
```

Arguments

outcome	a list object computed by `iNEXT.link`.
type	three types of plots: sample-size-based rarefaction/extrapolation curve (`type = 1`); sample completeness curve (`type = 2`); coverage-based rarefaction/extrapolation curve (`type = 3`).
se	a logical variable to display confidence interval around the estimated sampling curve.
facet.var	create a separate plot for each value of a specified variable: no separation (`facet.var="None"`); a separate plot for each diversity order (`facet.var="Order.q"`); a separate plot for each assemblage (`facet.var="Assemblage"`); a separate plot for each combination of order x assemblage (`facet.var="Both"`).
color.var	create curves in different colors for values of a specified variable: all curves are in the same color (`color.var="None"`); use different colors for diversity orders (`color.var="Order.q"`); use different colors for sites (`color.var="Assemblage"`); use different colors for combinations of order x assemblage (`color.var="Both"`).
grey	a logical variable to display grey and white ggplot2 theme.
...	other arguments passed on to methods. Not currently used.

Value

a ggplot2 object

Examples

```
## Not run:
data(Norfolk)
out1 <- iNEXT.link(Norfolk, diversity = 'TD',datatype = "abundance", nboot = 0)
ggiNEXT.link(outcome = out1, type = 1)
ggiNEXT.link(outcome = out1, type = 2)
ggiNEXT.link(outcome = out1, type = 3)

#' data(puerto.rico)
out2 <- iNEXT.link(puerto.rico$data, diversity = 'PD', datatype="abundance",
row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)
ggiNEXT.link(outcome = out2, type = 1)
ggiNEXT.link(outcome = out2, type = 2)
ggiNEXT.link(outcome = out2, type = 3)

## End(Not run)
```

---

ggiNEXTbeta.link   *ggplot2 extension for outcome from* iNEXT.beta.link

---

Description

ggiNEXTbeta.link: ggplot for Interpolation and extrapolation of Beta diversity with order q

Usage

```
ggiNEXTbeta.link(
  outcome,
  type = c("B", "D"),
  diversity = "TD",
  scale = "free",
  main = NULL,
  transp = 0.4,
  stript.size = 11,
  text.size = 13
)
```

Arguments

outcome	the outcome from "iNEXTbeta.link"
type	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 ("fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")? Default is "free".
main	The title of the plot.
transp	a value between 0 and 1 controlling transparency. transp = 0 is completely transparent, default is 0.4.
measurement	character indicating the label of y-axis.

Value

a figure for Beta diversity or dissimilarity diversity.

a ggplot2 object

Examples

```
## Not run:
data(Norfolk)
beta1 = iNEXTbeta.link(networks = puerto.rico$data, level = seq(0.5, 1, 0.5), datatype='abundance',q = c(0, 1,
                      diversity = 'TD', nboot = 10, conf = 0.95)
beta2 = iNEXTbeta.link(networks = puerto.rico$data, level = seq(0.5, 1, 0.5), datatype='abundance',q = c(0, 1,
                      diversity = 'PD', nboot = 10, conf = 0.95,
                      row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)

ggiNEXTbeta.link(beta1,diversity = 'TD', type = 'B')
ggiNEXTbeta.link(beta1,diversity = 'TD', type = 'D')
ggiNEXTbeta.link(beta2,diversity = 'PD', type = 'B')
```

```
ggiNEXTbeta.link(beta2,diversity = 'PD', type = 'D')

## End(Not run)
```

---

ggObs.link   *ggplot for Empirical Network diversity*

Description

ggObs.link Plots q-profile based on the outcome of Obs.link using the ggplot2 package.

Usage

```
ggObs.link(outcome, diversity = "TD", text.size = 14)
```

Arguments

outcome   the outcome of the functions Obs.link .

text.size   control the text size of the output plot.

Value

a figure of estimated sample completeness with order q

Examples

```
## Not run:
## Ex.1
data(Norfolk)
out1 <- Obs.link(Norfolk, diversity = 'TD', datatype = "abundance", nboot = 10)
ggObs.link(out1)
## Ex.2
data(puerto.rico)
out2 <- Obs.link(puerto.rico$data, diversity = 'PD', datatype = "abundance",
nboot = 10, row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)
ggObs.link(out2)

## End(Not run)
```

---

ggSC.link   *ggplot for Sample Completeness*

Description

ggSC.link The figure for estimation of Sample Completeness with order q

Usage

```
ggSC.link(outcome)
```

Arguments

outcome   a table generated from SC function

Value

a figure of estimated sample completeness with order q

Examples

```
data(Norfolk)
output = SC.link(Norfolk)
ggSC.link(output)
```

---

ggSpec.link   *ggplot for Evenness* ggSpec.link *The figure for estimation of Evenness with order q*

Description

ggplot for Evenness ggSpec.link The figure for estimation of Evenness with order q

Usage

```
ggSpec.link(outcome)
```

Arguments

outcome   a table generated from Spec.link function

Value

a figure of estimated sample completeness with order q

References

Chao,A.and Ricotta,C.(2019).Quantifying evenness and linking it to diversity, beta diversity, and similarity.

Examples

```
## Not run:
data(Norfolk)
Est <- Spec.link(data = Norfolk, diversity = 'TD', datatype = "abundance", q = c(0,1,2),
                 nboot = 30, method = "Estimated")
Emp <- Spec.link(data = Norfolk, diversity = 'TD', datatype = "abundance", q = c(0,1,2),
                 nboot = 30, method = "Empirical")
ggSpec(output = Est)
ggSpec(output = Emp)

## End(Not run)
```

---

iNEXT.link	*Interpolation (rarefaction) and extrapolation of Chao et al.'s (2021) network diversity and mean network diversity Function* iNEXT.link *computes network diversity estimates for rarefied samples and extrapolated samples along with confidence intervals and related coverage estimates based on Chao et al.'s (2021) network diversity (ND)*

Description

Interpolation (rarefaction) and extrapolation of Chao et al.'s (2021) network diversity and mean network diversity Function `iNEXT.link` computes network diversity estimates for rarefied samples and extrapolated samples along with confidence intervals and related coverage estimates based on Chao et al.'s (2021) network diversity (ND)

Usage

```
iNEXT.link(
  data,
  diversity = "TD",
  q = c(0, 1, 2),
  datatype = "abundance",
  size = NULL,
  nT = NULL,
  endpoint = NULL,
  knots = 40,
  conf = 0.95,
  nboot = 30,
  row.tree = NULL,
  col.tree = NULL,
  PDtype = "meanPD"
)
```

Arguments

data	a matrix/data.frame of species abundances (for abundance data) or species-by-site incidence raw matrix/data.frame (for incidence data).
	Abundance data: a species-by-site matrix/data.frame of species abundances. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
	Incidence raw data: species-by-site raw incidence matrix/data.frame. When there are N assemblages and thus N matrices, users must first merge the N matrices by species identity to obtain a large merged incidence matrix, where the rows of the matrix refer to all species presented in the merged data. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold.
q	a nonnegative value or sequence specifying the diversity order. 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"`).
size	a sequence of positive integers specifying the sample sizes for which PD or meanPD estimates will be calculated. If NULL, then estimates will be calculated for those sample sizes determined by the specified/default `endpoint` and `knots`.
endpoint	a positive integer specifying the endpoint for the rarefaction and extrapolation range. If NULL, then `endpoint` = double of the reference sample size in each assemblage. It is ignored if `size` is given.
knots	a positive integer specifying the number of equally-spaced knots between 1 and the `endpoint`. Default is 40.
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Enter 0 to skip the bootstrap procedures. Default is 50
row.tree	phylogenetic tree of row assemblage in interaction matrix.
col.tree	phylogenetic tree of column assemblage in interaction matrix
PDtype	Select phylogenetic diversity type: PDtype = "PD" for Chao et al. (2010) phylogenetic diversity and PDtype = "meanPD" for mean phylogenetic diversity (phylogenetic Hill number). It will be used when `diversity = 'PD'`. Default is "PD".
type	desired diversity type: type = "PD" for Chao et al. (2010) phylogenetic diversity and type = "meanPD" for mean phylogenetic diversity (phylogenetic Hill number). Default is "PD".

Value

- `$DataInfo`: A dataframe summarizing data information

- `$iNextEst`: coverage-based diversity estimates along with confidence intervals (if nboot > 0) for showing diversity estimates for rarefied and extrapolated samples along with related statistics;

- `$AsyEst`: for showing asymptotic diversity estimates along with related statistics.

References

Chao, A., Chiu C.-H. and Jost, L. (2010). Phylogenetic diversity measures based on Hill numbers. *Philosophical Transactions of the Royal Society B.*, 365, 3599-3609.

Chao, A., Chiu, C.-H., Hsieh, T. C., Davis, T., Nipperess, D., and Faith, D. (2015). Rarefaction and extrapolation of phylogenetic diversity. *Methods in Ecology and Evolution*, 6, 380-388.

Chao, A., Chiu C.-H. and Jost L. (2016). Phylogenetic diversity measures and their decomposition: a framework based on Hill numbers. pp. 141-172 in Pellens R. and Grandcolas P. (eds) *Biodiversity Conservation and Phylogenetic Systematics: Preserving our Evolutionary Heritage in an Extinction Crisis*, Springer.

Hsieh, T. C. and Chao, A. (2017). Rarefaction and extrapolation: making fair comparison of abundance-sensitive phylogenetic diversity among multiple assemblages. *Systematic Biology*, 66, 100-111.

Examples

```
## Not run:
data(puerto.rico)
iNEXT.link(puerto.rico$data, diversity = 'TD', datatype="abundance")
iNEXT.link(puerto.rico$data, diversity = 'PD', datatype="abundance",
           row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)

## End(Not run)
```

---

iNEXTbeta.link	*Interpolation (rarefaction) and extrapolation of Chao et al.'s (2021) network diversity and mean network diversity Function* `iNEXTbeta.link` *Interpolation and extrapolation of Beta diversity with order q*

Description

Interpolation (rarefaction) and extrapolation of Chao et al.'s (2021) network diversity and mean network diversity Function `iNEXTbeta.link` Interpolation and extrapolation of Beta diversity with order q

Usage

```
iNEXTbeta.link(
  data,
  diversity = "TD",
  level = seq(0.5, 1, 0.5),
  datatype = c("abundance", "incidence_raw"),
  q = c(0, 1, 2),
  nboot = 20,
  conf = 0.95,
  row.tree = NULL,
  col.tree = NULL
)
```

Arguments

data	a matrix/data.frame of species abundances (for abundance data) or species-by-site incidence raw matrix/data.frame (for incidence data).
	Abundance data: a species-by-site matrix/data.frame of species abundances. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
	Incidence raw data: species-by-site raw incidence matrix/data.frame. When there are N assemblages and thus N matrices, users must first merge the N matrices by species identity to obtain a large merged incidence matrix, where the rows of the matrix refer to all species presented in the merged data. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold.
datatype	data type of input data: individual-based abundance data (datatype = "abundance") or species by sampling-units incidence matrix (datatype = "incidence_raw").
q	a nonnegative value or sequence specifying the diversity order. Default is c(0,1,2).
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Enter 0 to skip the bootstrap procedures. Default is 50
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
type	desired diversity type: type = "PD" for Chao et al. (2010) phylogenetic diversity and type = "meanPD" for mean phylogenetic diversity (phylogenetic Hill number). Default is "PD".

Value

A list of seven lists with three-diversity and four-dissimilarity.

References

Chao, A., Chazdon, R. L., Colwell, R. K. and Shen, T.-J.(2005). A new statistical approach for assessing similarity of species composition with incidence and abundance data. Ecology Letters 8, 148-159. (pdf file) Spanish translation in pp. 85-96 of Halffter, G. Soberon, J., Koleff, P. and Melic, A. (eds) 2005 Sobre Diversidad Biologica: el Sognificado de las Diversidades Alfa, Beta y Gamma. m3m-Monografias 3ercer Milenio, vol. 4, SEA, CONABIO, Grupo DIVERSITAS & CONACYT, Zaragoza. IV +242 pp. Chiu, C.-H., Jost, L. and Chao*, A. (2014). Phylogenetic beta diversity, similarity, and differentiation measures based on Hill numbers. Ecological Monographs 84, 21-44.

Examples

```
## Not run:
# example
data(puerto.rico)
beta1 = iNEXTbeta.link(data = puerto.rico$data, level = seq(0.5, 0.9, 0.4), datatype='abundance',q = c(0, 1, 2)
                       diversity = 'TD', nboot = 10, conf = 0.95)
beta2 = iNEXTbeta.link(networks = puerto.rico$data, level = seq(0.5, 0.9, 0.4), datatype='abundance',q = c(0, 1
                       data = 'PD', nboot = 10, conf = 0.95,
                       row.tree = puerto.rico$row.tree, col.tree = puerto.rico$col.tree)

## End(Not run)
```

Obs.link   *Empirical diversity q profile*

Description

`Obs.link` The estimated and empirical diversity of order q

Usage

```
Obs.link(
  data,
  diversity = "TD",
  q = seq(0, 2, 0.2),
  datatype = "abundance",
  nboot = 50,
  conf = 0.95,
  col.tree = NULL,
  row.tree = NULL
)
```

Arguments

data	a matrix/data.frame of species abundances (for abundance data) or species-by-site incidence raw matrix/data.frame (for incidence data). Abundance data: a species-by-site matrix/data.frame of species abundances. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing. Incidence raw data: species-by-site raw incidence matrix/data.frame. When there are N assemblages and thus N matrices, users must first merge the N matrices by species identity to obtain a large merged incidence matrix, where the rows of the matrix refer to all species presented in the merged data. The row (species) names of data must match the species names in the phylogenetic tree and thus cannot be missing.
diversity	a choice of three-level diversity: 'TD' = 'Taxonomic', 'PD' = 'Phylogenetic', and 'FD' = 'Functional' under certain threshold.
q	a nonnegative value or sequence specifying the diversity order. Default is `c(0,1,2)`. Enter 0 to skip the bootstrap procedures. Default is 50.
datatype	data type of input data: individual-based abundance data (`datatype = "abundance"`) or species by sampling-units incidence matrix (`datatype = "incidence_raw"`).
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
col.tree	phylogenetic tree of column assemblage in interaction matrix
row.tree	phylogenetic tree of row assemblage in interaction matrix.

Value

a table of Empirical network diversity q profile

Examples

```
## Not run:
## Example for abundance-based data
## Ex.1
data(Norfolk)
out1 <- Obs.link(Norfolk, diversity = 'TD', datatype = "abundance", nboot = 30)
ggObs.link(out1)
## Ex.2
data(puerto.rico)
out2 <- Obs.link(data = puerto.rico$data, diversity = 'PD', datatype = "abundance",
ggObs.link(out2)

## End(Not run)
```

SC.link   *Sample Completeness main function*

Description

`SC.link` Estimation of Sample Completeness with order q

Usage

```
SC.link(
  data,
  q = seq(0, 2, 0.2),
  datatype = "abundance",
  nboot = 30,
  conf = 0.95
)
```

Arguments

data	a matrix/data.frame/list/vector of abundances-based/incidences-based species data.
q	a integer vector for the order of Hill number
datatype	data type of input data: individual-based abundance data (`datatype = "abundance"`) or species by sampling-units incidence matrix (`datatype = "incidence_raw"`).#'
nboot	a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Enter 0 to skip the bootstrap procedures. Default is 50
conf	positive number < 1 specifying the level of confidence interval, default is 0.95.

Value

a matrix of estimated sample completeness with order q:

References

Chao,A.,Y.Kubota,D.Zelený,C.-H.Chiu. Quantifying sample completeness and comparing diversities among assemblages.

Examples

```
data(Norfolk)
output = SC.link(Norfolk)
ggSC.link(output)
```

Spec.link   *Specialization Estimation of Evenness with order q*

Description

`Spec.link` computes Evenness Estimation of Evenness with order q.

Usage

```
Spec.link(
  data,
  q = seq(0, 2, 0.2),
  diversity = "TD",
  datatype = "abundance",
  method = "Estimated",
  nboot = 30,
  conf = 0.95,
  E.class = c(1:5),
  C = NULL
)
```

Arguments

outcome   the outcome of the functions ObsND .

Value

A list of estimated(empirical) evenness with order q. Different lists represents different classes of Evenness. Each list is combined with order.q and sites. If "method" is estimated, then fist list will be named "C" which means the maximum standardized coverage between all double reference sample size.

Examples

```
## Not run:
data(Norfolk)
Est <- Spec.link(x = Norfolk, datatype = "abundance", q = c(0,1,2),
nboot = 30, method = "Estimated")
Emp <- Spec.link(x = Norfolk, datatype = "abundance", q = c(0,1,2),
nboot = 30, method = "Empirical")
```

```
Est
Emp
ggSpec(Est)
ggSpec(Emp)

## End(Not run)
```

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