

Package ‘iNEXT.link’

June 13, 2024

Type Package

Title Network Diversity Interpolation and Extrapolation Estimation

Version 1.0.0

Author Anne Chao, Kai-Hsiang Hu, K.W. Chen, C.G. Lo, S.Y. Wang

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

URL https://chao.stat.nthu.edu.tw/wordpress/software_download/inext-link/

Description

iNEXT.link is an R package that extends the concepts of iNEXT.3D (Chao et al., 2021), iNEXT.4step (Chao et al., 2020) and iNEXT.beta3D (Chao et al., 2023) to ecological networks (Chiu et al., 2023). iNEXT.link is primarily designed to calculate and analyze various measures of diversity in ecological networks. Specifically, the package calculates three Hill numbers of order q (species richness, Shannon diversity, and Simpson diversity) in taxonomic diversity level, as well as phylogenetic and functional diversity levels. For single ecological networks, iNEXT.link provides tools for analyzing diversity. The package provides two types of rarefaction and extrapolation (R/E) sampling curves to estimate diversity and confidence intervals for single ecological networks. These include sample-size-based (or size-based) R/E curves and coverage-based R/E curves. Moreover, iNEXT.link offers dissimilarity-turnover curves for the coverage-based R/E curves for gamma, alpha, and beta diversity measures, which can be used to compare diversity patterns across different ecological networks.

License GPL (≥ 3)

Suggests knitr,
rmarkdown,
ggpubr

Imports tidyverse,
magrittr,
abind,
phytools,
Rcpp,
dplyr,
ggplot2,
colorRamps,
tidyr,
tidytree,
tibble,
stats,
ape,

```
sets,
phyclust,
future.apply,
future,
reshape2,
utils,
iNEXT.3D,
iNEXT.4steps,
iNEXT.beta3D,
ade4

Encoding UTF-8
LazyData true
RoxygenNote 7.2.3
Remotes AnneChao/iNEXT.3D, AnneChao/iNEXT.4steps, AnneChao/iNEXT.beta3D
VignetteBuilder knitr
ByteCompile true
```

R topics documented:

iNEXT.link-package	2
Completeness.link	4
DataInfo.link	5
estimatedD.link	6
ggCompleteness.link	9
ggiNEXT.link	9
ggiNEXTbeta.link	10
ggObsAsy.link	11
ggSpec.link	12
iNEXT.link	13
iNEXTbeta.link	15
ObsAsy.link	18
Spec.link	20
Index	22

iNEXT.link-package	<i>Network diversity iNterpolation/Extrapolation Estimation</i>
--------------------	-----------------------------------------------------------------

Description

iNEXT.link is an R package that extends the concepts of iNEXT.3D (Chao et al., 2021), iNEXT.4step (Chao et al., 2020) and iNEXT.beta3D (Chao et al., 2023) to ecological networks (Chiu et al., 2023).

iNEXT.link is primarily designed to calculate and analyze various measures of diversity in ecological networks. Specifically, the package calculates three Hill numbers of order q (species richness, Shannon diversity, and Simpson diversity) in taxonomic diversity level, as well as phylogenetic and functional diversity levels.

For single ecological networks, iNEXT.link provides tools for analyzing diversity. The package provides two types of rarefaction and extrapolation (R/E) sampling curves to estimate diversity

and confidence intervals for single ecological networks. These include sample-size-based (or size-based) R/E curves and coverage-based R/E curves.

Moreover, `iNEXT.link` offers dissimilarity-turnover curves for the coverage-based R/E curves for gamma, alpha, and beta diversity measures, which can be used to compare diversity patterns across different ecological networks.

This package contains twelve main functions:

**** Functions for Single community ****

1. `iNEXT.link`: Computes rarefaction/extrapolation taxonomic, phylogenetic, and functional diversity estimates and sample coverage estimates.
2. `DataInfo.link`: exhibits basic data information
3. `estimatedD.link`: computes species diversity with a particular user-specified level of sample size or sample coverage.
4. `A0.link`: compute asymptotic or empirical(observed) diversity of order q .
5. `Completeness.link`: Calculates estimated sample completeness with order q .
6. `Spec.link`: Computes standardized specialization estimation under specified sample coverage(or observed) with order q .

**** Function for Multi-community ****

7. `iNEXTbeta.link`: Computing standardized gamma, alpha, beta diversity, and four dissimilarity-turnover indices for three dimensions: taxonomic, phylogenetic and functional diversity at specified sample coverage.

**** Functions for Visualizing Results ****

8. `ggCompleteness.link`: Visualizing the output from the function `Completeness.link`
9. `ggSpec.link`: Visualizing the output from the function `Spec.link`
10. `ggA0.link`: Visualizing the output from the function `A0.link`
11. `ggiNEXT.link`: Visualizing the output from the function `iNEXT.link`
12. `ggiNEXTbeta.link`: Visualizing the output from the function `iNEXTbeta.link`

An Online version of `iNEXT.link` is also available for users without an R background:
https://chao.shinyapps.io/iNEXT_link/.

In the detailed Online `iNEXT.link` User's Guide, we illustrate all the running procedures in an easily accessible way through numerical examples with proper interpretations of portions of the output. All the data of those illustrative examples are included in this package.

Author(s)

Anne Chao, K.H. Hu

Maintainer: K.H. Hu <river19951224@gmail.com>

References

Chao, A., Henderson, P. A., Chiu, C.-H., Moyes, F., Hu, K.-H., Dornelas, M and Magurran, A. E. (2021). Measuring temporal change in alpha diversity: a framework integrating taxonomic, phylogenetic and functional diversity and the `iNEXT.3D` standardization. *Methods in Ecology and Evolution*, 12, 1926-1940.

Chao, A., Thorn, S., Chiu, C.-H., Moyes, F., Hu, K.-H., Chazdon, R. L., Wu, J., Dornelas, M., Zeleny, D., Colwell, R. K., and Magurran, A. E. (2023). Rarefaction and extrapolation with beta diversity under a framework of Hill numbers: the iNEXT.beta3D standardization. To appear in Ecological Monographs.

Chao, A., Y. Kubota, D. Zeleny, C.-H. Chiu, C.-F. Li, B. Kusumoto, M. Yasuhara, S. Thorn, C.-L. Wei, M. J. Costello, and R. K. Colwell (2020). Quantifying sample completeness and comparing diversities among assemblages. Ecological Research, 35, 292-314.

Chiu, C.-H., Chao, A., Vogel, S., Kriegel, P. and Thorn, S. (2023). Quantifying and estimating ecological network diversity based on incomplete sampling data. Philosophical Transactions of the Royal Society B, 378: 20220183. <https://doi.org/10.1098/rstb.2022.0183>.

Completeness.link	<i>Sample Completeness main function</i>
-------------------	------------------------------------------

Description

Completeness.link Estimation of Sample Completeness with order q

Usage

```
Completeness.link(data, q = seq(0, 2, 0.2), nboot = 30, conf = 0.95)
```

Arguments

data	a list of data.frames, each data.frames represents col.species-by-row.species abundance matrix.
q	q a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
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 30.
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.

Value

a matrix of estimated sample completeness with order q:

Order.q	the diversity order of q.
Estimate.SC	the estimated (or observed) sample completeness of order q.
s.e.	standard error of sample completeness.
SC.LCL, SC.UCL	the bootstrap lower and upper confidence limits for the sample completeness of order q at the specified level (with a default value of 0.95).
Assemblage	the assemblage name.

References

Chao, A., Y. Kubota, D. Zelen??, C.-H. Chiu, C.-F. Li, B. Kusumoto, M. Yasuhara, S. Thorn, C.-L. Wei, M. J. Costello, and R. K. Colwell (2020). Quantifying sample completeness and comparing diversities among assemblages. *Ecological Research*, 35, 292-314.

Examples

```
data(beetles)
output = Completeness.link(beetles)
output
```

DataInfo.link	<i>Exhibit basic data information</i>
---------------	---------------------------------------

Description

DataInfo.link: exhibits basic data information

Usage

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

Arguments

data	a list of data.frames, each data.frames represents col.species-by-row.species abundance matrix.
diversity	selection of diversity type: 'TD' = 'Taxonomic diversity', 'PD' = 'Phylogenetic diversity', and 'FD' = 'Functional diversity'.
row.tree	(required only when diversity = "PD"), a phylogenetic tree of row assemblage in the pooled network row assemblage.
col.tree	(required only when diversity = "PD"), a phylogenetic tree of column assemblage in the pooled network column assemblage.
row.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of row assemblage in the pooled network row assemblage.
col.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of column assemblage in the pooled network column assemblage.

Value

a data.frame of basic data information including network name (Networks), sample size (n), observed species richness in row assemblage (S.obs(row)), observed species richness in column assemblage (S.obs(col)), the number of interactions (Link.obs), link percentage(Connectance), sample coverage estimate (Coverage).

Besides, show the first ten species abundance (or incidence) frequency counts in the reference sample in TD. (f1-f10)

In PD, show the the observed total branch length in the phylogenetic tree (PD.obs), the number of singletons and doubletons in the node/branch set (f1*-f2*), the total branch length of those singletons/doubletons in the node/branch set (g1-g2), mean reference time (mean_T).

In FD (FDtype = "tau_values"), show the number of singletons and doubletons in the data (f1-f2), the number of singletons and doubletons in the functional group (a1*-a2*), the threshold of functional distinctiveness between any two species (threshold).

Examples

```
#' ## Taxonomic diversity
data(beetles)
DataInfo.link(data = beetles, diversity = 'TD')

## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
DataInfo.link(data = beetles, diversity = 'PD', col.tree = beetles_col_tree)

## Functional diversity
data(beetles)
data(beetles_col_distM)
DataInfo.link(data = beetles, diversity = 'FD', col.distM = beetles_col_distM)
```

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),
  base = "coverage",
```

```

    level = NULL,
    nboot = 50,
    conf = 0.95,
    row.tree = NULL,
    col.tree = NULL,
    PDtype = "meanPD",
    row.distM = NULL,
    col.distM = NULL,
    FDtype = "AUC",
    FDtau = 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.
q	a numerical vector of the order of Hill number. Default is seq(0, 2, 0.2).
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.
PDtype	(required only when diversity = "PD"), select PD type: PDtype = "PD" (effective total branch length) or PDtype = "meanPD" (effective number of equally divergent lineages). Default is "meanPD".
row.distM	(required only when diversity = "FD"), a row species pairwise distance matrix for all row species of row assemblage in interaction matrix.
col.distM	(required only when diversity = "FD"), a column species pairwise distance matrix for all column species of column assemblage in interaction matrix.
FDtype	(required only when diversity = "FD"), select FD type: FDtype = "tau_values" for FD under specified threshold values, or FDtype = "AUC" (area under the curve of tau-profile) for an overall FD which integrates all threshold values between zero and one. Default is "AUC".
FDtau	(required only when diversity = "FD" and FDtype = "tau_values"), 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).

Value

a data.frame of diversity table including the following arguments:

Assemblage	the assemblage name.
m	the corresponding sample size for the standardized coverage value.
Method	Rarefaction, Observed, or Extrapolation, depending on whether the target coverage is less than, equal to, or greater than the coverage of the reference sample.
Order.q	the diversity order of q.
SC	the target standardized coverage value.
qTD, qPD, qFD	the estimated diversity of order q for the target coverage value. The estimate for complete coverage (or level = 1) represents the estimated asymptotic diversity.
s.e.	standard error of diversity estimate.
qTD.LCL, qPD.LCL, qFD.LCL and qTD.UCL, qPD.UCL, qFD.UCL	the bootstrap lower and upper confidence limits for the diversity of order q at the specified level (with a default value of 0.95).
Reftime	reference times for PD.
Type	"PD" (effective total branch length) or "meanPD" (effective number of equally divergent lineages).
Tau	the threshold of functional distinctiveness between any two species.

Examples

```
## Taxonomic diversity
data(beetles)
output1 <- estimateD.link(beetles, diversity = 'TD',
                          base = "coverage", level = 0.7, nboot = 30)
output1

## Phylogenetic diversity
output2 <- estimateD.link(beetles, diversity = 'PD',
                          base = "size", level = NULL, nboot = 30, col.tree = beetles_col_tree)
output2

## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = estimateD.link(data = beetles, diversity = 'FD', col.distM = beetles_col_distM, FDtype = "tau_values")
output3

## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = estimateD.link(data = beetles, diversity = 'FD',
                          col.distM = beetles_col_distM, FDtype = "AUC", nboot = 0)
output4
```

ggCompleteness.link *ggplot for Sample Completeness*

Description

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

Usage

```
ggCompleteness.link(output)
```

Arguments

output a table generated from Completeness.link function

Value

a figure of estimated sample completeness with order q

References

Chao, A., Y. Kubota, D. Zelen??, C.-H. Chiu, C.-F. Li, B. Kusumoto, M. Yasuhara, S. Thorn, C.-L. Wei, M. J. Costello, and R. K. Colwell (2020). Quantifying sample completeness and comparing diversities among assemblages. Ecological Research, 35, 292-314.

Examples

```
data(beetles)
output = Completeness.link(beetles)
ggCompleteness.link(output)
```

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

Description

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

Usage

```
ggiNEXT.link(
  output,
  type = c(1, 2, 3),
  facet.var = "Assemblage",
  color.var = "Order.q"
)
```

Arguments

output	a list object computed by iNEXT.link .
type	three types of plots: sample-size-based rarefaction/extrapolation curve (type = 1); sample coverage curve (type = 2); coverage-based rarefaction/extrapolation curve (type = 3).
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").

Value

a ggplot2 object for coverage-based or size-based rarefaction and extrapolation

Examples

```
## Taxonomic diversity
data(beetles)
output1 = iNEXT.link(data = beetles, diversity = 'TD', q = c(0,1,2))
ggiNEXT.link(output1)
```

```
## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = iNEXT.link(data = beetles, diversity = 'PD', q = c(0,1,2), col.tree = beetles_col_tree)
ggiNEXT.link(output2)
```

```
## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = iNEXT.link(data = beetles, diversity = 'FD', q = c(0,1,2), nboot = 0, col.distM = beetles_col_distM, F)
ggiNEXT.link(output3)
```

```
## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = iNEXT.link(data = beetles, diversity = 'FD', q = c(0,1,2), nboot = 0, col.distM = beetles_col_distM, F)
ggiNEXT.link(output4)
```

ggiNEXTbeta.link

ggplot2 extension for output from iNEXTbeta.link

Description

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

Usage

```
ggiNEXTbeta.link(output, type = c("B", "D"))
```

Arguments

output	the output 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.

Value

a figure for gamma, alpha, and beta diversity or four dissimilarity measures.

Examples

```
## Taxonomic diversity
data(beetles)
output1 = iNEXTbeta.link(data = beetles, diversity = 'TD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2))
ggiNEXTbeta.link(output1, type = 'B')
ggiNEXTbeta.link(output1, type = 'D')

## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = iNEXTbeta.link(data = beetles, diversity = 'PD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.tree =
ggiNEXTbeta.link(output2, type = 'B')
ggiNEXTbeta.link(output2, type = 'D')

## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = iNEXTbeta.link(data = beetles, diversity = 'FD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.distM =
ggiNEXTbeta.link(output3, type = 'B')
ggiNEXTbeta.link(output3, type = 'D')

## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = iNEXTbeta.link(data = beetles, diversity = 'FD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.distM =
ggiNEXTbeta.link(output4, type = 'B')
ggiNEXTbeta.link(output4, type = 'D')
```

Description

ggObsAsy.link Plots q-profile based on the output of ObsAsy.link using the ggplot2 package.

Usage

```
ggObsAsy.link(output)
```

Arguments

output the output of the functions `ObsAsy.link` .

Value

a figure of asymptotic or empirical (observed) diversity in q-profile.

Examples

```
## Taxonomic diversity
data(beetles)
output1 = ObsAsy.link(data = beetles, diversity = 'TD', q = seq(0, 2, 0.2))
ggObsAsy.link(output1)
```

```
## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = ObsAsy.link(data = beetles, diversity = 'PD', q = seq(0, 2, 0.2), col.tree = beetles_col_tree)
ggObsAsy.link(output2)
```

```
## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = ObsAsy.link(data = beetles, diversity = 'FD', q = seq(0, 2, 0.2), col.distM = beetles_col_distM, FDtype = 'single')
ggObsAsy.link(output3)
```

```
## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = ObsAsy.link(data = beetles, diversity = 'FD', q = seq(0, 2, 0.25), col.distM = beetles_col_distM, FDtype = 'integrated')
ggObsAsy.link(output4)
```

ggSpec.link

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

Description

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

Usage

```
ggSpec.link(output)
```

Arguments

output a table generated from Specialization function

Value

a figure of estimated sample completeness with order q

Examples

```
data(beetles)
output = Spec.link(beetles)
ggSpec.link(output)
```

iNEXT.link	<i>Interpolation (rarefaction) and extrapolation of network diversity</i>
------------	---------------------------------------------------------------------------

Description

Interpolation (rarefaction) and extrapolation of network diversity

Usage

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

Arguments

data	a list of data.frames, each data.frames represents col.species-by-row.species abundance matrix.
diversity	selection of diversity type: 'TD' = 'Taxonomic diversity', 'PD' = 'Phylogenetic diversity', and 'FD' = 'Functional diversity'.
q	a numerical vector specifying the diversity orders. Default is c(0, 1, 2).
size	an integer vector of sample sizes for which diversity estimates will be computed. If NULL, then diversity estimates will be calculated for those sample sizes determined by the specified/default endpoint and knots.

endpoint	an integer vector specifying the sample size that is the endpoint for rarefaction/extrapolation. If NULL, then endpoint = double reference sample size in each assemblage.
knots	an integer specifying the number of equally-spaced knots between size 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. Bootstrap replications are generally time consuming. Enter 0 to skip the bootstrap procedures. Default is 30.
row.tree	(required only when diversity = "PD"), a phylogenetic tree of row assemblage in the pooled network row assemblage.
col.tree	(required only when diversity = "PD"), a phylogenetic tree of column assemblage in the pooled network column assemblage.
PDtype	(required only when diversity = "PD"), select PD type: PDtype = "PD"(effective total branch length) or PDtype = "meanPD"(effective number of equally divergent lineages).Default is "meanPD".
row.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of row assemblage in the pooled network row assemblage.
col.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of column assemblage in the pooled network column assemblage.
FDtype	(required only when diversity = "FD"), select FD type: FDtype = "tau_values" for FD under specified threshold values, or FDtype = "AUC" (area under the curve of tau-profile) for an overall FD which integrates all threshold values between zero and one. Default is "AUC".
FDtau	(required only when diversity = "FD" and FDtype = "tau_values"), 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).

Value

- \$DataInfo: A dataframe summarizing data information
- \$iNextEst: coverage-based diversity estimates along with confidence intervals for showing diversity estimates for rarefied and extrapolated samples along with related statistics;
- \$AsyEst: for showing asymptotic diversity estimates along with related statistics.

a list of three objects: \$DataInfo (or \$PDInfo, \$FDInfo, \$AUCInfo) for summarizing data information; \$iNextEst (or \$PDiNextEst, \$FDiNextEst, \$AUCiNextEst) for showing diversity estimates for rarefied and extrapolated samples along with related statistics; and \$AsyEst (or \$PDAsyEst, \$FDAsyEst, \$AUCAsyEst) 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

```
## Taxonomic diversity
data(beetles)
output1 = iNEXT.link(data = beetles, diversity = 'TD', q = c(0,1,2))
output1$TDInfo # showing basic data information.
output1$TDiNextEst # showing diversity estimates with rarefied and extrapolated.
output1$TDAsyEst # showing asymptotic diversity estimates.

## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = iNEXT.link(data = beetles, diversity = 'PD', q = c(0,1,2), col.tree = beetles_col_tree)
output2

## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = iNEXT.link(data = beetles, diversity = 'FD', q = c(0,1,2), nboot = 0, col.distM = beetles_col_distM, F
output3

## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = iNEXT.link(data = beetles, diversity = 'FD', q = c(0,1,2), nboot = 0, col.distM = beetles_col_distM, F
output4
```

iNEXTbeta.link	<i>Interpolation (rarefaction) and extrapolation of network beta diversity Function iNEXTbeta.link Interpolation and extrapolation of beta di- versity with order q</i>
----------------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Description

Interpolation (rarefaction) and extrapolation of network beta diversity Function iNEXTbeta.link
Interpolation and extrapolation of beta diversity with order q

Usage

```
iNEXTbeta.link(
  data,
  diversity = "TD",
  level = seq(0.5, 1, 0.05),
  q = c(0, 1, 2),
  nboot = 20,
  conf = 0.95,
  row.tree = NULL,
  col.tree = NULL,
  PDtype = "meanPD",
  row.distM = NULL,
  col.distM = NULL,
  FDtype = "AUC",
  FDtau = NULL,
  FDcut_number = 30
)
```

Arguments

<code>data</code>	data can be input as a list of data.frame, each data.frame represents col.species-by-row.species abundance matrix; see example 1 for an example.
<code>diversity</code>	selection of diversity type: 'TD' = 'Taxonomic diversity', 'PD' = 'Phylogenetic diversity', and 'FD' = 'Functional diversity'.
<code>level</code>	a sequence specifying the particular sample coverages (between 0 and 1). Default is seq(0.5, 1, 0.05).
<code>q</code>	a numerical vector specifying the diversity orders. Default is c(0, 1, 2).
<code>nboot</code>	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 30.
<code>conf</code>	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
<code>row.tree</code>	(required only when diversity = "PD"), a phylogenetic tree of row assemblage in the pooled network row assemblage.
<code>col.tree</code>	(required only when diversity = "PD"), a phylogenetic tree of column assemblage in the pooled network column assemblage.
<code>PDtype</code>	(required only when diversity = "PD"), select PD type: PDtype = "PD"(effective total branch length) or PDtype = "meanPD"(effective number of equally divergent lineages).Default is "meanPD".
<code>row.distM</code>	(required only when diversity = "FD"), a species pairwise distance matrix for all species of row assemblage in the pooled network row assemblage.
<code>col.distM</code>	(required only when diversity = "FD"), a species pairwise distance matrix for all species of column assemblage in the pooled network column assemblage.
<code>FDtype</code>	(required only when diversity = "FD"), select FD type: FDtype = "tau_values" for FD under specified threshold values, or FDtype = "AUC" (area under the curve of tau-profile) for an overall FD which integrates all threshold values between zero and one. Default is "AUC".

FDtau	(required only when diversity = "FD" and FDtype = "tau_value"), 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).
FDcut_number	(required only when diversity = "FD" and FDtype = "AUC"), a numeric number to split zero to one into several equal-spaced length. Default is 30.

Value

A list of seven matrices with three diversity dimensions and four dissimilarity measures.

Dataset	the datasets name.
Order.q	the diversity order of q.
SC	the target standardized coverage value. The observed coverage and extrapolation limit for beta diversity are defined the same as those for alpha diversity. For $q = 0$, the extrapolation can be extended to a maximum coverage value $C(2n, \alpha) = \text{coverage value of twice the alpha reference sample size}$; for $q = 1$ and 2, target coverage can be extended to 1 (complete coverage) if data are not sparse.
Size	the corresponding sample size for the standardized coverage value.
Alpha/Beta/Gamma/Dissimilarity	the estimated diversity or dissimilarity of order q for the target coverage value. The estimate for complete coverage (or level = 1) represents the estimated asymptotic diversity.
Method	Rarefaction, Observed, or Extrapolation, depending on whether the target coverage is less than, equal to, or greater than the coverage of the reference sample. (For beta diversity, observed coverage is defined as the coverage of the alpha reference sample).
s.e.	standard error of diversity estimate.
LCL, UCL	the bootstrap lower and upper confidence limits for the diversity of order q at the specified level (with a default value of 0.95).
Diversity	"TD" (taxonomic diversity), "PD" (phylogenetic diversity of effective total branch length), "meanPD" (phylogenetic diversity of effective number of equally divergent lineages), "FD_tau" (functional diversity under a single tau), "FD_AUC" (functional diversity by integrating all threshold values between zero and one).
Tau	the threshold of functional distinctiveness between any two species.

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 3er 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. Chao, A., Thorn, S., Chiu, C.-H., Moyes, F., Hu, K.-H., Chazdon, R. L., Wu, J., Dornelas, M., Zelen??, D., Colwell, R. K., and Magurran, A. E. (2023). Rarefaction and extrapolation with beta diversity under a framework of Hill numbers: the iNEXT.beta3D standardization. To appear in *Ecological Monographs*.

Examples

```
## Taxonomic diversity
data(beetles)
output1 = iNEXTbeta.link(data = beetles, diversity = 'TD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2))
output1

## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = iNEXTbeta.link(data = beetles, diversity = 'PD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.tree =
output2

## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = iNEXTbeta.link(data = beetles, diversity = 'FD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.distM
output3

## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = iNEXTbeta.link(data = beetles, diversity = 'FD', level = seq(0.5, 0.9, 0.4), q = c(0, 1, 2), col.distM
output4
```

ObsAsy.link

Asymptotic and Observed diversity q profile

Description

ObsAsy.link: The asymptotic (or observed) diversity of order q

Usage

```
ObsAsy.link(
  data,
  diversity = "TD",
  q = seq(0, 2, 0.2),
  nboot = 30,
  conf = 0.95,
  method = c("Asymptotic", "Observed"),
  row.tree = NULL,
  col.tree = NULL,
  PDtype = "meanPD",
  row.distM = NULL,
  col.distM = NULL,
  FDtype = "AUC",
  FDtau = NULL
)
```

Arguments

data	a list of data.frames, each data.frames represents col.species-by-row.species abundance matrix.
diversity	selection of diversity type: 'TD' = Taxonomic diversity, 'PD' = Phylogenetic diversity, and 'FD' = Functional diversity.
q	a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
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 30.
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
method	asymptotic or Observed
row.tree	(required only when diversity = "PD"), a phylogenetic tree of row assemblage in the pooled network row assemblage.
col.tree	(required only when diversity = "PD"), a phylogenetic tree of column assemblage in the pooled network column assemblage.
PDtype	(required only when diversity = "PD"), select PD type: PDtype = "PD"(effective total branch length) or PDtype = "meanPD"(effective number of equally divergent lineages).Default is "meanPD".
row.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of row assemblage in the pooled network row assemblage.
col.distM	(required only when diversity = "FD"), a species pairwise distance matrix for all species of column assemblage in the pooled network column assemblage.
FDtype	(required only when diversity = "FD"), select FD type: FDtype = "tau_values" for FD under specified threshold values, or FDtype = "AUC" (area under the curve of tau-profile) for an overall FD which integrates all threshold values between zero and one. Default is "AUC".
FDtau	(required only when diversity = "FD" and FDtype = "tau_values"), 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).

Value

a table of diversity table including the following arguments.	
Order.q	the diversity order of q.
qTD, qPD, qFD	the estimated asymptotic diversity or observed diversity of order q.
s.e.	standard error of diversity.
qTD.LCL, qPD.LCL, qFD.LCL and qTD.UCL, qPD.UCL, qFD.UCL	the bootstrap lower and upper confidence limits for the diversity of order q at the specified level (with a default value of 0.95).
Assemblage (or Network)	the network name.
Method	"Asymptotic" means asymptotic diversity and "Observed" means observed diversity.

Reftime	the reference times for PD.
Type	"PD" (effective total branch length) or "meanPD" (effective number of equally divergent lineages) for PD.
Tau	the threshold of functional distinctiveness between any two species for FD (under FDtype = tau_values).

Examples

```
## Taxonomic diversity
data(beetles)
output1 = ObsAsy.link(data = beetles, diversity = 'TD', q = seq(0, 2, 0.2))
output1

## Phylogenetic diversity
data(beetles)
data(beetles_col_tree)
output2 = ObsAsy.link(data = beetles, diversity = 'PD', q = seq(0, 2, 0.2), col.tree = beetles_col_tree)
output2

## Functional diversity under single threshold
data(beetles)
data(beetles_col_distM)
output3 = ObsAsy.link(data = beetles, diversity = 'FD', q = seq(0, 2, 0.2), col.distM = beetles_col_distM, FDtype = "AUC")
output3

## Functional diversity with thresholds integrating from 0 to 1
data(beetles)
data(beetles_col_distM)
output4 = ObsAsy.link(data = beetles, diversity = 'FD', q = seq(0, 2, 0.25),
                      col.distM = beetles_col_distM, FDtype = "AUC", nboot = 0)
output4
```

Spec.link	<i>Standardized estimation (or observed) of specialization with order q</i>
-----------	-----------------------------------------------------------------------------

Description

Standardized estimation (or observed) of specialization with order q

Usage

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

Arguments

data	a list of data.frames, each data.frames represents col.species-by-row.species abundance matrix.
q	a numerical vector specifying the diversity orders. Default is seq(0, 2, 0.2).
method	a binary calculation method with "Estimated" or "Observed".
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 30.
conf	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
E.class	an integer vector between 1 to 5.
SC	a standardized coverage for calculating specialization index. It is used when method = 'Estimated'. If NULL, then this function computes the diversity estimates for the minimum sample coverage among all samples extrapolated to double reference sizes (C = Cmax).

Value

A list of several tables containing estimated (or observed) evenness with order q. Each tables represents a class of specialization.

Order.q	the diversity order of q.
Specialization	the specialization of order q.
s.e.	standard error of evenness.
Spec.LCL, Spec.UCL	the bootstrap lower and upper confidence limits for the evenness of order q at the specified level (with a default value of 0.95).
Method	"Estimated" or "Observed".
SC	the target standardized coverage value. (only when method = "Estimated")
Network	the network name.
class	specialization class.

Examples

```
data(beetles)
output = Spec.link(beetles)
output
```

Index

- * **package**
 - iNEXT.link-package, [2](#)
- Completeness.link, [4](#)
- DataInfo.link, [5](#)
- estimateD.link, [6](#)
- ggCompleteness.link, [9](#)
- ggiNEXT.link, [9](#)
- ggiNEXTbeta.link, [10](#)
- ggObsAsy.link, [11](#)
- ggplot, [9](#)
- ggSpec.link, [12](#)
- iNEXT.link, [9](#), [10](#), [13](#)
- iNEXT.link-package, [2](#)
- iNEXTbeta.link, [15](#)
- ObsAsy.link, [18](#)
- Spec.link, [20](#)