An Introduction to iNEXT.beta3D via Examples

Anne Chao and Kai-Hsiang Hu

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The package `iNEXT.beta3D` (iNterpolation and EXTrapolation with beta diversity for three dimensions of biodiversity) is a sequel to `iNEXT`. The three dimensions (3D) of biodiversity include taxonomic diversity (TD), phylogenetic diversity (PD) and functional diversity (FD). This document provides an introduction demonstrating how to run `iNEXT.beta3D`. An online version iNEXT.beta3D Online is also available for users without an R background.

A unified framework based on Hill numbers and their generalizations is adopted to quantify TD, PD and FD. TD quantifies the effective number of species, mean-PD (PD divided by tree depth) quantifies the effective number of lineages, and FD quantifies the effective number of virtual functional groups (or functional "species"). Thus, TD, mean-PD, and FD are all in the same units of species/lineage equivalents and can be meaningfully compared; see Chao et al. (2021) for a review of the unified framework.

For each of the three dimensions, `iNEXT.beta3D` focuses on the multiplicative diversity decomposition (alpha, beta and gamma) of orders q = 0, 1 and 2 based on sampling data. Beta diversity quantifies the extent of among-assemblage differentiation, or the changes in species/lineages/functional-groups composition and abundance among assemblages. `iNEXT.beta3D` features standardized 3D estimates with a common sample size (for alpha and gamma diversity) or sample coverage (for alpha, beta and gamma diversity). `iNEXT.beta3D` also features coverage-based standardized estimates of four classes of dissimilarity measures.

Based on the rarefaction and extrapolation (R/E) method for Hill numbers (TD) of orders q = 0, 1 and 2, Chao et al. (2023b) developed the pertinent R/E theory for taxonomic beta diversity with applications to real-world spatial, temporal and spatio-temporal data. An application to Gentry's global forest data along with a concise description of the theory is provided in Chao et al. (2023a). The extension to phylogenetic and functional beta diversity is generally parallel.

The `iNEXT.beta3D` package features two types of R/E sampling curves:

1. Sample-size-based (or size-based) R/E sampling curves: This type of sampling curve plots standardized 3D gamma and alpha diversity with respect to sample size. Note that the size-based beta diversity is not a statistically valid measure (Chao et al. 2023b) and thus the corresponding sampling curve is not provided.
2. Sample-coverage-based (or coverage-based) R/E sampling curves: This type of sampling curve plots standardized 3D gamma, alpha, and beta diversity as well as four classes of dissimilarity measures with respect to sample coverage (an objective measure of sample completeness).

Sufficient data are needed to run `iNEXT.beta3D`. If your data comprise only a few species and their abundances/phylogenies/traits, it is probable that the data lack sufficient information to run `iNEXT.beta3D`.

HOW TO CITE iNEXT.beta3D

If you publish your work based on results from `iNEXT.beta3D`, you should make reference to at least one of the following methodology papers (2023a, b) and also cite the `iNEXT.beta3D` package:

- Chao, A., Chiu, C.-H., Hu, K.-H., and Zeleny, D. (2023a). Revisiting Alwyn H. Gentry's forest transect data: a statistical sampling-model-based approach. *Japanese Journal of Statistics and Data Science*, 6, 861-884. (https://doi.org/10.1007/s42081-023-00214-1)
- Chao, A., Thorn, S., Chiu, C.-H., Moyes, F., Hu, K.-H., Chazdon, R. L., Wu, J., Magnago, L. F. S., Dornelas, M., Zeleny, D., Colwell, R. K., and Magurran, A. E. (2023b). Rarefaction and extrapolation with beta diversity under a framework of Hill numbers: the iNEXT.beta3D standardization. *Ecological Monographs* e1588.(https://doi.org/10.1002/ecm.1588)
- Chao, A. and Hu, K.-H. (2023). The iNEXT.beta3D package: interpolation and extrapolation with beta diversity for three dimensions of biodiversity. R package available from CRAN.

SOFTWARE NEEDED TO RUN iNEXT.beta3D IN R

- Required: R
- Suggested: RStudio IDE

HOW TO RUN iNEXT.beta3D:

The `iNEXT.beta3D` package is available from CRAN and can be downloaded from Anne Chao's Github iNEXT.beta3D_github using the following commands. For a first-time installation, additional visualization extension package (`ggplot2` from CRAN) and relevant package (`iNEXT.3D` from CRAN) must be installed and loaded.

```
## install iNEXT.beta3D package from CRAN
```

```
install.packages("iNEXT.beta3D")

## install the latest version from github
install.packages('devtools')
library(devtools)
install_github('AnneChao/iNEXT.beta3D')

## import packages
library(iNEXT.beta3D)
```

There are three main functions in this package:

- **iNEXTbeta3D**: computes standardized 3D estimates with a common sample size (for alpha and gamma diversity) or sample coverage (for alpha, beta and gamma diversity) for default sample sizes or coverage values. This function also computes coverage-based standardized 3D estimates of four classes of dissimilarity measures for default coverage values. In addition, this function also computes standardized 3D estimates with a particular vector of user-specified sample sizes or coverage values.
- **ggiNEXTbeta3D**: Visualizes the output from the function `iNEXTbeta3D`.
- **DataInfobeta3D**: Provides basic data information for (1) the reference sample in each assemblage, (2) the gamma reference sample in the pooled assemblage, and (3) the alpha reference sample in the joint assemblage.

DATA INPUT FORMAT

To assess beta diversity among assemblages, information on shared/unique species and their abundances is required. Thus, species identity (or any unique identification code) and assemblage affiliation must be provided in the data. In any input dataset, set row name of the data to be species name (or identification code) and column name to be assemblage name. Two types of species abundance/incidence data are supported:

1. Individual-based abundance data (`datatype = "abundance"`): Input data for a single dataset with N assemblages consist of a species-by-assemblage abundance `matrix/data.frame`. Users can input several datasets which may represent data collected from various localities, regions, plots, time periods, …, etc. Input data for multiple datasets then consist of a list of matrices; each matrix represents a species-by-assemblage abundance matrix for one of the datasets. Different datasets can have different numbers of assemblages. `iNEXTbeta3D` computes beta diversity and dissimilarity among assemblages within each dataset.
2. Sampling-unit-based incidence raw data (`datatype = "incidence_raw"`): Input data for a dataset with N assemblages consist of a list of matrices/data.frames, with each matrix representing a species-by-sampling-unit incidence raw matrix for one of the N assemblages; each element in the incidence raw matrix is 1 for a detection, and 0 for a non-detection. Users can input several datasets. Input data then consist of multiple lists with each list comprising a list of species-by-sampling-unit incidence matrices; see an example below. The number of sampling units can vary with datasets (but within a dataset, the number of sampling units in each assemblage must be the same). `iNEXTbeta3D` computes beta diversity and dissimilarity among assemblages within each dataset based on incidence-based frequency counts obtained from all sampling units.

Species abundance data format

We use the tree species abundance data collected from two rainforest fragments/localities in Brazil to assess beta diversity between Edge and Interior assemblages/habitats within each fragment; see Chao et al. (2023b) for analysis details. The data (named `"Brazil_rainforests"`) consist of a list of two matrices (for two fragments named “Marim” and “Rebio2”, respectively); each matrix represents a species-by-assemblage abundance matrix, and there are two assemblages (“Edge” and “Interior”) in each fragment. The demo data are slightly different from those analyzed in Chao et al. (2023b) because seven species are removed from the original pooled data due to lack of phylogenetic information. Run the following code to view the data: (Here we only show the first 15 rows for each matrix.)

```
data(Brazil_rainforests)
Brazil_rainforests
```

```
#> $Marim
#>                            Edge Interior
#> Acosmium_lentiscifolium       1        0
#> Allophylus_petiolulatus       5        0
#> Alseis_involuta               2        0
#> Ampelocera_glabra             1        0
#> Andira_legalis                0        1
#> Andira_ormosioides            0        1
#> Apuleia_leiocarpa             1        0
#> Aspidosperma_illustre         0        3
#> Astrocaryum_aculeatissimum    1        0
#> Astronium_concinnum           4        1
#> Barnebydendron_riedelii       0        2
#> Bauhinia_forficata            1        0
#> Brosimum_glaucum              4        0
```

```
#> Calyptranthes_lucida          0        4
#> Campomanesia_lineatifolia     1        0
#>
#> $Rebio2
#>                             Edge Interior
#> Albizia_polycephala            1        0
#> Allophylus_petiolulatus        3        3
#> Alseis_involuta                1        0
#> Amaioua_intermedia             0        1
#> Ampelocera_glabra              0        3
#> Anaxagorea_silvatica           0        6
#> Annona_dolabripetala           1        0
#> Aspidosperma_cylindrocarpon    2        0
#> Astrocaryum_aculeatissimum     7        1
#> Astronium_concinnum           12        1
#> Astronium_graveolens          13        1
#> Beilschmiedia_linharensis      1        0
#> Brosimum_glaucum               2        2
#> Brosimum_sp1                   0        1
#> Calyptranthes_lucida           2        1
```

Species incidence raw data format

We use tree species data collected from two second-growth rainforests, namely Cuatro Rios (CR) and Juan Enriquez (JE) in Costa Rica, as demo data to assess temporal beta diversity between two years (2005 and 2017) within each forest. Each year is designated as an assemblage. The data in each forest were collected from a 1-ha (50 m x 200 m) forest plot. Because individual trees of some species may exhibit intra-specific aggregation within a 1 ha area, they may not be suitable for modelling as independent sampling units. In this case, it is statistically preferable to first convert species abundance records in each forest to occurrence or incidence (detection/non-detection) data in subplots/quadrats; see Chao et al. (2023b) for analysis details.

Each 1-ha forest was divided into 100 subplots (each with 0.01 ha) and only species' incidence records in each subplot were used to compute the incidence frequency for a species (i.e., the number of subplots in which that species occurred). By treating the incidence frequency of each species among subplots as a "proxy" for its abundance, the `iNEXT.beta3D` standardization can be adapted to deal with spatially aggregated data and to avoid the effect of intra-specific aggregation.

The data (named `"Second_growth_forests"`) consist of two lists (for two forests named "CR 2005 vs. 2017" and "JE 2005 vs. 2017", respectively). Each list consists of two matrices; the first matrix represents the species-by-subplot incidence data in 2005, and the second matrix represents the species-by-subplots incidence data in 2017. Run the following code to view the incidence raw data: (Here we only show the first ten rows and six columns for each matrix; there are 100 columns/subplots in each forest and each year.)

```
data(Second_growth_forests)
Second_growth_forests
```

```
#> $`CR 2005 vs. 2017`
#> $`CR 2005 vs. 2017`$Year_2005
#>        Subplot_1 Subplot_2 Subplot_3 Subplot_4 Subplot_5 Subplot_6
#> Abaade         0         0         0         0         0         0
#> Alcflo         0         0         0         0         0         0
#> Alclat         0         1         0         0         0         0
#> Aliatl         0         0         0         0         0         0
#> Ampmac         0         0         0         0         0         0
#> Anacra         0         1         0         0         0         1
#> Annama         0         1         0         0         0         0
#> Annpap         0         0         0         0         0         0
#> Apemem         0         0         0         0         0         0
#> Ardfim         0         0         0         0         0         0
#>
#> $`CR 2005 vs. 2017`$Year_2017
#>        Subplot_1 Subplot_2 Subplot_3 Subplot_4 Subplot_5 Subplot_6
#> Abaade         0         0         0         0         0         0
#> Alcflo         0         0         0         0         0         0
#> Alclat         0         1         0         0         0         0
#> Aliatl         0         0         0         0         0         0
#> Ampmac         0         0         0         0         0         0
#> Anacra         0         1         1         0         1         1
#> Annama         0         0         0         0         0         0
#> Annpap         0         0         0         0         0         0
#> Apemem         0         0         0         0         0         0
#> Ardfim         0         0         0         0         0         0
#>
#>
#> $`JE 2005 vs. 2017`
#> $`JE 2005 vs. 2017`$Year_2005
#>        Subplot_1 Subplot_2 Subplot_3 Subplot_4 Subplot_5 Subplot_6
#> Alccos         0         0         0         0         0         0
```

```
#> Alcflo         0         0         0         0         0         0
#> Alclat         0         0         0         0         0         0
#> Annpap         0         0         0         0         0         0
#> Apemem         0         0         0         0         0         0
#> Astcon         0         0         0         0         0         0
#> Bacgas         0         0         0         0         0         0
#> Brogui         0         0         0         0         0         0
#> Brolac         0         0         0         0         0         0
#> Byrcra         0         0         0         0         1         0
#>
#> $`JE 2005 vs. 2017`$Year_2017
#>        Subplot_1 Subplot_2 Subplot_3 Subplot_4 Subplot_5 Subplot_6
#> Alccos         0         0         0         0         0         0
#> Alcflo         0         0         0         0         0         0
#> Alclat         0         0         0         0         0         0
#> Annpap         0         0         0         0         0         0
#> Apemem         0         0         0         0         0         0
#> Astcon         0         0         0         0         0         0
#> Bacgas         0         0         0         0         0         0
#> Brogui         0         0         0         0         0         0
#> Brolac         0         0         0         0         0         0
#> Byrcra         0         0         0         0         0         0
```

Phylogenetic tree format for PD

To perform PD analysis, the phylogenetic tree (in Newick format) spanned by species observed in all datasets must be stored in a data file. For example, the phylogenetic tree for all observed species (including species in both “Marim” and “Rebio2” fragments) is stored in a data file named `"Brazil_tree"` for demonstration purpose. A partial list of the tip labels and node labels are shown below.

```
data(Brazil_tree)
Brazil_tree
#>
#> Phylogenetic tree with 185 tips and 117 internal nodes.
#>
#> Tip labels:
#>   Carpotroche_brasiliensis, Casearia_ulmifolia, Casearia_sp2, Casearia_oblongifolia,
       Casearia_commersoniana, Rinorea_bahiensis, ...
#> Node labels:
#>   magnoliales_to_asterales, poales_to_asterales, , , , , ...
#>
#> Rooted; includes branch lengths.
```

Species pairwise distance matrix format for FD

To perform FD analysis, the species-pairwise distance matrix (Gower distance computed from species traits) for species observed in all datasets must be stored in a matrix/data.frame format. Typically, the distance between any two species is computed from species traits using the Gower distance. In our demo data, the distance matrix for all species (including species in both “Marim” and “Rebio2” fragments) is stored in a data file named `"Brazil_distM"` for demonstration purpose. Here we only show the first three rows and three columns of the distance matrix.

```
data(Brazil_distM)
Brazil_distM
```

```
#>                          Carpotroche_brasiliensis Astronium_concinnum Astronium_graveolens
#> Carpotroche_brasiliensis                    0.000               0.522                0.522
#> Astronium_concinnum                         0.522               0.000                0.000
#> Astronium_graveolens                        0.522               0.000                0.000
```

MAIN FUNCTION: iNEXTbeta3D()

We first describe the main function `iNEXTbeta3D()` with default arguments:

```
iNEXTbeta3D(data, diversity = "TD", q = c(0, 1, 2), datatype = "abundance",
            base = "coverage", level = NULL, nboot = 10, conf = 0.95,
            PDtree = NULL, PDreftime = NULL, PDtype = "meanPD",
            FDdistM = NULL, FDtype = "AUC", FDtau = NULL, FDcut_number = 30)
```

The arguments of this function are briefly described below, and will be explained in more details by illustrative examples in later text. By default (with the standardization `base = "coverage"`), this function computes coverage-based standardized 3D gamma, alpha, beta diversity, and four dissimilarity indices for coverage up to one (for q = 1, 2) or up to the coverage of double the reference sample size (for q = 0). If users set the

standardization base to `base="size"`, this function computes size-based standardized 3D gamma and alpha diversity estimates up to double the reference sample size in each dataset. In addition, this function also computes standardized 3D estimates with a particular vector of user-specified sample sizes or coverage values.

Argument	Description
`data`	a. For `datatype = "abundance"`, species abundance data for a single dataset can be input as a `matrix/data.frame` (species-by-assemblage); data for multiple datasets can be input as a `list` of `matrices/data.frames`, with each matrix representing a species-by-assemblage abundance matrix for one of the datasets. b. For `datatype = "incidence_raw"`, data for a single dataset with N assemblages can be input as a `list` of `matrices/data.frames`, with each matrix representing a species-by-sampling-unit incidence matrix for one of the assemblages; data for multiple datasets can be input as multiple lists.
`diversity`	selection of diversity type: `diversity = "TD"` = Taxonomic diversity, `diversity = "PD"` = Phylogenetic diversity, and `diversity = "FD"` = Functional diversity.
`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).
`base`	standardization base: coverage-based rarefaction and extrapolation for gamma, alpha, beta diversity, and four classes of dissimilarity indices (`base = "coverage"`), or sized-based rarefaction and extrapolation for gamma and alpha diversity (`base = "size"`). Default is `base = "coverage"`.
`level`	A numerical vector specifying the particular values of sample coverage (between 0 and 1 when `base = "coverage"`) or sample sizes (`base = "size"`) that will be used to compute standardized diversity/dissimilarity. Asymptotic diversity estimator can be obtained by setting `level = 1` (i.e., complete coverage for `base = "coverage"`). By default (with `base = "coverage"`), this function computes coverage-based standardized 3D gamma, alpha, beta diversity, and four dissimilarity indices for coverage from 0.5 up to one (for `q = 1, 2`) or up to the coverage of double the reference sample size (for `q = 0`), in increments of 0.025. The extrapolation limit for beta diversity is defined as that for alpha diversity. If users set `base = "size"`, this function computes size-based standardized 3D gamma and alpha diversity estimates based on 40 equally-spaced sample sizes/knots from sample size 1 up to double the reference sample 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. Set `nboot = 0` to skip the bootstrap procedures. Default is `nboot = 10`. If more accurate results are required, set `nboot = 100` (or `nboot = 200`).
`conf`	a positive number < 1 specifying the level of confidence interval. Default is `conf = 0.95`.
`PDtree`	(required argument for `diversity = "PD"`), a phylogenetic tree in Newick format for all observed species in the pooled assemblage.
`PDreftime`	(argument only for `diversity = "PD"`), a numerical value specifying reference time for PD. Default is `PDreftime=NULL`. (i.e., the age of the root of `PDtree`)
`PDtype`	(argument only for `diversity = "PD"`), select PD type: `PDtype = "PD"` (effective total branch length) or `PDtype = "meanPD"` (effective number of equally divergent lineages). Default is `PDtype = "meanPD"`, where `meanPD` = PD/tree depth.
`FDdistM`	(required argument for `diversity = "FD"`), a species pairwise distance matrix for all species in the pooled assemblage.
`FDtype`	(argument only for `diversity = "FD"`), select FD type: `FDtype = "tau_value"` for FD under a specified threshold value, 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 `FDtype = "AUC"`.
`FDtau`	(argument only for `diversity = "FD"` and `FDtype="tau_value"`), a numerical value between 0 and 1 specifying the tau value (threshold level) that will be used to compute FD. If `FDtau = NULL` (default), then the threshold level is set to be the mean distance between any two individuals randomly selected from the pooled dataset (i.e., quadratic entropy).
`FDcut_number`	(argument only for `diversity = "FD"` and `FDtype="AUC"`), a numeric number to cut [0, 1] interval into equal-spaced sub-intervals to obtain the AUC value by integrating the tau-profile. Equivalently, the number of tau values that will be considered to compute the integrated AUC value. Default is `FDcut_number = 30`. A larger value can be set to obtain

more accurate AUC value.

This function returns an `"iNEXTbeta3D"` object which can be further used to make plots using the function `ggiNEXTbeta3D()` to be described below.

Output of the main function iNEXTbeta3D()

By default (with `base = 'coverage'`), the `iNEXTbeta3D()` function for each of the three dimensions (TD, PD, and FD) returns the `"iNEXTbeta3D"` object including seven data frames for each dataset:

- gamma (standardized gamma diversity)
- alpha (standardized alpha diversity)
- beta (standardized beta diversity)
- 1-C (standardized Sorensen-type non-overlap index)
- 1-U (standardized Jaccard-type non-overlap index)
- 1-V (standardized Sorensen-type turnover index)
- 1-S (standardized Jaccard-type turnover index)

When users set `base = 'size'`, the `iNEXTbeta3D()` function for each of the three dimensions (TD, PD, and FD) returns the `"iNEXTbeta3D"` object including two data frames for each dataset:

- gamma (size-based standardized gamma diversity)
- alpha (size-based standardized alpha diversity)

Size-based beta diversity and dissimilarity indices are not statistically valid measures and thus are not provided.

GRAPHIC DISPLAYS: FUNCTION ggiNEXTbeta3D()

The function `ggiNEXTbeta3D()` with default arguments is described as follows:

```
ggiNEXTbeta3D(output, type = "B")
```

Argument	Description
`output`	output from the function `iNEXTbeta3D`.
`type`	(argument only for `base = "coverage"`), `type = 'B'` for plotting the rarefaction and extrapolation sampling curves for gamma, alpha, and beta diversity; `type = 'D'` for plotting the rarefaction and extrapolation sampling curves for four dissimilarity indices. Skip the argument for plotting size-based rarefaction and extrapolation sampling curves for gamma and alpha diversity.

The `ggiNEXTbeta3D()` function is a wrapper around the `ggplot2` package to create a R/E curve using a single line of code. The resulting object is of class `"ggplot"`, so it can be manipulated using the `ggplot2` tools. Users can visualize the displays of coverage-based R/E sampling curves of gamma, alpha and beta diversity as well as four classes of dissimilarity indices by setting the parameter `type`.

TAXONOMIC DIVERSITY (TD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 1: Abundance data with default sample sizes or coverage values

First, we run the `iNEXTbeta3D()` function with `Brazil_rainforests` abundance data to compute coverage-based taxonomic gamma, alpha, beta diversity, and four dissimilarity indices under `base = 'coverage'` by running the following code:

```
## R/E Analysis with taxonomic diversity for abundance data
data(Brazil_rainforests)

output_TDc_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'TD',
                              datatype = "abundance", base = 'coverage', nboot = 10)
output_TDc_abun
```

The output contains seven data frames: `gamma`, `alpha`, `beta`, `1-C`, `1-U`, `1-V`, `1-S`. For each data frame, it includes the name of dataset (`Dataset`), the diversity order of q (`Order.q`), the target standardized coverage value (`SC`), the corresponding sample size (`Size`), the estimated diversity/dissimilarity estimate (`Alpha/Beta/Gamma/Dissimilarity`), `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), standard error of standardized estimate (`s.e.`), the bootstrap lower and upper confidence limits for the diversity/dissimilarity with a

default significance level of 0.95 (`LCL`, `UCL`). These estimates with confidence intervals in the output are then used for plotting rarefaction and extrapolation curves.

Our diversity/dissimilarity estimates and related statistics in the default output are displayed for the standardized coverage value from 0.5 to the coverage value of twice the reference sample size (for q = 0), or from 0.5 to 1.0 (for q = 1 and 2), in increments of 0.025. In addition, the results for the following four coverage value are also added: `SC(n, alpha)`, `SC(2n, alpha)`, `SC(n, gamma)` and `SC(2n, gamma)` if these values are in the above-specified range. Here `SC(n, alpha)` and `SC(2n, alpha)` represent, respectively, the coverage estimate for the alpha reference sample size n and the extrapolated sample with size 2n in the joint assemblage. These values can be found as `SC(n)` and `SC(2n)` for `"Joint assemblage (for alpha)"` in the column "Assemblage" from the output of the function `DataInfobeta3D`; see later text. Similar definitions pertain to `SC(n, gamma)` and `SC(2n, gamma)` for the gamma reference sample; these two values can also be found as `SC(n)` and `SC(2n)` for `"Pooled assemblage (for gamma)"` in the column "Assemblage" from the output of the function `DataInfobeta3D`. For beta diversity and dissimilarity, the observed sample coverage and extrapolation limit are defined the same as the alpha diversity. The corresponding coverage values for incidence data are denoted as, respectively, `SC(T, alpha)`, `SC(2T, alpha)`, `SC(T, gamma)` and `SC(2T, gamma)` in the output.

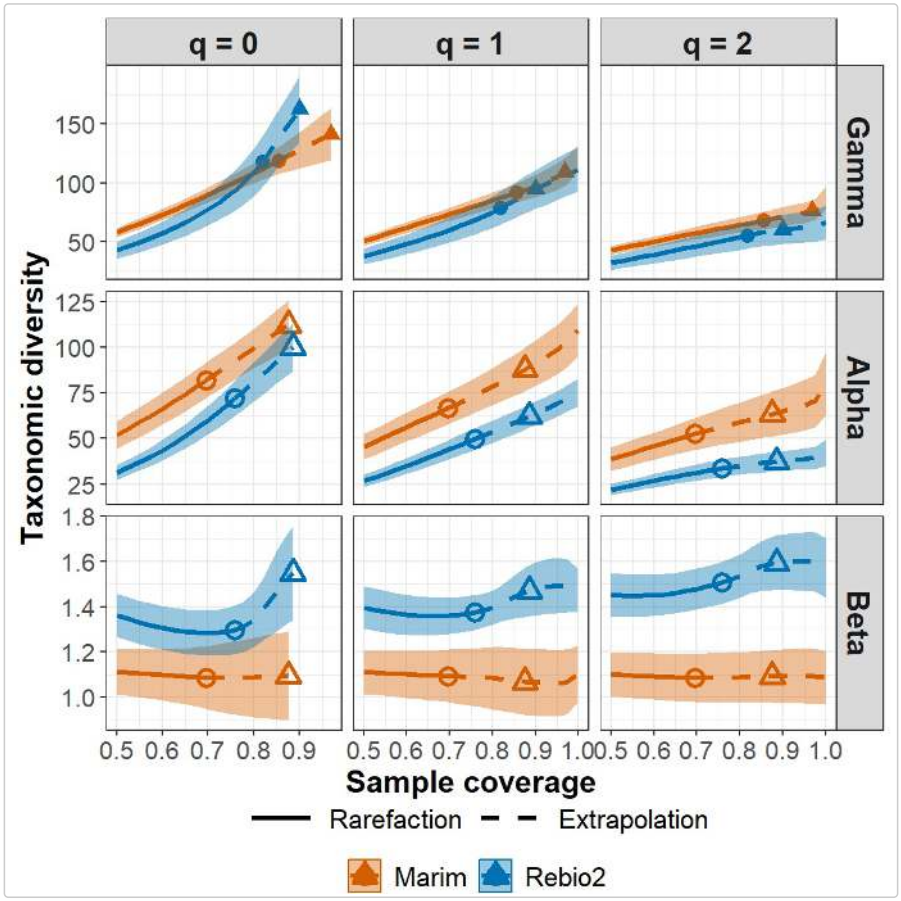
Because all the diversity/dissimilarity estimates are computed for the standardized coverage range values starting from 0.5, the default setting with `level = NULL` does not work if the observed sample coverage in the alpha/gamma reference sample is less than 50%. In this case, readers should specify sample coverage values using the argument `level`, instead of using `level = NULL`. The suggested maximum coverage value that readers can specify is `SC(2n, alpha)`. Beyond the limit, beta diversity and dissimilarity estimates may be subject to some bias. Below we show the output for taxonomic beta diversity between the "Edge" and "Interior" habitats in the "Marim" fragment.

```
#>    Dataset Order.q    SC Size Beta               Method  s.e.   LCL  UCL
#> 1    Marim       0 0.500  148 1.11           Rarefaction 0.051 1.011 1.21
#> 2    Marim       0 0.525  162 1.11           Rarefaction 0.052 1.006 1.21
#> 3    Marim       0 0.550  178 1.10           Rarefaction 0.053 1.000 1.21
#> 4    Marim       0 0.575  195 1.10           Rarefaction 0.055 0.993 1.21
#> 5    Marim       0 0.600  213 1.10           Rarefaction 0.058 0.986 1.21
#> 6    Marim       0 0.625  233 1.09           Rarefaction 0.060 0.977 1.21
#> 7    Marim       0 0.650  255 1.09           Rarefaction 0.063 0.968 1.22
#> 8    Marim       0 0.675  279 1.09           Rarefaction 0.067 0.958 1.22
#> 9    Marim       0 0.696  302 1.09 Observed_SC(n, alpha) 0.070 0.949 1.23
#> 10   Marim       0 0.700  306 1.09         Extrapolation 0.071 0.947 1.23
#> 11   Marim       0 0.725  336 1.08         Extrapolation 0.076 0.935 1.24
#> 12   Marim       0 0.750  368 1.08         Extrapolation 0.081 0.925 1.24
#> 13   Marim       0 0.775  403 1.08         Extrapolation 0.086 0.917 1.25
#> 14   Marim       0 0.800  443 1.09         Extrapolation 0.090 0.911 1.26
#> 15   Marim       0 0.825  488 1.09         Extrapolation 0.093 0.907 1.27
#> 16   Marim       0 0.850  541 1.09         Extrapolation 0.097 0.903 1.28
#> 17   Marim       0 0.855  552 1.09 Observed_SC(n, gamma) 0.097 0.902 1.28
#> 18   Marim       0 0.875  602 1.09         Extrapolation 0.100 0.898 1.29
#> 19   Marim       0 0.876  604 1.09  Extrap_SC(2n, alpha) 0.100 0.898 1.29
#> 20   Marim       1 0.500  148 1.11           Rarefaction 0.049 1.014 1.21
#> 21   Marim       1 0.525  162 1.11           Rarefaction 0.050 1.010 1.21
#> 22   Marim       1 0.550  178 1.11           Rarefaction 0.051 1.007 1.21
#> 23   Marim       1 0.575  195 1.10           Rarefaction 0.052 1.002 1.20
#> 24   Marim       1 0.600  213 1.10           Rarefaction 0.053 0.998 1.21
#> 25   Marim       1 0.625  233 1.10           Rarefaction 0.054 0.993 1.21
#> 26   Marim       1 0.650  255 1.10           Rarefaction 0.056 0.988 1.21
#> 27   Marim       1 0.675  279 1.09           Rarefaction 0.057 0.983 1.21
#> 28   Marim       1 0.696  302 1.09 Observed_SC(n, alpha) 0.059 0.978 1.21
#> 29   Marim       1 0.700  306 1.09         Extrapolation 0.059 0.978 1.21
#> 30   Marim       1 0.725  336 1.09         Extrapolation 0.062 0.971 1.21
#> 31   Marim       1 0.750  368 1.09         Extrapolation 0.064 0.964 1.22
#> 32   Marim       1 0.775  403 1.09         Extrapolation 0.067 0.956 1.22
#> 33   Marim       1 0.800  443 1.08         Extrapolation 0.070 0.947 1.22
#> 34   Marim       1 0.825  488 1.08         Extrapolation 0.072 0.939 1.22
#> 35   Marim       1 0.850  541 1.07         Extrapolation 0.073 0.931 1.22
#> 36   Marim       1 0.855  552 1.07 Observed_SC(n, gamma) 0.073 0.929 1.22
#> 37   Marim       1 0.875  602 1.07         Extrapolation 0.074 0.923 1.21
#> 38   Marim       1 0.876  604 1.07  Extrap_SC(2n, alpha) 0.074 0.923 1.21
#> 39   Marim       1 0.900  678 1.06         Extrapolation 0.075 0.918 1.21
#> 40   Marim       1 0.925  775 1.06         Extrapolation 0.075 0.915 1.21
#> 41   Marim       1 0.950  912 1.06         Extrapolation 0.075 0.915 1.21
#> 42   Marim       1 0.969 1075 1.07  Extrap_SC(2n, gamma) 0.074 0.921 1.21
#> 43   Marim       1 0.975 1147 1.07         Extrapolation 0.073 0.924 1.21
#> 44   Marim       1 1.000  Inf 1.10         Extrapolation 0.063 0.979 1.23
#> 45   Marim       2 0.500  148 1.10           Rarefaction 0.049 1.004 1.20
#> 46   Marim       2 0.525  162 1.10           Rarefaction 0.050 1.001 1.20
#> 47   Marim       2 0.550  178 1.10           Rarefaction 0.050 0.998 1.20
#> 48   Marim       2 0.575  195 1.09           Rarefaction 0.051 0.994 1.19
#> 49   Marim       2 0.600  213 1.09           Rarefaction 0.052 0.991 1.19
#> 50   Marim       2 0.625  233 1.09           Rarefaction 0.052 0.987 1.19
#> 51   Marim       2 0.650  255 1.09           Rarefaction 0.053 0.984 1.19
#> 52   Marim       2 0.675  279 1.09           Rarefaction 0.054 0.981 1.19
#> 53   Marim       2 0.696  302 1.08 Observed_SC(n, alpha) 0.055 0.978 1.19
```

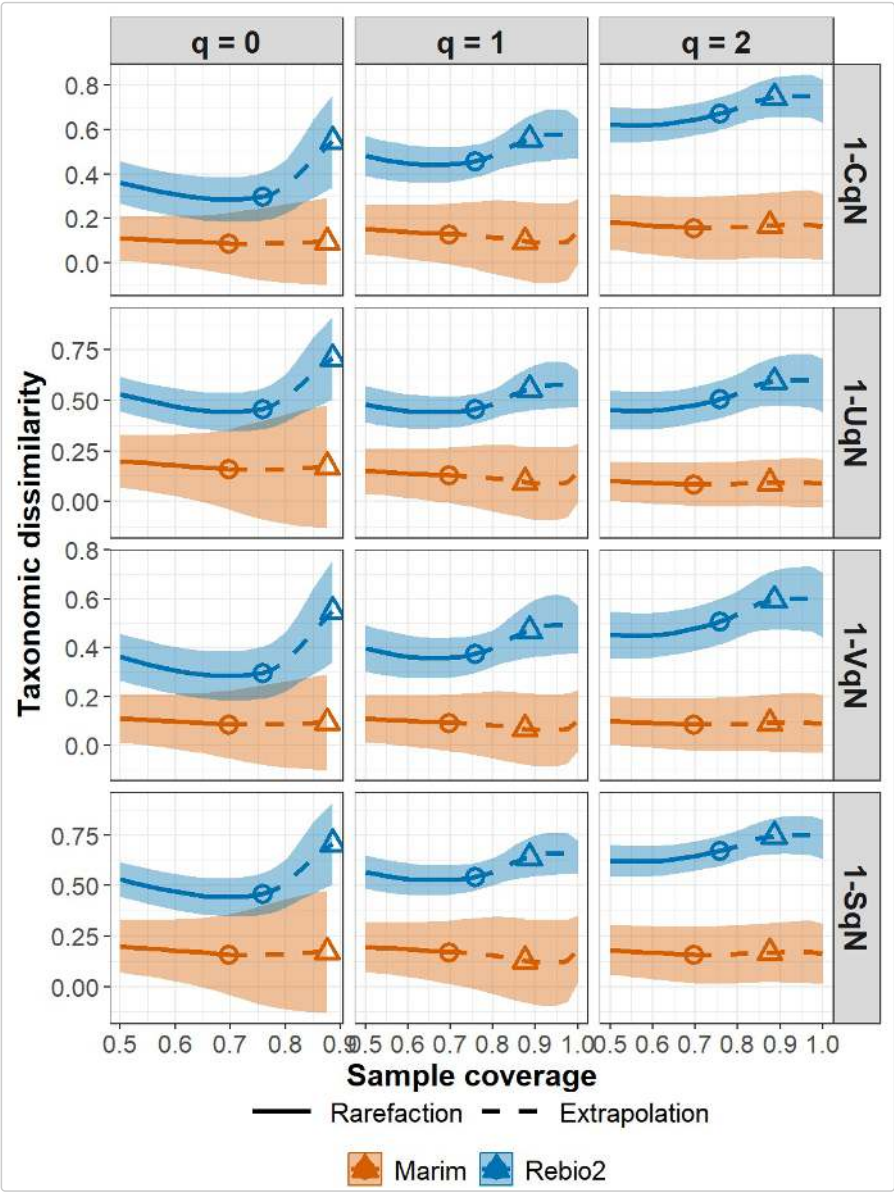
```
#> 54   Marim       2 0.700  306 1.08         Extrapolation 0.055 0.978 1.19
#> 55   Marim       2 0.725  336 1.08         Extrapolation 0.056 0.976 1.19
#> 56   Marim       2 0.750  368 1.08         Extrapolation 0.056 0.975 1.20
#> 57   Marim       2 0.775  403 1.09         Extrapolation 0.056 0.976 1.20
#> 58   Marim       2 0.800  443 1.09         Extrapolation 0.057 0.976 1.20
#> 59   Marim       2 0.825  488 1.09         Extrapolation 0.057 0.977 1.20
#> 60   Marim       2 0.850  541 1.09         Extrapolation 0.058 0.977 1.21
#> 61   Marim       2 0.855  552 1.09 Observed_SC(n, gamma) 0.058 0.977 1.21
#> 62   Marim       2 0.875  602 1.09         Extrapolation 0.059 0.976 1.21
#> 63   Marim       2 0.876  604 1.09  Extrap_SC(2n, alpha) 0.059 0.976 1.21
#> 64   Marim       2 0.900  678 1.09         Extrapolation 0.060 0.974 1.21
#> 65   Marim       2 0.925  775 1.09         Extrapolation 0.062 0.973 1.21
#> 66   Marim       2 0.950  912 1.09         Extrapolation 0.062 0.972 1.22
#> 67   Marim       2 0.969 1075 1.09  Extrap_SC(2n, gamma) 0.063 0.971 1.22
#> 68   Marim       2 0.975 1147 1.09         Extrapolation 0.063 0.971 1.22
#> 69   Marim       2 1.000  Inf 1.09         Extrapolation 0.059 0.972 1.21
```

Run the following code to display the two types of curves:

```
## Coverage-based R/E curves for taxonomic gamma, alpha and beta diversity
ggiNEXTbeta3D(output_TDc_abun, type = 'B')
```



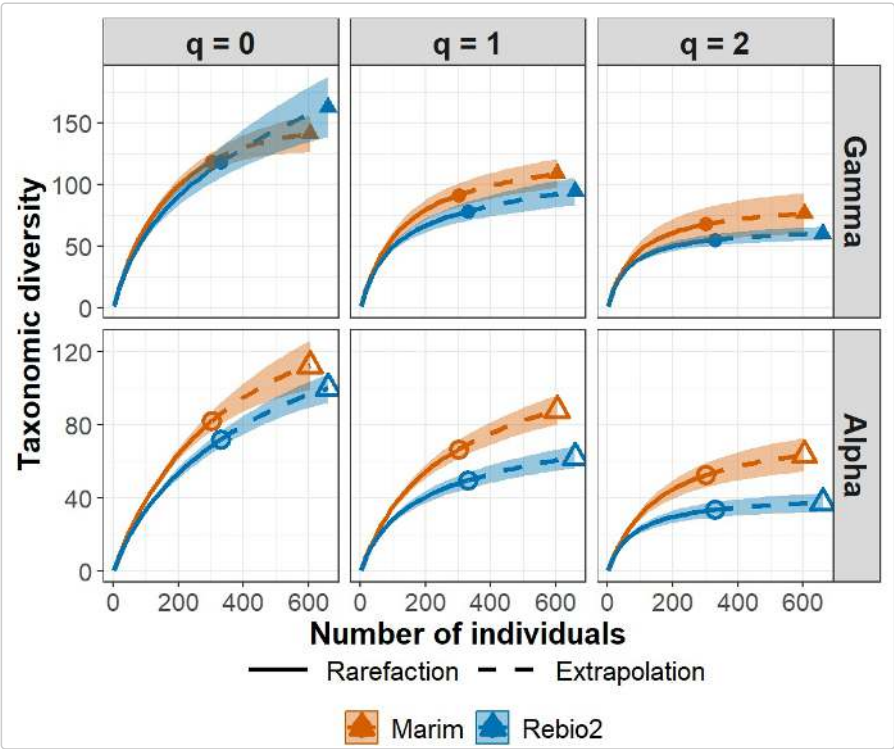

```
## Coverage-based R/E curves for four taxonomic dissimilarity indices
ggiNEXTbeta3D(output_TDc_abun, type = 'D')
```



The following commands return the size-based R/E sampling curves for gamma and alpha taxonomic diversity:

```
## Size-based R/E curves for taxonomic gamma and alpha diversity
output_TDs_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'TD',
                              datatype = 'abundance', base = "size", nboot = 10)

ggiNEXTbeta3D(output_TDs_abun)
```



EXAMPLE 2: Abundance data with user-specified sample sizes or coverage values

In addition to the default sample sizes or coverage values, `iNEXTbeta3D` also computes standardized 3D estimates with a particular vector of user-specified sample sizes or coverage values. The following commands return the TD estimates with two user-specified levels of sample coverage (e.g., 85% and 90%). Only the output for gamma, alpha and beta is shown below in each dataset; the output for 1-C, 1-U, 1-V, 1-S is omitted.

```
## R/E Analysis with taxonomic diversity for abundance data
data(Brazil_rainforests)

output_TDc_abun_byuser = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'TD',
                                     datatype = "abundance", base = 'coverage', nboot = 10,
                                     level = c(0.85, 0.9))
output_TDc_abun_byuser
```

```
#> $Marim
#> $Marim$gamma
#>   Dataset     Order.q   SC    Size   Gamma        Method  s.e.    LCL     UCL
#> 1         Order q = 0
#> 2   Marim           0 0.85 295.313 118.011   Rarefaction 5.368 107.49 128.533
#> 3   Marim           0  0.9 374.487   127.8 Extrapolation 8.321 111.49 144.109
#> 4         Order q = 1
#> 5   Marim           1 0.85 295.313  90.988   Rarefaction  4.23 82.696  99.279
#> 6   Marim           1  0.9 374.487  97.277 Extrapolation 5.098 87.284  107.27
#> 7         Order q = 2
#> 8   Marim           2 0.85 295.313  67.621   Rarefaction 4.428 58.942    76.3
#> 9   Marim           2  0.9 374.487  71.019 Extrapolation 4.985 61.248  80.791
#>
#> $Marim$alpha
#>   Dataset     Order.q   SC    Size   Alpha        Method   s.e.    LCL     UCL
#> 1         Order q = 0
#> 2   Marim           0 0.85 540.613 108.036 Extrapolation 10.479 87.497 128.575
#> 3   Marim           0  0.9 677.745 116.503 Extrapolation  12.38  92.24 140.767
#> 4         Order q = 1
#> 5   Marim           1 0.85 540.613  84.693 Extrapolation  4.955 74.981  94.405
#> 6   Marim           1  0.9 677.745  91.384 Extrapolation  5.535 80.536 102.233
#> 7         Order q = 2
#> 8   Marim           2 0.85 540.613  61.998 Extrapolation  3.632  54.88  69.117
#> 9   Marim           2  0.9 677.745  64.996 Extrapolation  3.974 57.208  72.784
#>
#> $Marim$beta
#>   Dataset     Order.q   SC    Size  Beta        Method  s.e.   LCL   UCL
#> 1         Order q = 0
#> 2   Marim           0 0.85 540.613 1.092 Extrapolation 0.101 0.894 1.291
#> 3   Marim           0  0.9 677.745 1.097 Extrapolation 0.108 0.885 1.308
#> 4         Order q = 1
#> 5   Marim           1 0.85 540.613 1.074 Extrapolation 0.078 0.922 1.227
#> 6   Marim           1  0.9 677.745 1.064 Extrapolation 0.077 0.913 1.216
#> 7         Order q = 2
#> 8   Marim           2 0.85 540.613 1.091 Extrapolation 0.061 0.971  1.21
#> 9   Marim           2  0.9 677.745 1.093 Extrapolation 0.062 0.971 1.214
#>
#>
#> $Rebio2
#> $Rebio2$gamma
#>   Dataset     Order.q   SC    Size   Gamma        Method   s.e.    LCL     UCL
#> 1         Order q = 0
#> 2  Rebio2           0 0.85  434.58 135.297 Extrapolation 26.875 82.624  187.97
#> 3  Rebio2           0  0.9 657.113 162.764 Extrapolation 35.987 92.231 233.297
#> 4         Order q = 1
#> 5  Rebio2           1 0.85  434.58   84.77 Extrapolation 10.403  64.38 105.159
#> 6  Rebio2           1  0.9 657.113  94.373 Extrapolation 12.229 70.404 118.341
#> 7         Order q = 2
#> 8  Rebio2           2 0.85  434.58  57.565 Extrapolation  4.652 48.447  66.682
#> 9  Rebio2           2  0.9 657.113  60.225 Extrapolation  4.661  51.09  69.361
#>
#> $Rebio2$alpha
#>   Dataset     Order.q   SC    Size   Alpha        Method  s.e.    LCL     UCL
#> 1         Order q = 0
#> 2  Rebio2           0 0.85 539.824  92.197 Extrapolation  7.05 78.379 106.015
#> 3  Rebio2           0  0.9  717.89 103.188 Extrapolation 8.772 85.995 120.382
#> 4         Order q = 1
#> 5  Rebio2           1 0.85 539.824  58.713 Extrapolation 2.798  53.23  64.196
#> 6  Rebio2           1  0.9  717.89   63.83 Extrapolation 3.077 57.799  69.862
#> 7         Order q = 2
#> 8  Rebio2           2 0.85 539.824  36.464 Extrapolation 3.007  30.57  42.358
#> 9  Rebio2           2  0.9  717.89  37.713 Extrapolation 3.248 31.346  44.079
```

```
#>
#> $Rebio2$beta
#>   Dataset     Order.q   SC    Size  Beta        Method  s.e.   LCL   UCL
#> 1         Order q = 0
#> 2  Rebio2           0 0.85 539.824 1.467 Extrapolation 0.092 1.287 1.648
#> 3  Rebio2           0  0.9  717.89 1.577 Extrapolation 0.112 1.358 1.796
#> 4         Order q = 1
#> 5  Rebio2           1 0.85 539.824 1.444 Extrapolation 0.067 1.313 1.575
#> 6  Rebio2           1  0.9  717.89 1.478 Extrapolation 0.075 1.332 1.625
#> 7         Order q = 2
#> 8  Rebio2           2 0.85 539.824 1.579 Extrapolation 0.055 1.472 1.686
#> 9  Rebio2           2  0.9  717.89 1.597 Extrapolation 0.056 1.487 1.706
```

The following commands return the TD estimates with two user-specified levels of sample sizes (e.g., 300 and 500).

```
## Size-based R/E for taxonomic gamma and alpha diversity
output_TDs_abun_byuser = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'TD',
                                     datatype = 'abundance', base = "size", nboot = 10,
                                     level = c(300, 500))
output_TDs_abun_byuser
```

```
#> $Marim
#> $Marim$gamma
#>   Dataset     Order.q Size    SC   Gamma        Method  s.e.     LCL     UCL
#> 1         Order q = 0
#> 2   Marim           0  300 0.854 118.708   Rarefaction 3.737 111.383 126.033
#> 3   Marim           0  500 0.947 137.082 Extrapolation 5.316 126.663 147.502
#> 4         Order q = 1
#> 5   Marim           1  300 0.854  91.406   Rarefaction 3.978  83.609  99.203
#> 6   Marim           1  500 0.947 104.649 Extrapolation 4.708  95.422 113.877
#> 7         Order q = 2
#> 8   Marim           2  300 0.854  67.861   Rarefaction 5.954  56.192   79.53
#> 9   Marim           2  500 0.947  74.527 Extrapolation 6.999  60.809  88.244
#>
#> $Marim$alpha
#>   Dataset     Order.q Size    SC   Alpha        Method  s.e.    LCL     UCL
#> 1         Order q = 0
#> 2   Marim           0  300 0.694  81.695   Rarefaction 3.181 75.461  87.929
#> 3   Marim           0  500 0.831 104.795 Extrapolation 5.485 94.044 115.545
#> 4         Order q = 1
#> 5   Marim           1  300 0.694  66.473   Rarefaction 3.562 59.492  73.454
#> 6   Marim           1  500 0.831  82.274 Extrapolation 4.917 72.637  91.911
#> 7         Order q = 2
#> 8   Marim           2  300 0.694  52.416   Rarefaction  3.84 44.889  59.943
#> 9   Marim           2  500 0.831  60.871 Extrapolation 4.912 51.244  70.499
#>
#>
#> $Rebio2
#> $Rebio2$gamma
#>   Dataset     Order.q Size    SC   Gamma        Method  s.e.     LCL     UCL
#> 1         Order q = 0
#> 2  Rebio2           0  300 0.807 112.391   Rarefaction 5.298 102.007 122.774
#> 3  Rebio2           0  500 0.867 144.556 Extrapolation 8.262 128.362  160.75
#> 4         Order q = 1
#> 5  Rebio2           1  300 0.807   76.38   Rarefaction 3.813  68.907  83.853
#> 6  Rebio2           1  500 0.867   88.06 Extrapolation 4.968  78.323  97.798
#> 7         Order q = 2
#> 8  Rebio2           2  300 0.807  54.382   Rarefaction  2.83  48.836  59.928
#> 9  Rebio2           2  500 0.867  58.564 Extrapolation 3.238  52.218   64.91
#>
#> $Rebio2$alpha
#>   Dataset     Order.q Size    SC  Alpha        Method  s.e.    LCL    UCL
#> 1         Order q = 0
#> 2  Rebio2           0  300 0.741 68.239   Rarefaction  3.16 62.045 74.433
#> 3  Rebio2           0  500 0.836 89.067 Extrapolation 4.151 80.931 97.202
#> 4         Order q = 1
#> 5  Rebio2           1  300 0.741 47.986   Rarefaction 3.645 40.841  55.13
#> 6  Rebio2           1  500 0.836 57.286 Extrapolation 4.504 48.457 66.114
#> 7         Order q = 2
#> 8  Rebio2           2  300 0.741 32.948   Rarefaction 3.554 25.983 39.913
#> 9  Rebio2           2  500 0.836  36.08 Extrapolation 4.144 27.959 44.202
```

EXAMPLE 3: Incidence data with default sample sizes or coverage values

We can also use incidence raw data (`Second_growth_forests`) to compute coverage-based standardized

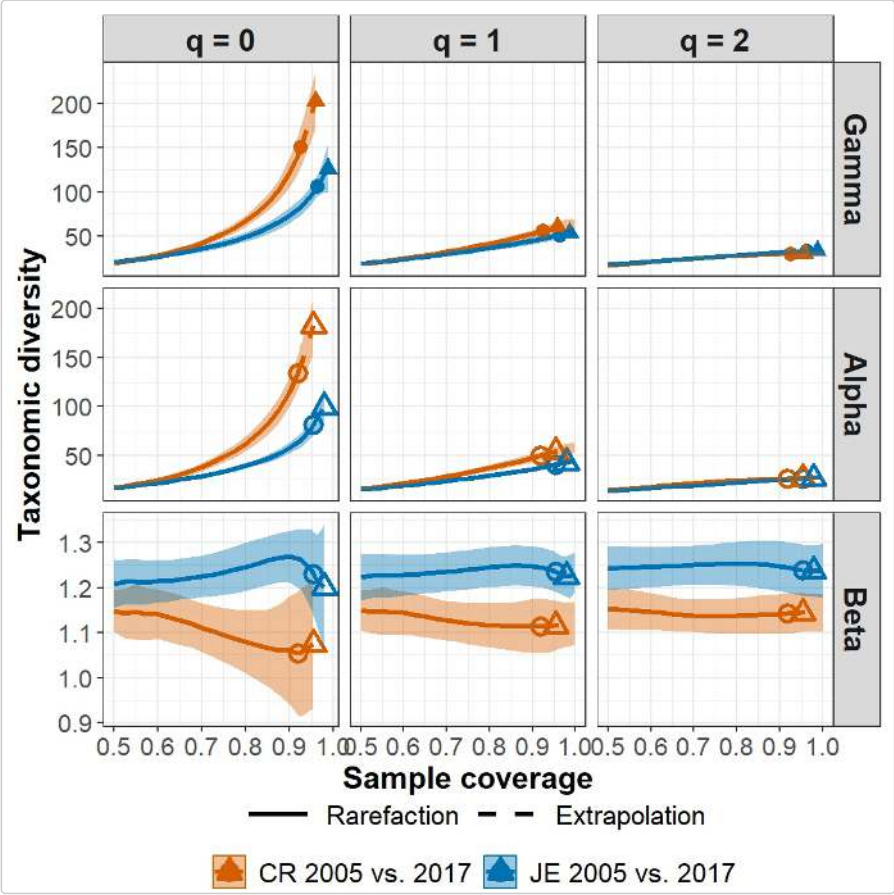
gamma, alpha, beta diversity, and four dissimilarities under `base = 'coverage'`, and also size-based standardized gamma and alpha diversity. Run the following code to perform incidence data analysis. The output data frame is similar to that based on abundance data and thus is omitted.

```
## R/E Analysis with taxonomic diversity for incidence raw data
data(Second_growth_forests)

output_TDc_inci = iNEXTbeta3D(data = Second_growth_forests, diversity = 'TD',
                              datatype = "incidence_raw", base = 'coverage', nboot = 10)
output_TDc_inci
```

The same procedures can be applied to incidence data. Based on the demo dataset, we display below the coverage-based R/E curves for comparing temporal beta diversity between 2005 and 2017 in two second-growth forests (CR and JE) by running the following code:

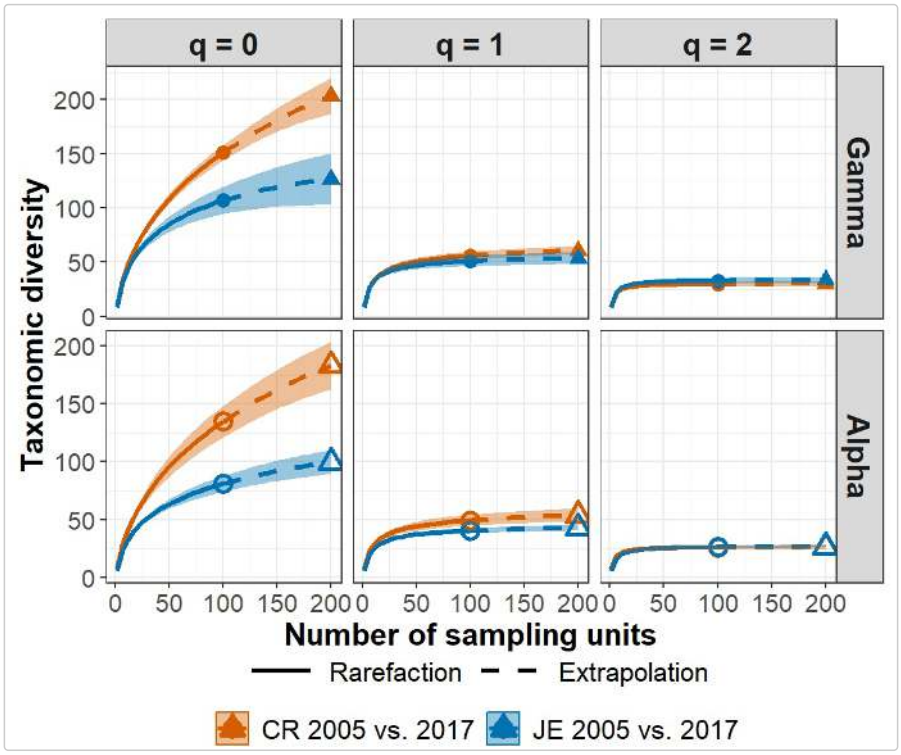
```
## Coverage-based R/E curves for taxonomic gamma, alpha and beta diversity
ggiNEXTbeta3D(output_TDc_inci, type = 'B')
```



The following commands return the size-based R/E sampling curves for gamma and alpha taxonomic diversity:

```
## Size-based R/E curves for taxonomic gamma and alpha diversity
output_TDs_inci = iNEXTbeta3D(data = Second_growth_forests, diversity = 'TD',
                              datatype = 'incidence_raw', base = "size", nboot = 10)

ggiNEXTbeta3D(output_TDs_inci)
```



EXAMPLE 4: Incidence data with user-specified sample sizes or coverage values

As with abundance data, user can also specify sample sizes (i.e. number of sampling units) or coverage values to obtain the pertinent output. The code for examples is given below with two user-specified levels of sample coverage values (e.g., 90% and 95%), but the output is omitted.

```
## R/E Analysis with taxonomic diversity for incidence data
data(Second_growth_forests)

output_TDc_inci_byuser = iNEXTbeta3D(data = Second_growth_forests, diversity = 'TD',
                                     datatype = 'incidence_raw', base = "coverage",
                                     nboot = 10, level = c(0.9, 0.95))
output_TDc_inci_byuser
```

The following commands return the TD estimates with two user-specified levels of sample sizes (e.g., 100 and 200).

```
## Size-based R/E for taxonomic gamma and alpha diversity
data(Second_growth_forests)

output_TDs_inci_byuser = iNEXTbeta3D(data = Second_growth_forests, diversity = 'TD',
                                     datatype = 'incidence_raw', base = "size",
                                     nboot = 10, level = c(100, 200))
output_TDs_inci_byuser
```

PHYLOGENETIC DIVERSITY (PD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 5: Abundance data with default sample sizes or coverage values

As with taxonomic diversity, `iNEXT.beta3D` computes coverage-based standardized phylogenetic gamma, alpha, beta diversity as well as four classes of phylogenetic dissimilarity indices; it also computes size-based standardized phylogenetic gamma and alpha diversity. The species names (or identification codes) in the phylogenetic tree must exactly match with those in the corresponding species abundance/incidence data. Two types of phylogenetic rarefaction and extrapolation curves (coverage- and size-based sampling curves) are also provided.

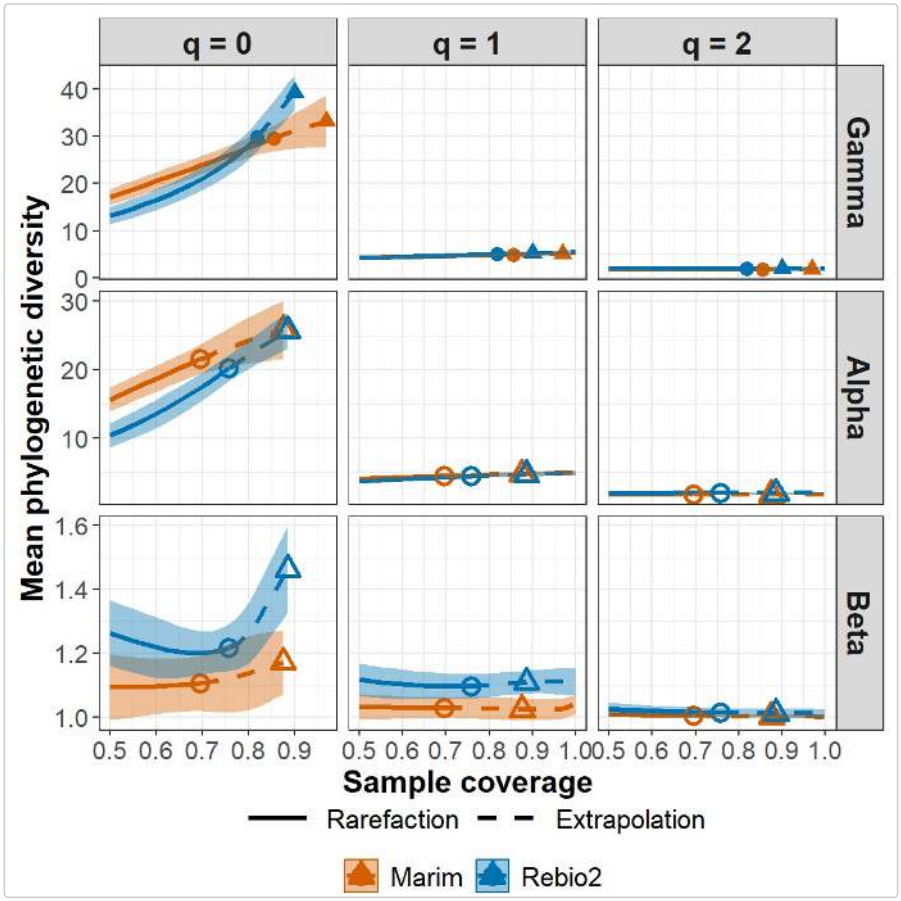
The required argument for performing PD analysis is `PDtree`. For example, the phylogenetic tree for all observed species (including species in both Marim and Rebio2 fragments) is stored in a data file named `"Brazil_tree"`. Then we enter the argument `PDtree = Brazil_tree`. Two optional arguments are: `PDtype` and `PDreftime`. There are two options for `PDtype`: `"PD"` (effective total branch length) or `"meanPD"` (effective number of equally divergent lineages, meanPD = PD/tree depth). Default is `PDtype = "meanPD"`. `PDreftime` is a numerical value specifying a reference time for computing phylogenetic diversity. By default (`PDreftime = NULL`), the reference time is set to the tree depth, i.e., age of the root of the phylogenetic tree. Run the following code to perform PD analysis. The output data frame is similar to that based on abundance data and thus is omitted.

```
## R/E Analysis with phylogenetic diversity for abundance data
data(Brazil_rainforests)
data(Brazil_tree)

output_PDc_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'PD',
                              datatype = "abundance", base = 'coverage', nboot = 10,
                              PDtree = Brazil_tree, PDreftime = NULL, PDtype = 'meanPD')
output_PDc_abun
```

Run the following code to display the R/E curves for phylogenetic gamma, alpha, and beta diversity:

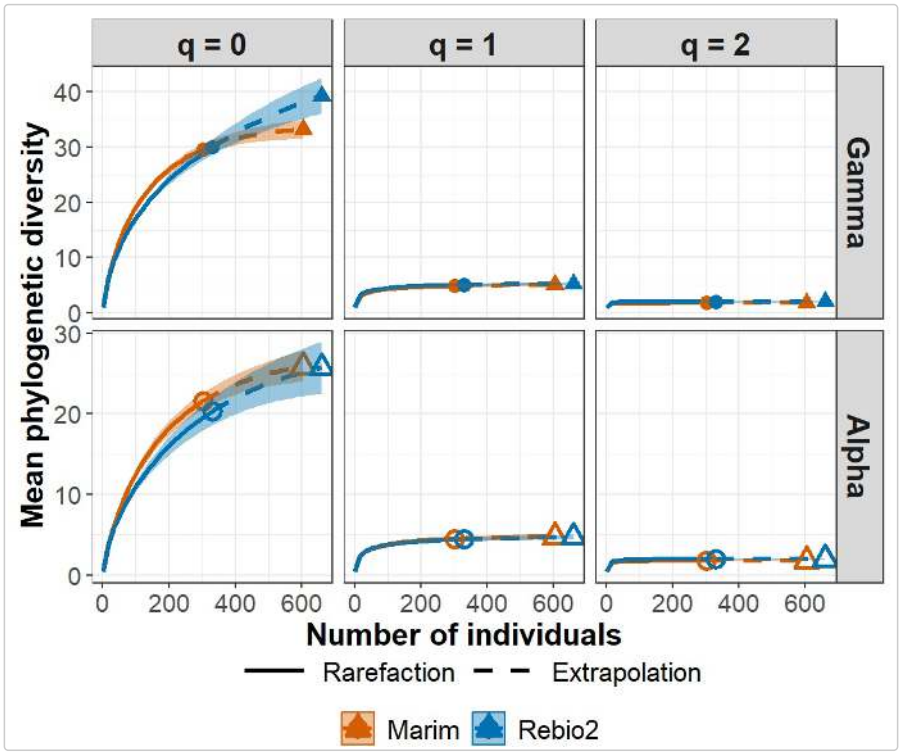
```
## Coverage-based R/E sampling curves for phylogenetic gamma, alpha and beta diversity
ggiNEXTbeta3D(output_PDc_abun, type = 'B')
```



The following commands return the size-based R/E sampling curves for gamma and alpha phylogenetic diversity:

```
## Size-based R/E curves for phylogenetic gamma and alpha diversity
data(Brazil_rainforests)
data(Brazil_tree)

output_PDs_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'PD',
                              datatype = 'abundance', base = "size", nboot = 10,
                              PDtree = Brazil_tree, PDreftime = NULL, PDtype = 'meanPD')
ggiNEXTbeta3D(output_PDs_abun)
```



FUNCTIONAL DIVERSITY (FD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 6: Abundance data with default sample sizes or coverage values

As with taxonomic and phylogenetic diversity, `iNEXT.beta3D` computes coverage-based standardized functional gamma, alpha, beta diversity as well as four classes of functional dissimilarity indices; it also computes size-based standardized functional gamma and alpha diversity. The species names (or identification codes) in the distance matrix must exactly match with those in the corresponding species abundance/incidence data. Two types of functional rarefaction and extrapolation curves (coverage- and size-based sampling curves) are also provided.

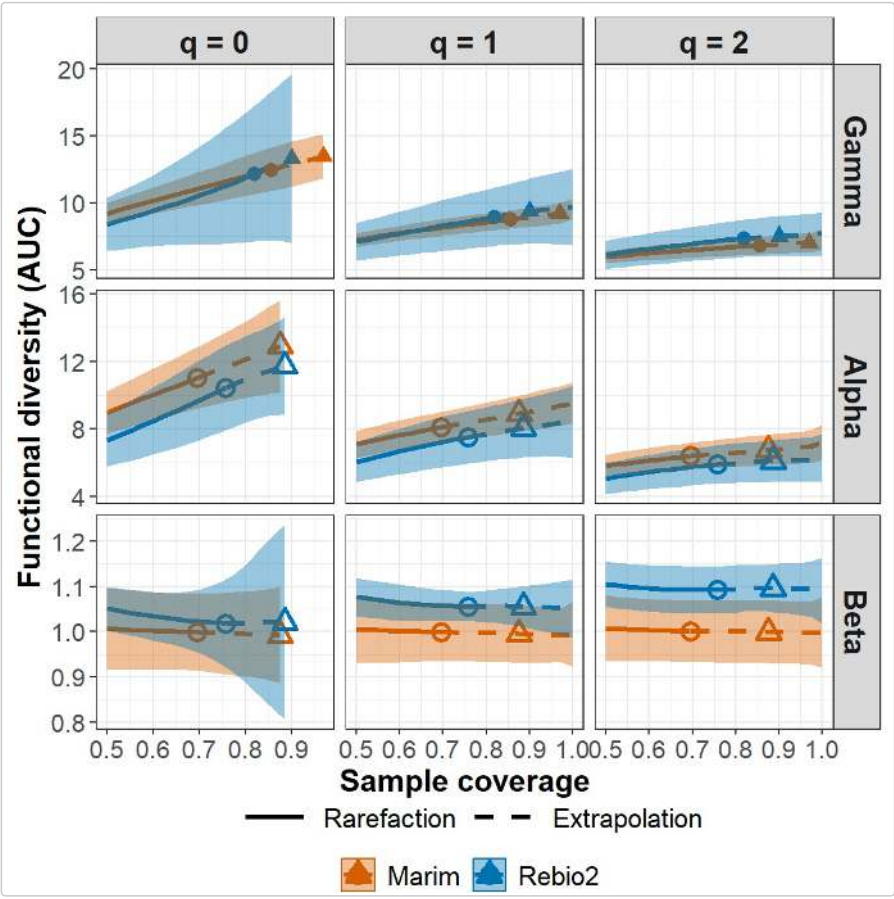
The required argument for performing FD analysis is `FDdistM`. For example, the distance matrix for all species (including species in both “Marim” and “Rebio2” fragments) is stored in a data file named `"Brazil_distM"`. Then we enter the argument `FDdistM = Brazil_distM`. Three optional arguments are (1) `FDtype`: `FDtype = "AUC"`means FD is computed from the area under the curve of a tau-profile by integrating all plausible threshold values between zero and one; `FDtype = "tau_value"` means FD is computed under a specific threshold value to be specified in the argument `FD_tau`. (2) `FD_tau`: a numerical value specifying the tau value (threshold level) that will be used to compute FD. If `FDtype = "tau_value"` and `FD_tau = NULL`, then the threshold level is set to be the mean distance between any two individuals randomly selected from the pooled data over all datasets (i.e., quadratic entropy). (3) `FDcut_number` is a numeric number to cut [0, 1] interval into equal-spaced sub-intervals to obtain the AUC value. Default is `FDcut_number = 30`. If more accurate integration is desired, then use a larger integer. Run the following code to perform FD analysis. The output data frame is similar to that based on abundance data and thus is omitted; see later graphical display of the output.

```
## R/E Analysis with functional diversity for abundance data - FDtype = 'AUC' (area under
        curve)
## by considering all threshold values between zero and one
data(Brazil_rainforests)
data(Brazil_distM)

output_FDc_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'FD',
                              datatype = "abundance", base = 'coverage', nboot = 10,
                              FDdistM = Brazil_distM, FDtype = 'AUC', FDcut_number = 30)
output_FDc_abun
```

Run the following code to display the R/E curves for functional gamma, alpha, and beta diversity:

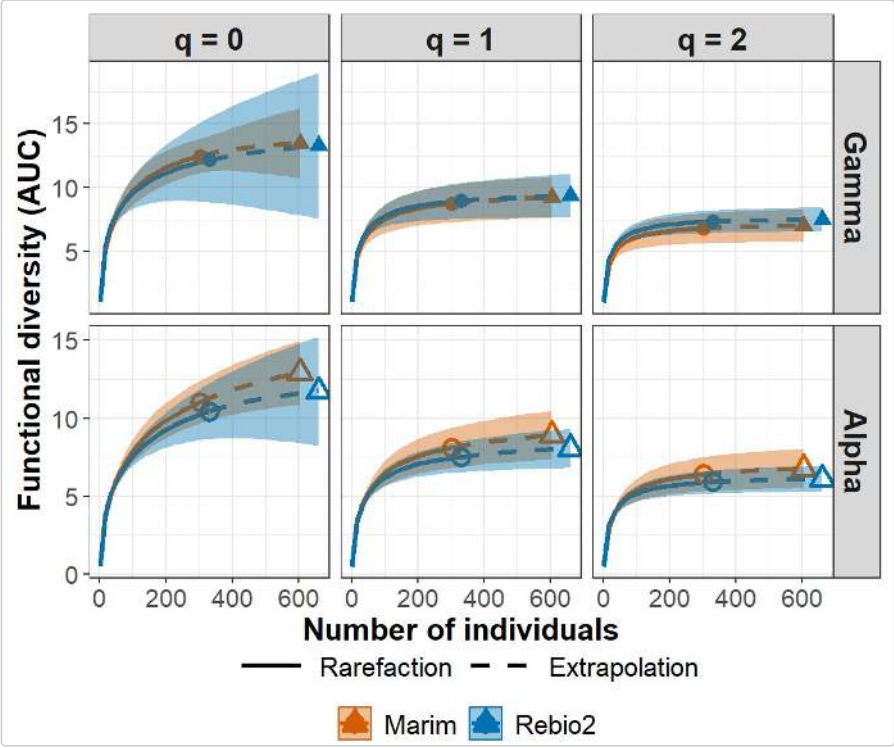
```
## Coverage-based R/E sampling curves for functional gamma, alpha and beta diversity
ggiNEXTbeta3D(output_FDc_abun, type = 'B')
```



The following commands return the size-based R/E sampling curves for gamma and alpha functional diversity:

```
## Size-based R/E curves for functional gamma and alpha diversity
data(Brazil_rainforests)
data(Brazil_distM)

output_FDs_abun = iNEXTbeta3D(data = Brazil_rainforests, diversity = 'FD',
                              datatype = 'abundance', base = "size", nboot = 10,
                              FDdistM = Brazil_distM, FDtype = 'AUC', FDcut_number = 30)
ggiNEXTbeta3D(output_FDs_abun)
```



DATA INFORMATION: FUNCTION DataInfobeta3D()

The function `DataInfobeta3D()` provides basic data information for (1) the reference sample in each individual assemblage, (2) the gamma reference sample in the pooled assemblage, and (3) the alpha reference sample in the joint assemblage. The function `DataInfobeta3D()` with default arguments is shown below:

```
DataInfobeta3D(data, diversity = "TD", datatype = "abundance",
               PDtree = NULL, PDreftime = NULL, FDdistM = NULL, FDtype = "AUC", FDtau = NULL)
```

All arguments in the above function are the same as those for the main function `iNEXTbeta3D`. Running the `DataInfobeta3D()` function returns basic data information including sample size, observed species richness, two sample coverage estimates (`SC(n)` and `SC(2n)`) as well as other relevant information in each of the three dimensions of diversity. We use `Brazil_rainforests` data to demo the function for each dimension.

```
## Data information for taxonomic diversity
data(Brazil_rainforests)
DataInfobeta3D(data = Brazil_rainforests, diversity = 'TD', datatype = 'abundance')
```

```
#>   Dataset        Assemblage   n S.obs SC(n) SC(2n) f1 f2 f3 f4 f5
#> 1   Marim              Edge 158    84 0.691  0.852 49 18  8  4  1
#> 2   Marim          Interior 144    80 0.704  0.899 43 23  7  5  0
#> 3   Marim Pooled assemblage 302   119 0.855  0.969 44 34 17  9  7
#> 4   Marim  Joint assemblage 302   164 0.696  0.876 92 41 15  9  1
#> 5  Rebio2              Edge 162    70 0.754  0.895 40 17  4  2  0
#> 6  Rebio2          Interior 168    74 0.763  0.877 40 13  8  4  4
#> 7  Rebio2 Pooled assemblage 330   118 0.819  0.901 60 18 15  5  3
#> 8  Rebio2  Joint assemblage 330   144 0.758  0.886 80 30 12  6  4
```

Output description:

- `Dataset` = the input datasets.
- `Assemblage` = Individual assemblages, `'Pooled assemblage'` (for gamma) or `'Joint assemblage'` (for alpha).
- `n` = number of observed individuals in the reference sample (sample size).
- `S.obs` = number of observed species in the reference sample.
- `SC(n)` = sample coverage estimate of the reference sample.
- `SC(2n)` = sample coverage estimate of twice the reference sample size.
- `f1`-`f5` = the first five species abundance frequency counts in the reference sample.

```
## Data information for phylogenetic diversity
data(Brazil_rainforests)
data(Brazil_tree)
DataInfobeta3D(data = Brazil_rainforests, diversity = 'PD', datatype = 'abundance',
               PDtree = Brazil_tree, PDreftime = NULL)
```

```
#>   Dataset        Assemblage   n S.obs SC(n) SC(2n) PD.obs f1* f2*   g1   g2 Reftime
#> 1   Marim              Edge 158    84 0.691  0.852   8805  49  26 3278 2188     400
#> 2   Marim          Interior 144    80 0.704  0.899   8436  43  28 2974 1935     400
#> 3   Marim Pooled assemblage 302   119 0.855  0.969  11842  44  39 3172 2995     400
#> 4   Marim  Joint assemblage 302   164 0.696  0.876  17241  92  54 6252 4123     400
#> 5  Rebio2              Edge 162    70 0.754  0.895   7874  40  23 3648 1717     400
#> 6  Rebio2          Interior 168    74 0.763  0.877   8360  40  17 3365 1954     400
#> 7  Rebio2 Pooled assemblage 330   118 0.819  0.901  11979  60  23 5063 1637     400
#> 8  Rebio2  Joint assemblage 330   144 0.758  0.886  16234  80  40 7013 3671     400
```

Information description:

- `Dataset`, `Assemblage`, `n`, `S.obs`, `SC(n)` and `SC(2n)`: definitions are the same as in the TD output.
- `PD.obs` = the observed total branch length in the phylogenetic tree spanned by all observed species.
- `f1*`,`f2*` = the number of singletons and doubletons in the node/branch abundance set.
- `g1`,`g2` = the total branch length of those singletons/doubletons in the node/branch abundance set.
- `Reftime` = reference time for phylogenetic diversity (the age of the root of phylogenetic tree).

```
## Data information for functional diversity (under a specified threshold level, FDtype =
        'tau_value')
data(Brazil_rainforests)
data(Brazil_distM)
DataInfobeta3D(data = Brazil_rainforests, diversity = 'FD', datatype = 'abundance',
               FDdistM = Brazil_distM, FDtype = 'tau_value', FDtau = NULL)
```

```
#>   Dataset        Assemblage   n S.obs SC(n) SC(2n) a1* a2* h1 h2   Tau
#> 1   Marim              Edge 158    84 0.691  0.852   0   0  0  0 0.343
#> 2   Marim          Interior 144    80 0.704  0.899   0   0  0  0 0.343
#> 3   Marim Pooled assemblage 302   119 0.855  0.969   0   0  0  0 0.343
#> 4   Marim  Joint assemblage 302   164 0.696  0.876   0   0  0  0 0.343
#> 5  Rebio2              Edge 162    70 0.754  0.895   0   0  0  0 0.343
#> 6  Rebio2          Interior 168    74 0.763  0.877   0   0  0  0 0.343
```

```
#> 7  Rebio2 Pooled assemblage 330   118 0.819  0.901   0   0  0  0 0.343
#> 8  Rebio2  Joint assemblage 330   144 0.758  0.886   0   0  0  0 0.343
```

Information description:

- `Dataset`, `Assemblage`, `n`, `S.obs`, `SC(n)` and `SC(2n)`: definitions are the same as in the TD output.
- `a1*`,`a2*` = the number of singletons (`a1*`) and of doubletons (`a2*`) among the functionally indistinct set at the specified threshold level `'Tau'`.
- `h1`,`h2` = the total contribution of singletons (`h1`) and of doubletons (`h2`) at the specified threshold level `'Tau'`.
- `Tau` = the specified threshold level of distinctiveness. Default is dmean (the mean distance between any two individuals randomly selected from the pooled data over all datasets).

```
## Data information for functional diversity (FDtype = 'AUC')
data(Brazil_rainforests)
data(Brazil_distM)
DataInfobeta3D(data = Brazil_rainforests, diversity = 'FD', datatype = 'abundance',
               FDdistM = Brazil_distM, FDtype = 'AUC')
```

```
#>   Dataset        Assemblage   n S.obs SC(n) SC(2n) dmin dmean  dmax
#> 1   Marim              Edge 158    84 0.691  0.852    0 0.329 0.755
#> 2   Marim          Interior 144    80 0.704  0.899    0 0.313 0.663
#> 3   Marim Pooled assemblage 302   119 0.855  0.969    0 0.323 0.755
#> 4   Marim  Joint assemblage 302   164 0.696  0.876    0 0.323 0.755
#> 5  Rebio2              Edge 162    70 0.754  0.895    0 0.376 0.659
#> 6  Rebio2          Interior 168    74 0.763  0.877    0 0.310 0.660
#> 7  Rebio2 Pooled assemblage 330   118 0.819  0.901    0 0.355 0.770
#> 8  Rebio2  Joint assemblage 330   144 0.758  0.886    0 0.355 0.770
```

Information description:

- `Dataset`, `Assemblage`, `n`, `S.obs`, `SC(n)` and `SC(2n)`: definitions are the same as in TD and thus are omitted.
- `dmin` = the minimum distance among all non-diagonal elements in the distance matrix.
- `dmean` = the mean distance between any two individuals randomly selected from each assemblage.
- `dmax` = the maximum distance among all elements in the distance matrix.

Below We use the demo dataset (`Second-growth forests`) to show the output of the function `DataInfobeta3D` for incidence data:

```
## Data information for taxonomic diversity (incidence data)
data(Second_growth_forests)
DataInfobeta3D(data = Second_growth_forests, diversity = 'TD', datatype = 'incidence_raw')
```

```
#>            Dataset        Assemblage   T    U S.obs SC(T) SC(2T)  Q1 Q2 Q3 Q4 Q5
#> 1 CR 2005 vs. 2017         Year_2005 100  787   135 0.919  0.953  64 17 16  6  4
#> 2 CR 2005 vs. 2017         Year_2017 100  768   134 0.917  0.956  64 20 11  8  3
#> 3 CR 2005 vs. 2017 Pooled assemblage 100  923   151 0.925  0.959  70 21 14  6  6
#> 4 CR 2005 vs. 2017  Joint assemblage 100 1555   269 0.918  0.954 128 37 27 14  7
#> 5 JE 2005 vs. 2017         Year_2005 100  503    71 0.955  0.979  23  9  8  4  0
#> 6 JE 2005 vs. 2017         Year_2017 100  659    91 0.953  0.979  31 12  8  3  5
#> 7 JE 2005 vs. 2017 Pooled assemblage 100  864   107 0.963  0.987  32 17  9  4  8
#> 8 JE 2005 vs. 2017  Joint assemblage 100 1162   162 0.954  0.979  54 21 16  7  5
```

Information description:

- `Dataset` = the input datasets.
- `Assemblage` = Individual assemblages, `'Pooled assemblage'` (for gamma) or `'Joint assemblage'` (for alpha).
- `T` = number of sampling units in the reference sample (sample size for incidence data).
- `U` = total number of incidences in the reference sample.
- `S.obs` = number of observed species in the reference sample.
- `SC(T)` = sample coverage estimate of the reference sample.
- `SC(2T)` = sample coverage estimate of twice the reference sample size.
- `Q1`-`Q5` = the first five species incidence frequency counts in the reference sample.

License and feedback

The `iNEXT.beta3D` package is licensed under the GPLv3. To help refine `iNEXT.beta3D`, users' comments or feedback would be welcome (please send them to Anne Chao or report an issue on the `iNEXT.beta3D` github iNEXT.beta3D_github.

References

- Chao, A., Chiu, C.-H., Hu, K.-H., and Zeleny, D. (2023a). Revisiting Alwyn H. Gentry's forest transect data: a statistical sampling-model-based approach. *Japanese Journal of Statistics and Data Science*, 6, 861-884. (https://doi.org/10.1007/s42081-023-00214-1)
- 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., Magnago, L. F. S., Dornelas, M., Zeleny, D., Colwell, R. K., and Magurran, A. E. (2023b). Rarefaction and extrapolation with beta diversity under a framework of Hill numbers: the iNEXT.beta3D standardization. *Ecological Monographs* e1588.