

A Quick Introduction to iNEXT.3D via Examples

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`iNEXT.3D` (INterpolation and EXTrapolation for three dimensions of biodiversity) is a sequel to `iNEXT` (Hsieh et al., 2016). Here the three dimensions (3D) of diversity include taxonomic diversity (TD), phylogenetic diversity (PD) and functional diversity (FD). An online version “iNEXT.3D Online” (https://chao.shinyapps.io/iNEXT_3D/) is also available for users without an R background.

A unified framework based on Hill numbers (for TD) and their generalizations (Hill-Chao numbers, for PD and FD) is adopted to quantify 3D. In this framework, TD quantifies the effective number of species, PD quantifies the effective total branch length, 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. (2014) for the basic standardization theory for TD, and Chao et al. (2021) for a review of the unified theory for 3D.

For each of the three dimensions of biodiversity, `iNEXT.3D` features two statistical analyses (non-asymptotic and asymptotic):

1. A non-asymptotic approach based on interpolation and extrapolation for 3D diversity (i.e., Hill-Chao numbers)

`iNEXT.3D` computes the estimated 3D diversity for standardized samples with a common sample size or sample completeness. This approach aims to compare diversity estimates for equally-large (with a common sample size) or equally-complete (with a common sample coverage) samples; it is based on the seamless rarefaction and extrapolation (R/E) sampling curves of Hill-Chao numbers for $q = 0, 1$ and 2 . For each dimension of biodiversity, `iNEXT.3D` offers three types of R/E sampling curves:

- Sample-size-based (or size-based) R/E sampling curves: This type of sampling curve plots the diversity estimates with respect to sample size.
- Coverage-based R/E sampling curves: This type of sampling curve plots the diversity estimates with respect to sample coverage.
- Sample completeness curve: This curve depicts how sample coverage varies with sample size. The sample completeness curve provides a bridge between the size- and coverage-based R/E sampling curves.

2. An asymptotic approach to infer asymptotic 3D diversity (i.e., Hill-Chao numbers)

`iNEXT.3D` computes the estimated asymptotic 3D diversity and also plots 3D diversity profiles (q-profiles) for q between 0 and 2 , in comparison with the observed diversity. Typically, the asymptotic estimates for $q \geq 1$ are reliable, but for $q < 1$ (especially for $q = 0$, species richness), the asymptotic estimates represent only lower bounds. `iNEXT.3D` also features a time-profile (which depicts the observed and asymptotic estimate of PD or mean PD with respect to reference times), and a tau-profile (which depicts the observed and asymptotic estimate of FD with respect to threshold level tau).

How to cite

If you publish your work based on results from `iNEXT.3D` package, you should make references to the following methodology paper and the package:

- 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. and Hu, K.-H. (2023). The iNEXT.3D package: interpolation and extrapolation for three dimensions of biodiversity. R package available from CRAN.

SOFTWARE NEEDED TO RUN iNEXT.3D IN R

- Required: [R](#)
- Suggested: [RStudio IDE](#)

HOW TO RUN iNEXT.3D:

The `iNEXT.3D` package can be downloaded from CRAN or Anne Chao's [iNEXT.3D_github](https://github.com/annechao/iNEXT.3D) using the commands below. For a first-time installation, some additional packages must be installed and loaded; see package manual.

```
## install iNEXT.3D package from CRAN
install.packages("iNEXT.3D")
```

```
## or install the latest version from github
install.packages('devtools')
library(devtools)
install_github('AnneChao/iNEXT.3D')

## import packages
library(iNEXT.3D)
```

There are six main functions in this package:

Two functions for non-asymptotic analysis with graphical displays:

- **iNEXT3D** computes standardized 3D diversity estimates of order $q = 0, 1$ and 2 for rarefied and extrapolated samples at specified sample coverage values and sample sizes.
- **ggiNEXT3D** visualizes the output from the function `iNEXT3D`.

Two functions for point estimation and basic data information

- **estimate3D** computes 3D diversity of order $q = 0, 1$ and 2 with a particular set of user-specified level of sample sizes or sample coverage values.
- **DataInfo3D** provides basic data information based on the observed data.

Two functions for asymptotic analysis with graphical displays:

- **ObsAsy3D** computes observed and asymptotic diversity of order q between 0 and 2 (in increments of 0.2) for 3D diversity; it also computes observed and asymptotic PD for specified reference times, and observed and asymptotic FD for specified threshold levels.
- **ggObsAsy3D** visualizes the output from the function `ObsAsy3D`.

DATA INPUT FORMAT

Species abundance/incidence data format

Although species identities/names are not required to assess TD or compare TD across individual assemblages (as in the `iNEXT` package), they are required for PD and FD. Thus, for `iNEXT.3D` package, information on species identity (or any unique identification code) and assemblage affiliation is required. Two types of species abundance/incidence data are supported:

1. Individual-based abundance data (`datatype = "abundance"`): When there are multiple assemblages, in addition to the assemblage/site names (as column names) and the species names (as row names), species abundance data (reference sample) can be input as a species (in rows) by assemblage (in columns) matrix/data.frame or a list of species abundance vectors. In the special case that there is only one assemblage, all data should be read in one column.
2. Sampling-unit-based incidence data: Incidence-raw data (`datatype = "incidence_raw"`): for each assemblage, input data for a reference sample consist of a species-by-sampling-unit matrix, in addition to the sampling-unit names (as column names) and the species names (as row names). When there are N assemblages, input data consist of N lists of matrices, and each matrix is a species-by-sampling-unit matrix. Each element in the incidence raw matrix is 1 for a detection, and 0 for a non-detection. Input a matrix which combines data for all assemblages is allowed, but the argument `nT` in the function `iNEXT3D` must be specified so that the number of sampling units in each assemblage is specified.

For example, the dataset `Brazil_rainforest_abun_data` included in the `iNEXT.3D` package consists of species sample abundances of two assemblages/habitats: "Edge" and "Interior". Run the following code to view the first 15 rows of the abundance data.

```
data("Brazil_rainforest_abun_data")
Brazil_rainforest_abun_data
```

	Edge	Interior
Carpotroche_brasiliensis	11	21
Astronium_concinnum	110	11
Astronium_graveolens	36	7
Spondias_macrocarpa	12	1
Spondias_venulosa	2	0
Tapirira_guianensis	7	1
Thyrsodium_spruceanum	11	11
Anaxagorea_silvatica	1	13
Annona_acutiflora	1	1
Annona_cacans	0	2
Annona_dolabripetala	3	3
Annona_sp	0	1
Duquetia_chrysocarpa	1	1
Ephedranthus_sp1	1	0
Ephedranthus_sp2	0	1

We use data (`Fish_incidence_data`) collected from two time periods, namely "2013-2015" and "2016-2018", as an example. Each time period is designated as an assemblage. The purpose was to compare 3D diversity of the two time periods. In each time period, species incidence/occurrence was recorded in 36 sampling units in each assemblage; each sampling unit represents a sampling date. Thus, there are 36 columns in each time period. Run the following code to view the first 6 rows and 6 columns for each matrix.

```
data("Fish_incidence_data")
Fish_incidence_data
```

```
$`2013-2015`
      17/01/2013 18/02/2013 19/03/2013 17/04/2013 16/05/2013 14/06/2013
Agonus_cataphractus      0      1      1      1      0      0
Alosa_fallax              0      0      0      0      0      0
Ammodytes_tobianus       0      0      0      0      0      0
Anguilla_anguilla        0      1      1      0      0      0
Aphia_minuta             0      0      0      0      1      1
Arnoglossus_laterna      0      0      0      0      0      0

$`2016-2018`
      18/01/2016 15/02/2016 16/03/2016 14/04/2016 12/05/2016 10/06/2016
Agonus_cataphractus      1      1      1      1      1      0
Alosa_fallax              0      0      0      0      0      0
Ammodytes_tobianus       0      0      0      0      0      0
Anguilla_anguilla        0      0      0      0      0      0
Aphia_minuta             0      0      0      0      1      0
Arnoglossus_laterna      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 the pooled data is required. For the dataset `Fish_incidence_data`, the phylogenetic tree for all observed species (including species in both time periods) is stored in the file `fish_phylo_tree`; for the dataset `Brazil_rainforest_abun_data`, the phylogenetic tree for all observed species (including species in both Edge and Interior habitats) is stored in the file `Brazil_rainforest_phylo_tree`. A partial list of the tip labels and node labels are shown below.

```
data("Brazil_rainforest_phylo_tree")
Brazil_rainforest_phylo_tree

Phylogenetic tree with 425 tips and 205 internal nodes.

Tip labels:
  Carpotroche_brasiliensis, Casearia_ulmifolia, Casearia_sp4, Casearia_sylvestris,
  Casearia_sp2, Casearia_sp3, ...
Node labels:
  magnoliales_to_asterales, poales_to_asterales, , , , celastrales_to_malpighiales, ...

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 the pooled data is required in a matrix/data.frame format. For the dataset `Fish_incidence_data`, the distance matrix for all observed species (including species in both time periods) is stored in the file `fish_dist_matrix`; for the dataset `Brazil_rainforest_abun_data`, the distance matrix for all species (including species in both Edge and Interior habitats) is stored in the file `Brazil_rainforest_dist_matrix`. The distance matrix for the first 3 Brazil rainforest tree species is shown below.

```
data("Brazil_rainforest_distance_matrix")
Brazil_rainforest_distance_matrix
```

```
      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 `iNEXT3D()`: RAREFACTION/EXTRAPOLATION

We first describe the main function `iNEXT3D()` with default arguments:

```
iNEXT3D(data, diversity = 'TD', q = c(0,1,2), datatype = "abundance",
  size = NULL, endpoint = NULL, knots = 40, nboot = 50, conf = 0.95, nT = NULL,
  PDtree = NULL, PDreftime = NULL, PDtype = 'meanPD',
  FDdistM, FDtype = 'AUC', FDTau = NULL, FDCut_number = 50)
```

The arguments of this function are briefly described below, and will be explained in more details by illustrative examples in later text. This main function computes standardized 3D diversity estimates of order $q = 0, 1$ and 2 , the sample coverage estimates, and related statistics for K (if `knots = K` in the specified argument) evenly-spaced knots (sample sizes) between size 1 and the `endpoint`, where the endpoint is described below. Each knot represents a particular sample size for which 3D diversity estimates will be calculated. By default, `endpoint = 2` double the reference sample size for abundance data or double the total sampling units for incidence data. For example, if `endpoint = 10`, `knot = 4` is specified, diversity estimates will be computed for a sequence of samples with sizes (1, 4, 7, 10).

Argument	Description
<code>data</code>	<p>a. For <code>datatype = "abundance"</code>, <code>data</code> can be input as a vector of species abundances (for a single assemblage), matrix/data.frame (species by assemblages), or a list of species abundance vectors.</p> <p>b. For <code>datatype = "incidence_raw"</code>, <code>data</code> can be input as a list of matrices/data.frames (species by sampling units); <code>data</code> can also be input as a single matrix/data.frame by merging all sampling units across assemblages based on species identity; in this case, the number of sampling units (<code>nT</code>, see below) must be specified.</p>
<code>diversity</code>	selection of diversity type: 'TD' = Taxonomic diversity, 'PD' = Phylogenetic diversity, and 'FD' = Functional diversity.
<code>q</code>	a numerical vector specifying the diversity orders. Default is <code>c(0, 1, 2)</code> .
<code>datatype</code>	data type of input data: individual-based abundance data (<code>datatype = "abundance"</code>), or species by sampling-units incidence/occurrence matrix (<code>datatype = "incidence_raw"</code>) with all entries being 0 (non-detection) or 1 (detection).
<code>size</code>	an integer vector of sample sizes (number of individuals or sampling units) for which diversity estimates will be computed. If <code>NULL</code> , then diversity estimates will be computed for those sample sizes determined by the specified/default <code>endpoint</code> and <code>knots</code> .
<code>endpoint</code>	an integer specifying the sample size that is the <code>endpoint</code> for rarefaction/extrapolation. If <code>NULL</code> , then <code>endpoint = 2</code> double the reference sample size.
<code>knots</code>	an integer specifying the number of equally-spaced <code>knots</code> (say K , default is 40) between size 1 and the <code>endpoint</code> ; each knot represents a particular sample size for which diversity estimate will be calculated. If the <code>endpoint</code> is smaller than the reference sample size, then <code>iNEXT3D()</code> computes only the rarefaction estimates for approximately K evenly spaced <code>knots</code> . If the <code>endpoint</code> is larger than the reference sample size, then <code>iNEXT3D()</code> computes rarefaction estimates for approximately $K/2$ evenly spaced <code>knots</code> between sample size 1 and the reference sample size, and computes extrapolation estimates for approximately $K/2$ evenly spaced <code>knots</code> between the reference sample size and the <code>endpoint</code> .
<code>nboot</code>	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.
<code>conf</code>	a positive number < 1 specifying the level of confidence interval. Default is 0.95.
<code>nT</code>	(required only when <code>datatype = "incidence_raw"</code> and input data in a single matrix/data.frame) a vector of nonnegative integers specifying the number of sampling units in each assemblage. If assemblage names are not specified(i.e., <code>names(nT) = NULL</code>), then assemblages are automatically named as "assemblage1", "assemblage2",..., etc.
<code>PDtree</code>	(required argument for <code>diversity = "PD"</code>), a phylogenetic tree in Newick format for all observed species in the pooled assemblage.
<code>PDreftime</code>	(argument only for <code>diversity = "PD"</code>), a vector of numerical values specifying reference times for PD. Default is <code>NULL</code> (i.e., the age of the root of <code>PDtree</code>).
<code>PDtype</code>	(argument only for <code>diversity = "PD"</code>), select PD type: <code>PDtype = "PD"</code> (effective total branch length) or <code>PDtype = "meanPD"</code> (effective number of equally divergent lineages). Default is "meanPD", where <code>meanPD = PD/tree depth</code> .
<code>FDdistM</code>	(required argument for <code>diversity = "FD"</code>), a species pairwise distance matrix for all species in the pooled assemblage.
	(argument only for <code>diversity = "FD"</code>), select FD type: <code>FDtype = "tau_values"</code> for FD

FDtype	under specified threshold values, or <code>FDtype = "AUC"</code> (area under the curve of tau-profile) for an overall FD which integrates all threshold values between zero and one. Default is "AUC".
FDtau	(argument only for <code>diversity = "FD"</code> and <code>FDtype = "tau_values"</code>), a numerical vector between 0 and 1 specifying tau values (threshold levels). If <code>NULL</code> (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	(argument only for <code>diversity = "FD"</code> and <code>FDtype = "AUC"</code>), a numeric number to cut <code>[0, 1]</code> 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 <code>FDcut_number = 50</code> . A larger value can be set to obtain more accurate AUC value.

For each dimension of diversity (`TD`, `PD`, `FD`), the main function `iNEXT3D()` returns the `iNEXT3D` object, which can be further used to make plots using the function `ggiNEXT3D()` to be described below. The "`iNEXT3D`" object includes three lists:

1. `$TDInfo` (`$PDInfo`, or `$FDInfo`) for summarizing data information.
2. `$TDiNextEst` (`$PDiNextEst`, or `$FDiNextEst`) for showing diversity estimates along with related statistics for a series of rarefied and extrapolated samples; there are two data frames (`$size_based` and `$coverage_based`) conditioning on standardized sample size or sample coverage, respectively.
3. `$TDAsyEst` (`$PDAsyEst`, or `$FDAsyEst`) for showing asymptotic diversity estimates along with related statistics.

FUNCTION ggiNEXT3D(): GRAPHIC DISPLAYS

The function `ggiNEXT3D()`, which extends `ggplot2` with default arguments, is described as follows:

```
ggiNEXT3D(output, type = 1:3, facet.var = "Assemblage", color.var = "Order.q")
```

Here `output` is the `iNEXT3D()` object. Three types of curves are allowed for 3D diversity:

1. Sample-size-based R/E curve (`type = 1`): This curve plots diversity estimates with confidence intervals as a function of sample size.
2. Sample completeness curve (`type = 2`): This curve plots the sample coverage with respect to sample size.
3. Coverage-based R/E curve (`type = 3`): This curve plots the diversity estimates with confidence intervals as a function of sample coverage.

The argument `facet.var = "Order.q"`, `facet.var = "Assemblage"`, `facet.var = "Both"`, or `facet.var = "None"` is used to create a separate plot for each value of the specified variable.

The `ggiNEXT3D()` function is a wrapper with the package `ggplot2` to create a rarefaction/extrapolation sampling curve in a single line of code. The figure object is of class "`ggplot`", so it can be manipulated by using the `ggplot2` tools.

TAXONOMIC DIVERSITY (TD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 1: TD rarefaction/extrapolation for abundance data

Based on the dataset (`Brazil_rainforest_abun_data`) included in the package, the following commands return all numerical results for `TD`. The first list of the output (`$TDInfo`) returns basic data information including the name of the Assemblage, sample size (`n`), observed species richness (`S.obs`), sample coverage estimate of the reference sample with size `n` (`SC(n)`), sample coverage estimate of the extrapolated sample with size `2n` (`SC(2n)`) as well as the first five species abundance frequency counts in the reference sample (`f1-f5`). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'TD'` and `datatype = "abundance"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order `q` between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

```
data(Brazil_rainforest_abun_data)
output_TD_abun <- iNEXT3D(Brazil_rainforest_abun_data, diversity = 'TD', q = c(0,1,2),
                          datatype = "abundance")
output_TD_abun$TDInfo
```

```
$TDInfo
  Assemblage   n S.obs SC(n) SC(2n)  f1 f2 f3 f4 f5
1      Edge 1794  319 0.939  0.974 110 48 38 28 13
```

The second list of the output (`$TDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the “Edge” assemblage, corresponding to the target sample size $m = 1, 95, 189, \dots, 1699, 1794, 1795, 1899, \dots, 3588$), which locates the reference sample size at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target sample size (`m`), the Method (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the size m is less than, equal to, or greater than the reference sample size), the diversity estimate of order q (`qTD`), the lower and upper confidence limits of diversity (`qTD.LCL` and `qTD.UCL`) conditioning on the sample size, and the corresponding sample coverage estimate (`SC`) along with the lower and upper confidence limits of sample coverage (`SC.LCL` and `SC.UCL`). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_TD_abun$TDiNextEst$size_based
```

	Assemblage	Order.q	m	Method	qTD	qTD.LCL	qTD.UCL	SC	SC.LCL	SC.UCL
1	Edge	0	1	Rarefaction	1.000	1.000	1.000	0.012	0.010	0.013
2	Edge	0	95	Rarefaction	66.306	65.043	67.569	0.484	0.468	0.500
3	Edge	0	189	Rarefaction	106.743	104.052	109.434	0.638	0.622	0.653
4	Edge	0	284	Rarefaction	137.029	133.025	141.033	0.718	0.704	0.733
5	Edge	0	378	Rarefaction	161.010	155.820	166.200	0.768	0.755	0.782
6	Edge	0	472	Rarefaction	181.073	174.781	187.366	0.803	0.790	0.816

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (`SC`), the corresponding sample size (`m`), the Method (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the coverage SC is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order q (`qTD`), the lower and upper confidence limits of diversity (`qTD.LCL` and `qTD.UCL`) conditioning on the target sample coverage value. Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication, leading to higher uncertainty on the resulting diversity estimate.)

```
output_TD_abun$TDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	m	Method	qTD	qTD.LCL	qTD.UCL
1	Edge	0	0.012	1	Rarefaction	1.000	0.970	1.030
2	Edge	0	0.484	95	Rarefaction	66.306	61.976	70.636
3	Edge	0	0.638	189	Rarefaction	106.743	99.830	113.657
4	Edge	0	0.718	284	Rarefaction	137.029	127.987	146.072
5	Edge	0	0.768	378	Rarefaction	161.010	150.075	171.946
6	Edge	0	0.803	472	Rarefaction	181.073	168.376	193.771

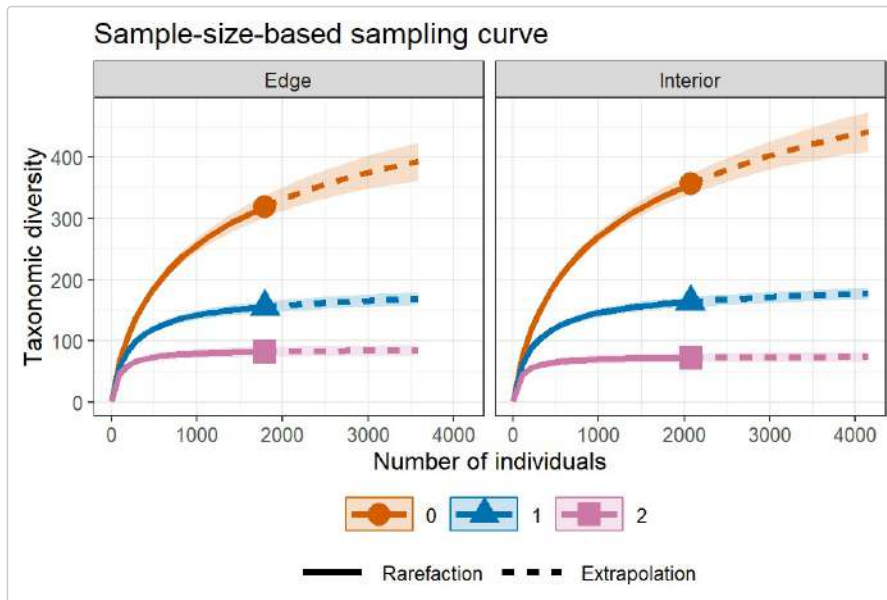
The third list of the output (`$TDAsyEst`) includes the name of the Assemblage, diversity label (`qTD`, species richness for $q = 0$, Shannon diversity for $q = 1$, and Simpson diversity for $q = 2$), the observed diversity (`TD_obs`), asymptotic diversity estimate (`TD_asy`) and its estimated bootstrap standard error (`s.e.`) as well as the confidence intervals for asymptotic diversity (`qTD.LCL` and `qTD.UCL`). These statistics are computed only for $q = 0, 1$ and 2 . More detailed information about asymptotic and observed diversity estimates for any order q between 0 and 2 can be obtained from function `ObsAsy3D()`. The output for `$TDAsyEst` is shown below:

```
output_TD_abun$TDAsyEst
```

	Assemblage	qTD	TD_obs	TD_asy	s.e.	qTD.LCL	qTD.UCL
1	Edge	Species richness	319.000	444.971	28.910	388.309	501.634
2	Edge	Shannon diversity	155.386	178.000	4.920	168.357	187.642
3	Edge	Simpson diversity	82.023	85.905	3.753	78.550	93.261
4	Interior	Species richness	356.000	513.518	28.411	457.834	569.202
5	Interior	Shannon diversity	163.514	186.983	6.553	174.139	199.827
6	Interior	Simpson diversity	72.153	74.718	4.713	65.481	83.955

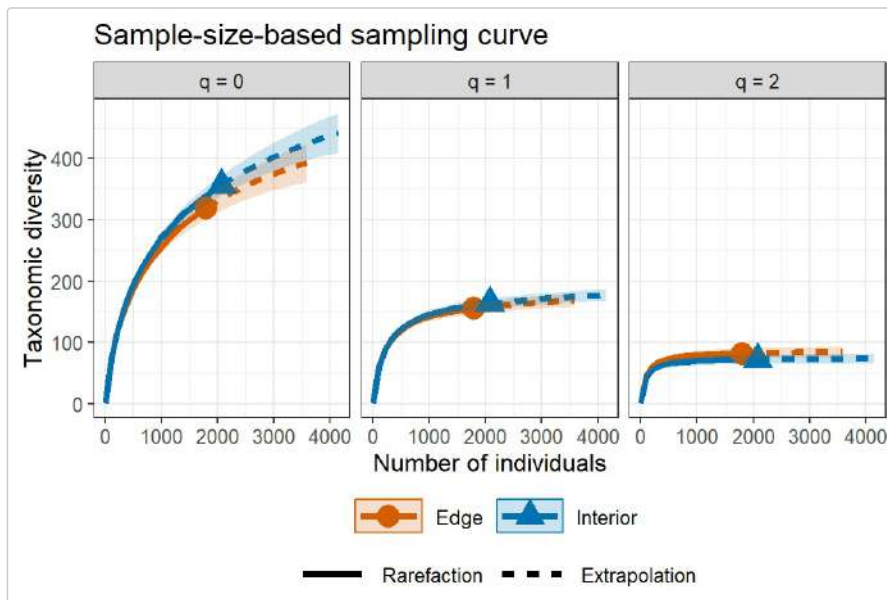
The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) is given below:

```
# TD sample-size-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_TD_abun, type = 1, facet.var = "Assemblage")
```



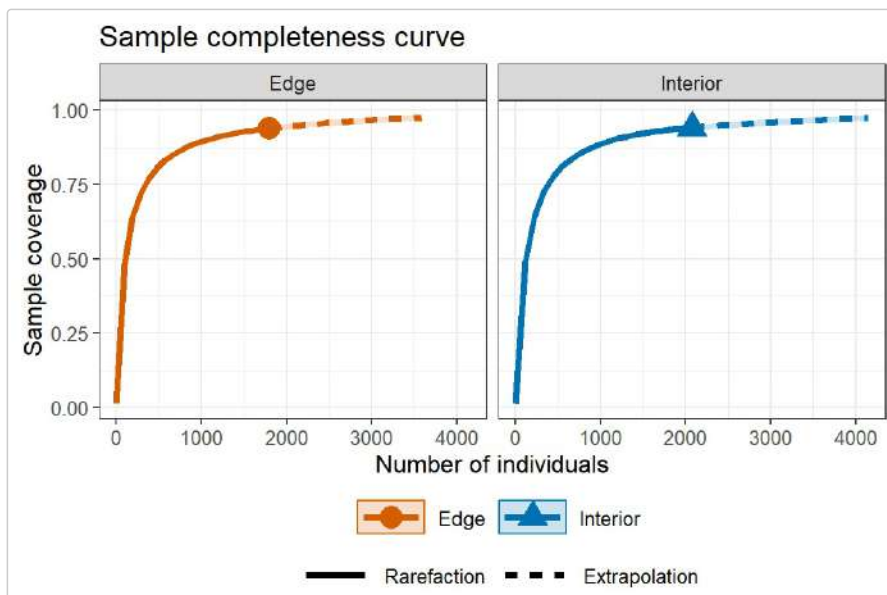
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# TD sample-size-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_TD_abun, type = 1, facet.var = "Order.q")
```



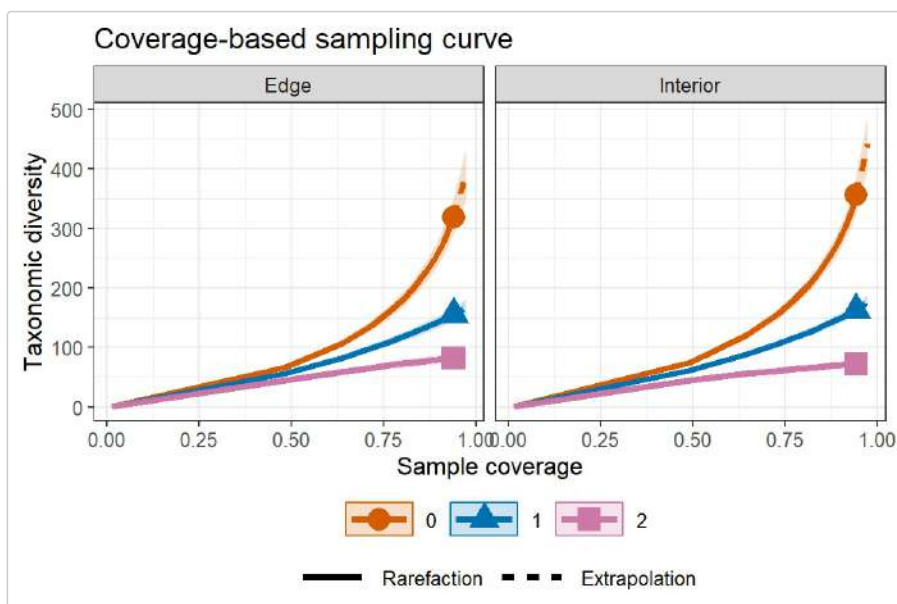
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors represent different assemblages.

```
# Sample completeness curves for abundance data, separating by "Assemblage"
ggiNEXT3D(output_TD_abun, type = 2, color.var = "Assemblage")
```

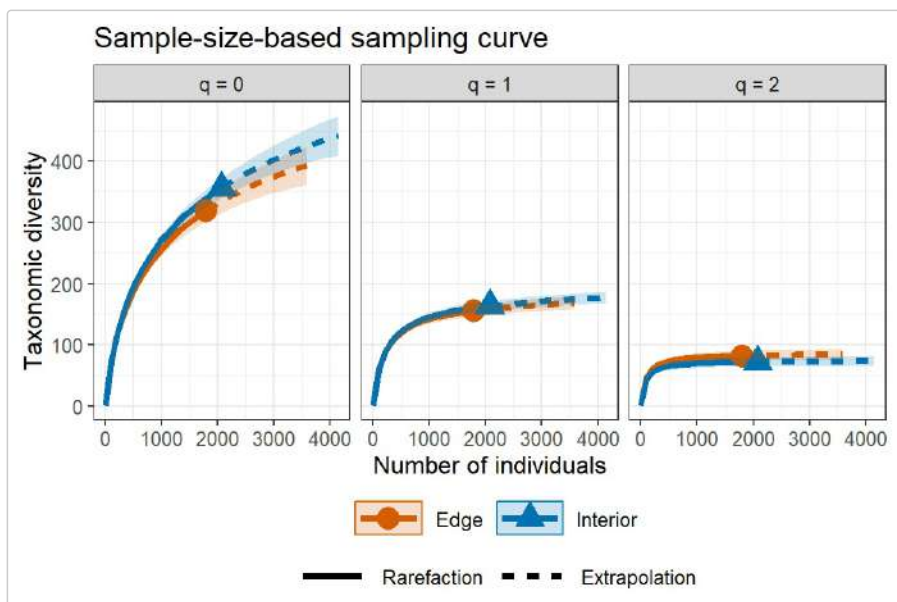


The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# TD coverage-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_TD_abun, type = 3, facet.var = "Assemblage")
```



```
# TD coverage-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_TD_abun, type = 3, facet.var = "Order.q")
```



EXAMPLE 2: TD rarefaction/extrapolation for incidence data

Based on the dataset (`Fish_incidence_data`) included in the package, the following commands return all numerical results for TD. The first list of the output (`$TDInfo`) returns basic data information including the name of the Assemblage, number of sampling units (T), total number of incidences (U), observed species richness (S_{obs}), sample coverage estimate of the reference sample with size T ($SC(T)$), sample coverage estimate of the extrapolated sample with size $2T$ ($SC(2T)$) as well as the first five species incidence frequency counts in the reference sample (Q_1-Q_5). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'TD'` and `datatype = "incidence_raw"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order q between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

```
data(Fish_incidence_data)
output_TD_inci <- iNEXT3D(Fish_incidence_data, diversity = 'TD', q = c(0, 1, 2),
                          datatype = "incidence_raw")
output_TD_inci$TDInfo
```

```
$TDInfo
```


	Assemblage	T	U	S.obs	SC(T)	SC(2T)	Q1	Q2	Q3	Q4	Q5
1	2013-2015	36	532	50	0.980	0.993	11	6	4	1	3
2	2016-2018	36	522	53	0.976	0.989	13	5	5	2	3

The second list of the output (`$TDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the "2013-2015" time period, corresponding to the target number of sample units `mT = 1, 2, 4, ..., 34, 36, 37, 38, ..., 72`), which locates the reference sampling units at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target number of sampling units (`mT`), the `Method` (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the target number of sample units `mT` is less than, equal to, or greater than the number of sampling units in the reference sample), the diversity estimate of order `q` (`qTD`), the lower and upper confidence limits of diversity (`qTD.LCL` and `qTD.UCL`) conditioning on the sample size, and the corresponding sample coverage estimate (`SC`) along with the lower and upper confidence limits of sample coverage (`SC.LCL` and `SC.UCL`). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_TD_inci$TDiNextEst$size_based
```

	Assemblage	Order.q	mT	Method	qTD	qTD.LCL	qTD.UCL	SC	SC.LCL	SC.UCL
1	2013-2015	0	1	Rarefaction	14.778	13.921	15.635	0.606	0.575	0.636
2	2013-2015	0	2	Rarefaction	20.603	19.460	21.746	0.749	0.724	0.773
3	2013-2015	0	4	Rarefaction	27.079	25.501	28.658	0.851	0.833	0.868
4	2013-2015	0	6	Rarefaction	31.121	29.209	33.034	0.894	0.880	0.909
5	2013-2015	0	8	Rarefaction	34.042	31.847	36.237	0.919	0.906	0.931
6	2013-2015	0	10	Rarefaction	36.319	33.873	38.765	0.934	0.923	0.945

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (`SC`), the corresponding number of sampling units (`mT`), the `Method` (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the coverage `SC` is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order `q` (`qTD`), the lower and upper confidence limits of diversity (`qTD.LCL` and `qTD.UCL`) conditioning on the target sample coverage value. Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication, leading to higher uncertainty on the resulting diversity estimate.)

```
output_TD_inci$TDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	mT	Method	qTD	qTD.LCL	qTD.UCL
1	2013-2015	0	0.606	1	Rarefaction	14.778	13.769	15.787
2	2013-2015	0	0.749	2	Rarefaction	20.603	18.962	22.244
3	2013-2015	0	0.851	4	Rarefaction	27.079	24.751	29.408
4	2013-2015	0	0.894	6	Rarefaction	31.121	28.310	33.933
5	2013-2015	0	0.919	8	Rarefaction	34.042	30.836	37.247
6	2013-2015	0	0.934	10	Rarefaction	36.319	32.771	39.867

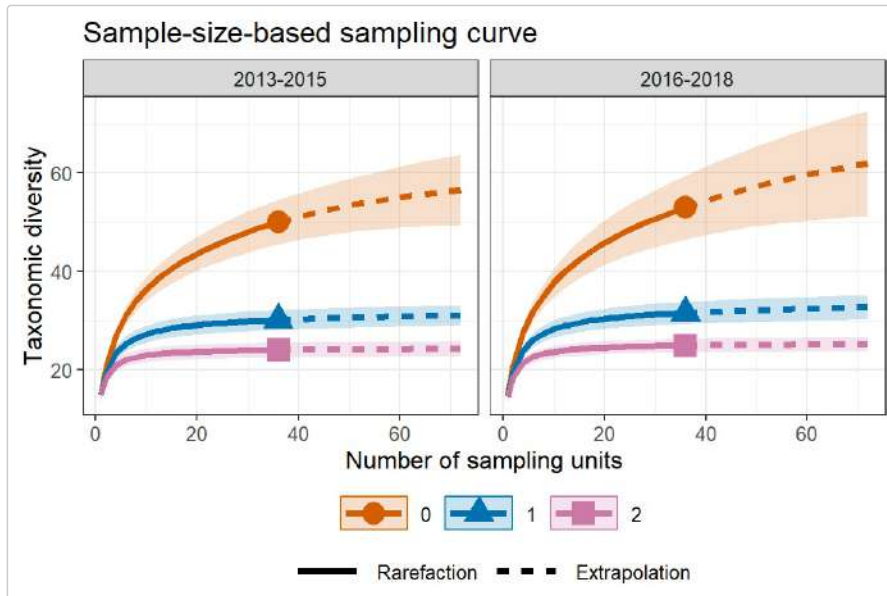
The third list of the output (`$TDAsyEst`) includes the name of the Assemblage, diversity label (`qTD`, species richness for `q = 0`, Shannon diversity for `q = 1`, and Simpson diversity for `q = 2`), the observed diversity (`TD_obs`), asymptotic diversity estimate (`TD_asy`) and its estimated bootstrap standard error (`s.e.`) as well as the confidence intervals for asymptotic diversity (`qTD.LCL` and `qTD.UCL`). These statistics are computed only for `q = 0, 1` and `2`. More detailed information about asymptotic and observed diversity estimates for any order `q` between `0` and `2` can be obtained from function `ObsAsy3D()`. The output is shown below:

```
output_TD_inci$TDAsyEst
```

	Assemblage		qTD	TD_obs	TD_asy	s.e.	qTD.LCL	qTD.UCL
1	2013-2015	Species richness	50.000	59.803	18.179	24.173	95.433	
2	2013-2015	Shannon diversity	30.089	31.542	1.173	29.243	33.840	
3	2013-2015	Simpson diversity	23.961	24.394	0.885	22.659	26.128	
4	2016-2018	Species richness	53.000	69.431	9.946	49.937	88.924	
5	2016-2018	Shannon diversity	31.534	33.393	1.388	30.674	36.113	
6	2016-2018	Simpson diversity	24.889	25.409	0.848	23.746	27.072	

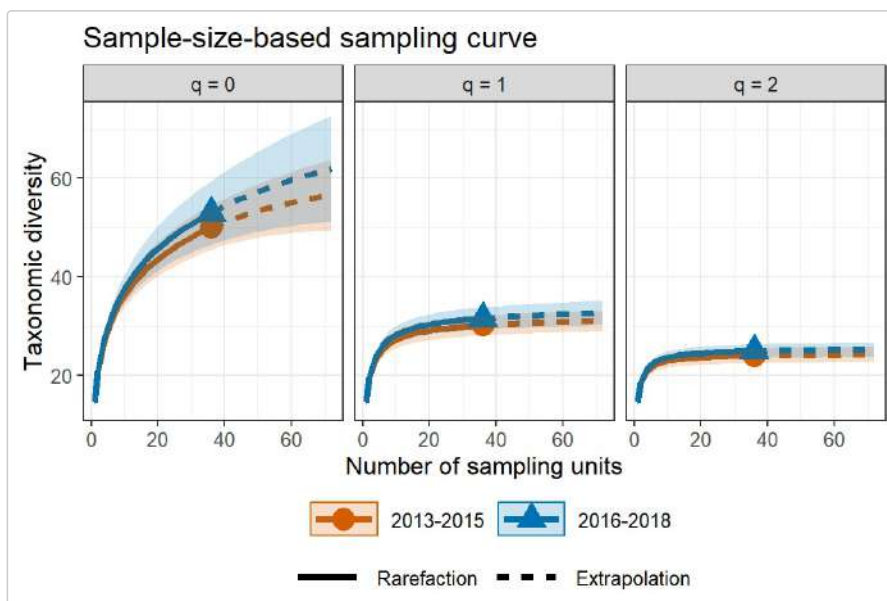
The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) for incidence data is given below:

```
# TD sample-size-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_TD_inci, type = 1, facet.var = "Assemblage")
```



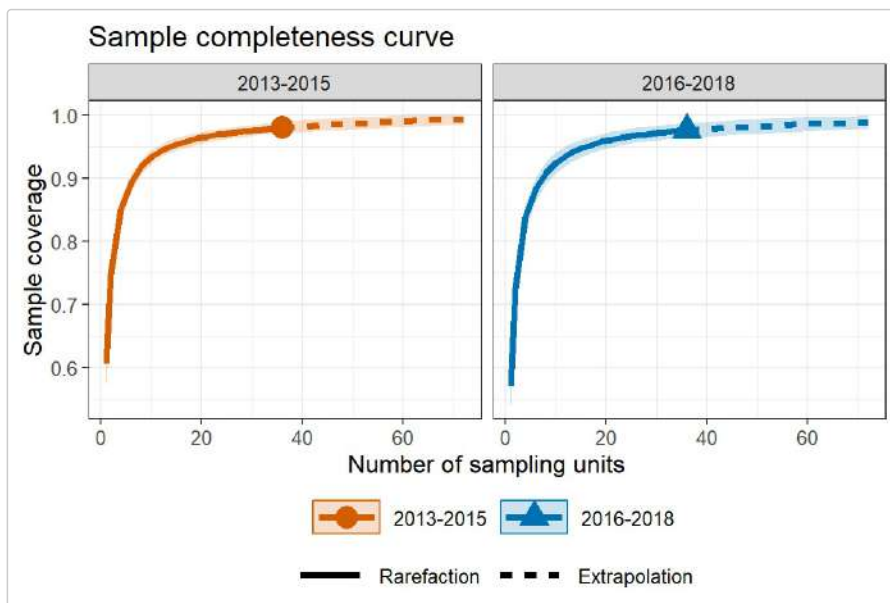
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# TD sample-size-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_TD_inci, type = 1, facet.var = "Order.q")
```



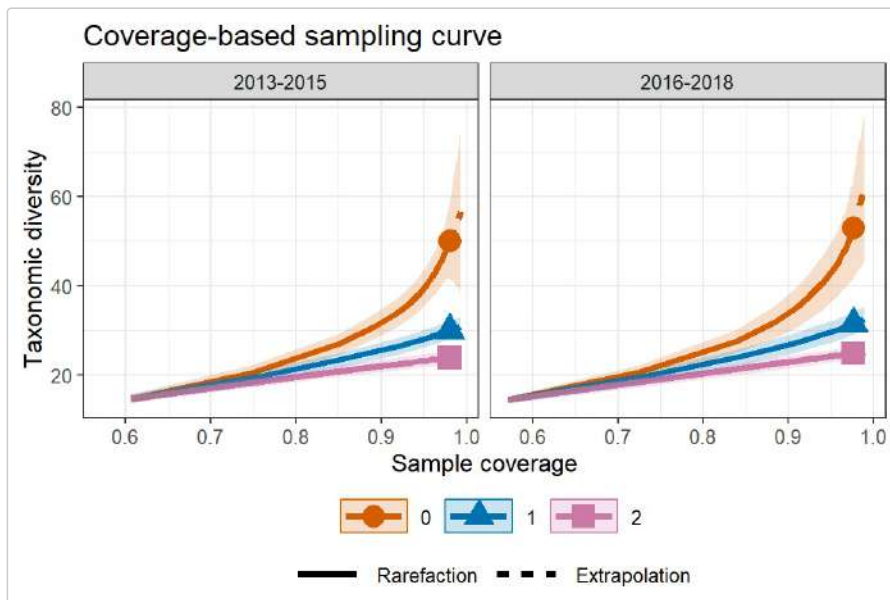
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors are used for different assemblages.

```
# Sample completeness curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_TD_inci, type = 2, color.var = "Assemblage")
```

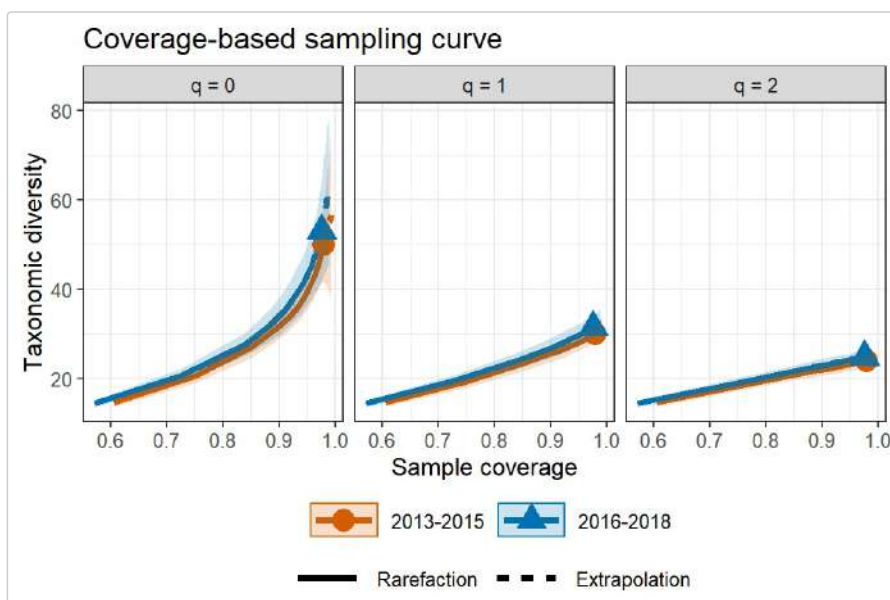


The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# TD coverage-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_TD_inci, type = 3, facet.var = "Assemblage")
```



```
# TD coverage-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_TD_inci, type = 3, facet.var = "Order.q")
```



PHYLOGENETIC DIVERSITY (PD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 3: PD rarefaction/extrapolation for abundance data

Based on the dataset (`Brazil_rainforest_abun_data`) and the phylogenetic tree (`Brazil_rainforest_phylo_tree`) included in the package, the following commands return all numerical results for PD. The first list of the output (`$PDInfo`) returns basic data information including the name of the Assemblage, sample size (n), observed species richness (S_{obs}), sample coverage estimate of the reference sample with size n ($SC(n)$), sample coverage estimate of the extrapolated sample with size $2n$ ($SC(2n)$), the observed total branch length in the phylogenetic tree spanned by all observed species (PD_{obs}), the number of singletons and doubletons in the node/branch abundance set ($f1^*$, $f2^*$), the total branch length of those singletons and doubletons in the node/branch abundance set ($g1$, $g2$), and the reference time (`Reftime`). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'PD'` and `datatype = "abundance"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order q between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

The required argument for performing PD analysis is `PDtree`. For example, the phylogenetic tree for all observed species (including species in both Edge and Interior habitats) is stored in `Brazil_rainforest_phylo_tree`. Then we enter the argument `PDtree = Brazil_rainforest_phylo_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.

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_phylo_tree)
data <- Brazil_rainforest_abun_data
tree <- Brazil_rainforest_phylo_tree
output_PD_abun <- iNEXT3D(data, diversity = 'PD', q = c(0, 1, 2), datatype = "abundance",
                          nboot = 20, PDtree = tree)

output_PD_abun$PDInfo
```

```
$PDInfo
# A tibble: 2 x 11
  Assemblage      n S.obs `SC(n)` `SC(2n)` PD.obs `f1*` `f2*`      g1      g2 Reftime
<chr>      <int> <int>  <dbl>  <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 Edge        1794   319   0.939   0.974 24516  110    52  6578 2885    400
2 Interior    2074   356   0.941   0.973 27727  123    56  7065 3656    400
```

The second list of the output (`$PDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the "Edge" assemblage, corresponding to the target sample size $m = 1, 95, 189, \dots, 1699, 1794, 1795, 1899, \dots, 3588$), which locates the reference sample size at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target sample size (m), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the size m is less than, equal to, or greater than the reference sample size), the diversity estimate of order q (q_{PD}), the lower and upper confidence limits of diversity ($q_{PD.LCL}$ and $q_{PD.UCL}$) conditioning on the sample size, the corresponding sample coverage estimate (SC) along with the lower and upper confidence limits of sample coverage ($SC.LCL$ and $SC.UCL$), the reference time (`Reftime`) and the type of PD (`Type`). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_PD_abun$PDiNextEst$size_based
```

	Assemblage	Order.q	m	Method	qPD	qPD.LCL	qPD.UCL	SC	SC.LCL	SC.UCL	Reftime	Type
1	Edge	0	1	Rarefaction	1.000	0.984	1.016	0.012	0.011	0.013	400	meanPD
2	Edge	0	95	Rarefaction	18.547	17.956	19.137	0.484	0.469	0.499	400	meanPD
3	Edge	0	189	Rarefaction	26.723	25.867	27.579	0.638	0.624	0.652	400	meanPD
4	Edge	0	284	Rarefaction	32.305	31.275	33.336	0.718	0.706	0.731	400	meanPD
5	Edge	0	378	Rarefaction	36.498	35.336	37.661	0.768	0.757	0.780	400	meanPD
6	Edge	0	472	Rarefaction	39.882	38.610	41.153	0.803	0.792	0.814	400	meanPD

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (SC), the corresponding sample size (m), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the coverage SC is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order q (q_{PD}), the lower and upper confidence limits of diversity ($q_{PD.LCL}$ and $q_{PD.UCL}$) conditioning on the target sample coverage value, the reference times (`Reftime`) and the

type of PD (`Type`). Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication, leading to higher uncertainty on the resulting diversity estimate.)

```
output_PD_abun$PDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	m	Method	qPD	qPD.LCL	qPD.UCL	Reftime	Type
1	Edge	0	0.012	1	Rarefaction	1.000	0.983	1.017	400	meanPD
2	Edge	0	0.484	95	Rarefaction	18.547	17.553	19.541	400	meanPD
3	Edge	0	0.638	189	Rarefaction	26.723	25.350	28.097	400	meanPD
4	Edge	0	0.718	284	Rarefaction	32.305	30.674	33.936	400	meanPD
5	Edge	0	0.768	378	Rarefaction	36.498	34.671	38.325	400	meanPD
6	Edge	0	0.803	472	Rarefaction	39.882	37.898	41.866	400	meanPD

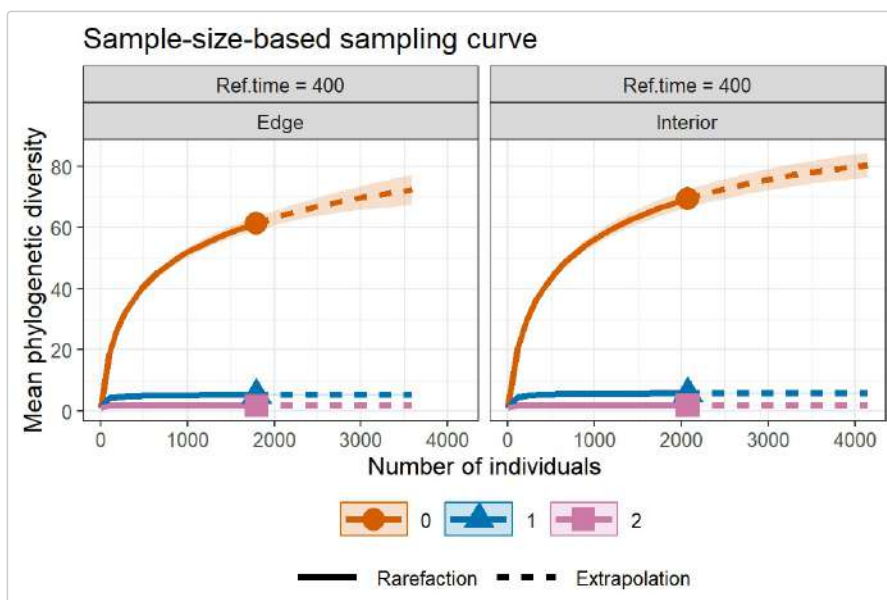
The third list of the output (`$PDAsyEst`) includes the name of the Assemblage, PD (or meanPD) for $q = 0, 1,$ and 2 (`qPD`), the observed diversity (`PD_obs`), asymptotic diversity estimates (`PD_asy`), estimated asymptotic bootstrap standard error (`s.e.`) as well as the confidence intervals for asymptotic diversity with $q = 0, 1,$ and 2 (`qPD.LCL` and `qPD.UCL`), the reference times (`Reftime`) and the type of PD (`Type`). These statistics are computed only for $q = 0, 1$ and 2 . More detailed information about asymptotic and observed diversity estimates for any order q between 0 and 2 can be obtained from function `ObsAsy3D()`. The output is shown below:

```
output_PD_abun$PDAsyEst
```

	Assemblage	qPD	PD_obs	PD_asy	s.e.	qPD.LCL	qPD.UCL	Reftime	Type
1	Edge q = 0 PD	61.290	80.027	5.580	69.091	90.964	400	meanPD	
2	Edge q = 1 PD	5.246	5.372	0.095	5.184	5.559	400	meanPD	
3	Edge q = 2 PD	1.797	1.798	0.022	1.754	1.841	400	meanPD	
4	Interior q = 0 PD	69.318	86.375	4.457	77.640	95.110	400	meanPD	
5	Interior q = 1 PD	5.721	5.854	0.093	5.672	6.036	400	meanPD	
6	Interior q = 2 PD	1.914	1.915	0.023	1.869	1.961	400	meanPD	

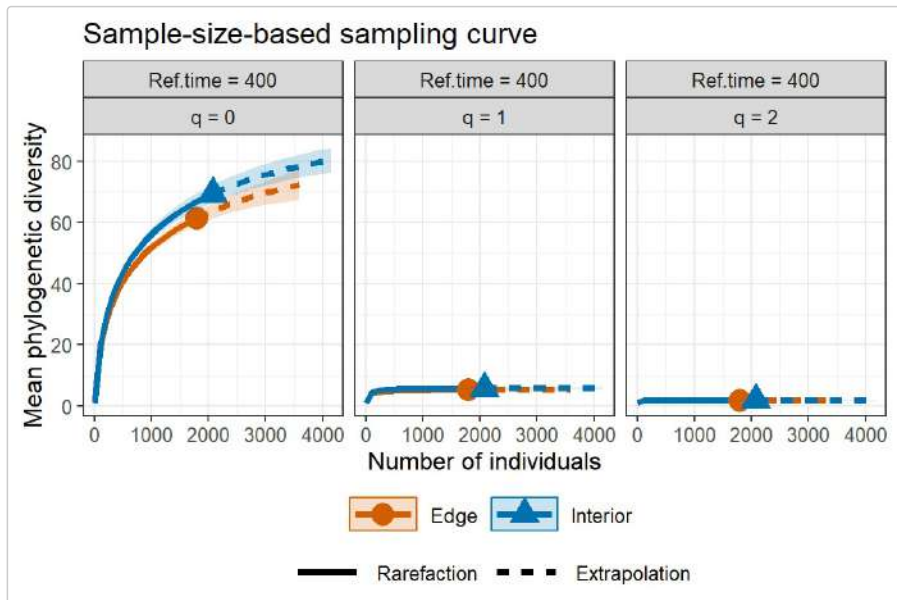
The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) is given below:

```
# PD sample-size-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_PD_abun, type = 1, facet.var = "Assemblage")
```



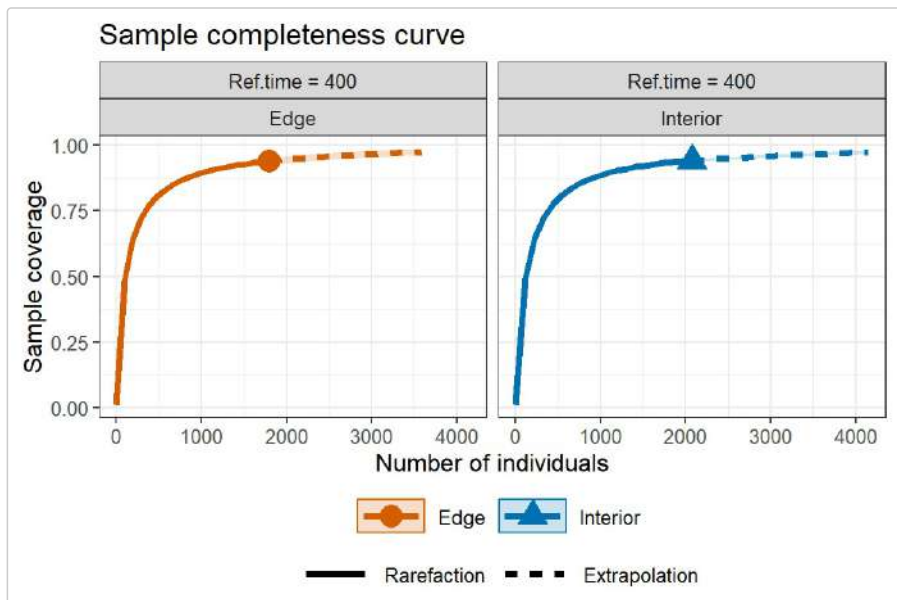
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# PD sample-size-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_PD_abun, type = 1, facet.var = "Order.q")
```



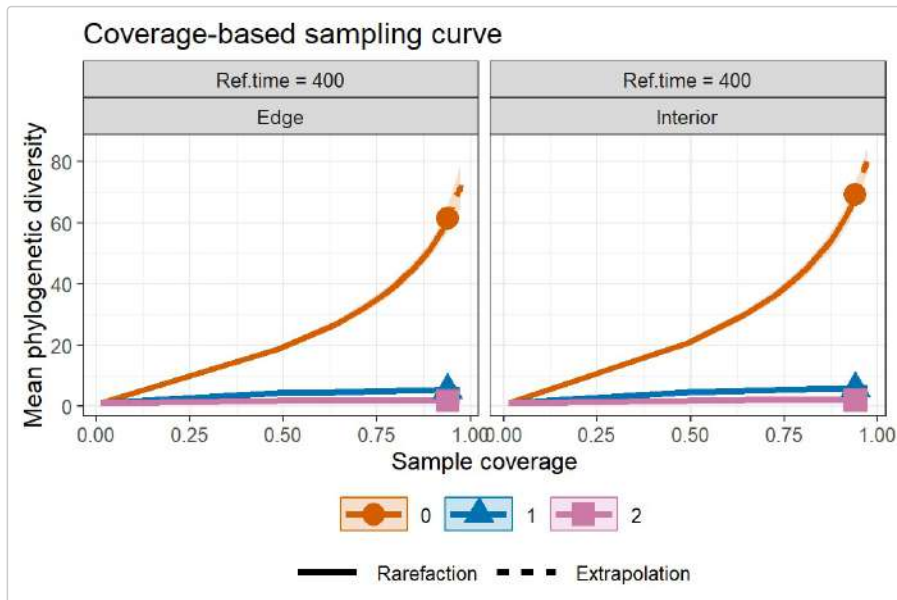
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors are used for different assemblages.

```
# Sample completeness curves for abundance data, separating by "Assemblage"
ggiNEXT3D(output_PD_abun, type = 2, color.var = "Assemblage")
```

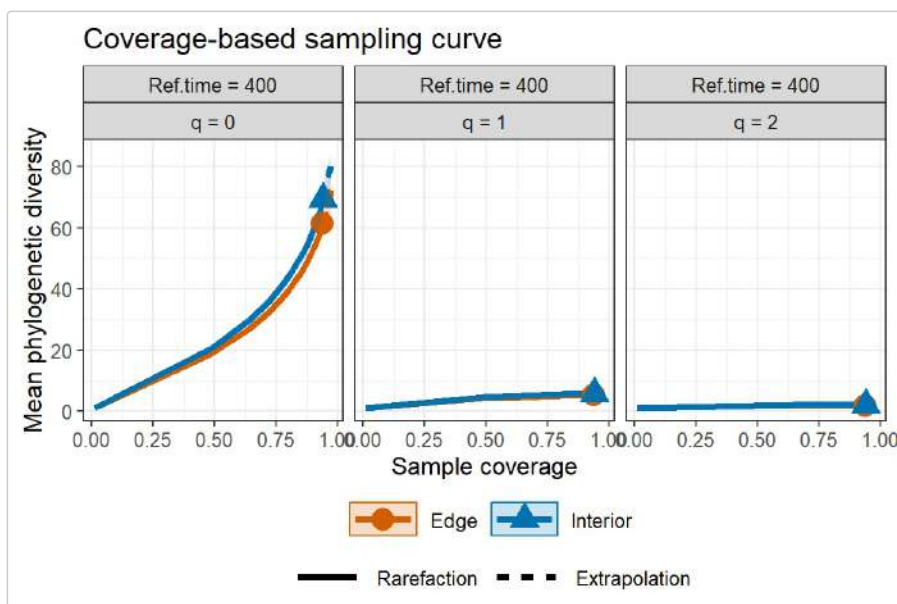


The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# PD coverage-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_PD_abun, type = 3, facet.var = "Assemblage")
```



```
# PD coverage-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_PD_abun, type = 3, facet.var = "Order.q")
```



EXAMPLE 4: PD rarefaction/extrapolation for incidence data

Based on the dataset (`Fish_incidence_data`) included in the package and the phylogenetic tree (`Fish_phylo_tree`), the following commands return all numerical results for PD. The first list of the output (`$PDInfo`) returns basic data information including the name of the Assemblage, number of sampling units (T), total number of incidences (v), observed species richness (S_{obs}), sample coverage estimate of the reference sample with size T ($SC(T)$), sample coverage estimate of the extrapolated sample with size $2T$ ($SC(2T)$), the observed total branch length in the phylogenetic tree spanned by all observed species (PD_{obs}), the singletons/doubletons in the sample branch incidence ($Q1^*$, $Q2^*$), the total branch length of those singletons/doubletons in the sample branch incidence ($R1$, $R2$), and the reference time (`Ref.time`). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'PD'` and `datatype = "incidence_raw"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order q between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

The required argument for performing PD analysis is `PDtree`. For example, the phylogenetic tree for all observed species (including species in both "2013-2015" and "2016-2018" time periods) is stored in `Fish_phylo_tree`. Then we enter the argument `PDtree = Fish_phylo_tree`. Two optional arguments are: `PDtype` and `PDref.time`. 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"`. `PDref.time` is a numerical value specifying a reference time for computing phylogenetic diversity. By default (`PDref.time = 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.

```
data(Fish_incidence_data)
data(Fish_phylo_tree)
data <- Fish_incidence_data
tree <- Fish_phylo_tree
```

```
output_PD_inci <- iNEXT3D(data, diversity = 'PD', q = c(0, 1, 2),
  datatype = "incidence_raw", nboot = 20, PDtree = tree)

output_PD_inci$PDInfo
```

```
$PDInfo
# A tibble: 2 x 12
  Assemblage      T      U S.obs `SC(T)` `SC(2T)` PD.obs `Q1*` `Q2*` R1 R2 Reftime
<chr>      <int> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 2013-2015    36   532   50  0.98  0.993  9.62  11   7 0.69  1.23  0.977
2 2016-2018    36   522   53  0.976  0.989  9.44  13   6 0.368  0.345  0.977
```

The second list of the output (`$PDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the "2013-2015" time period, corresponding to the target number of sample units $m_T = 1, 2, 4, \dots, 34, 36, 37, 38, \dots, 72$), which locates the reference sampling units at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target number of sample units (m_T), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the target number of sample units m_T is less than, equal to, or greater than the number of sampling units in the reference sample), the diversity estimate of order q (`qPD`), the lower and upper confidence limits of diversity (`qPD.LCL` and `qPD.UCL`) conditioning on the sample size, the corresponding sample coverage estimate (`SC`) along with the lower and upper confidence limits of sample coverage (`SC.LCL` and `SC.UCL`), the reference time (`Reftime`) and the type of PD (`Type`). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_PD_inci$PDiNextEst$size_based
```

	Assemblage	Order.q	m_T	Method	qPD	qPD.LCL	qPD.UCL	SC	SC.LCL	SC.UCL	Reftime	Type
1	2013-2015	0	1	Rarefaction	5.744	5.541	5.946	0.606	0.577	0.635	0.977	meanPD
2	2013-2015	0	2	Rarefaction	6.813	6.581	7.045	0.749	0.727	0.770	0.977	meanPD
3	2013-2015	0	4	Rarefaction	7.716	7.488	7.945	0.851	0.837	0.865	0.977	meanPD
4	2013-2015	0	6	Rarefaction	8.130	7.865	8.394	0.894	0.881	0.908	0.977	meanPD
5	2013-2015	0	8	Rarefaction	8.389	8.079	8.700	0.919	0.905	0.932	0.977	meanPD
6	2013-2015	0	10	Rarefaction	8.589	8.237	8.942	0.934	0.921	0.947	0.977	meanPD

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (`SC`), the corresponding number of sample units (m_T), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the coverage `SC` is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order q (`qPD`), the lower and upper confidence limits of diversity (`qPD.LCL` and `qPD.UCL`) conditioning on the target sample coverage value, the reference time (`Reftime`) and the type of PD (`Type`). Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication, leading to higher uncertainty on the resulting diversity estimate.)

```
output_PD_inci$PDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	m_T	Method	qPD	qPD.LCL	qPD.UCL	Reftime	Type
1	2013-2015	0	0.606	1	Rarefaction	5.744	5.542	5.946	0.977	meanPD
2	2013-2015	0	0.749	2	Rarefaction	6.813	6.598	7.028	0.977	meanPD
3	2013-2015	0	0.851	4	Rarefaction	7.716	7.492	7.941	0.977	meanPD
4	2013-2015	0	0.894	6	Rarefaction	8.130	7.852	8.407	0.977	meanPD
5	2013-2015	0	0.919	8	Rarefaction	8.389	8.055	8.724	0.977	meanPD
6	2013-2015	0	0.934	10	Rarefaction	8.589	8.204	8.975	0.977	meanPD

The third list of the output (`$PDAsyEst`) includes the name of the Assemblage, PD (or meanPD) for $q = 0, 1$, and 2 (`qPD`), the observed diversity (`PD_obs`), asymptotic diversity estimate (`PD_asy`) and its estimated bootstrap standard error (`s.e.`), the confidence intervals for asymptotic diversity (`qPD.LCL` and `qPD.UCL`), the reference time (`Reftime`) and the type of PD (`Type`). These statistics are computed only for $q = 0, 1$ and 2. More detailed information about asymptotic and observed diversity estimates for any order q between 0 and 2 can be obtained from function `ObsAsy3D()`. The output is shown below:

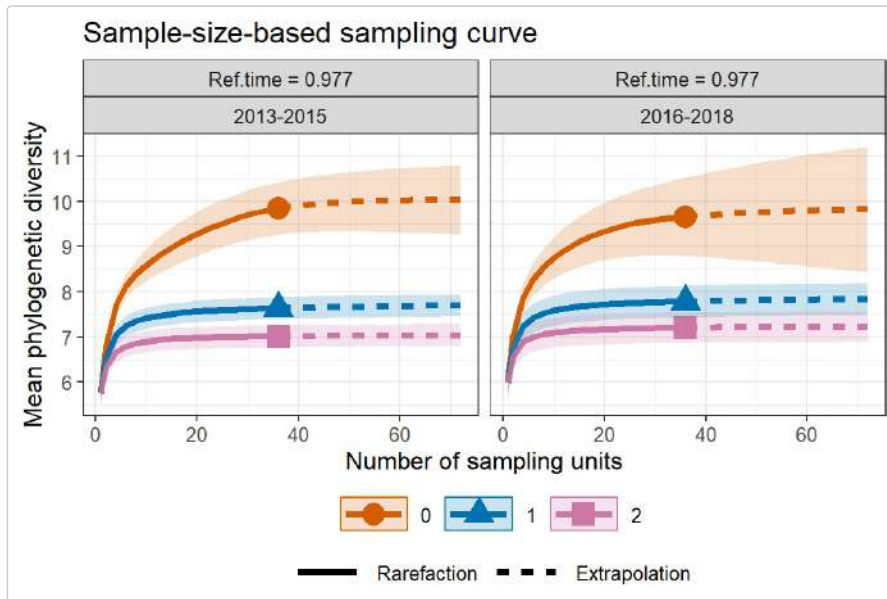
```
output_PD_inci$PDAsyEst
```

	Assemblage	qPD	PD_obs	PD_asy	s.e.	qPD.LCL	qPD.UCL	Reftime	Type	
1	2013-2015	q = 0	PD	9.847	10.039	0.702	8.663	11.416	0.977	meanPD
2	2013-2015	q = 1	PD	7.635	7.729	0.157	7.421	8.037	0.977	meanPD
3	2013-2015	q = 2	PD	7.013	7.057	0.152	6.760	7.355	0.977	meanPD
4	2016-2018	q = 0	PD	9.659	9.854	0.796	8.295	11.413	0.977	meanPD

5	2016-2018	q = 1	PD	7.781	7.859	0.141	7.583	8.136	0.977	meanPD
6	2016-2018	q = 2	PD	7.202	7.244	0.116	7.016	7.471	0.977	meanPD

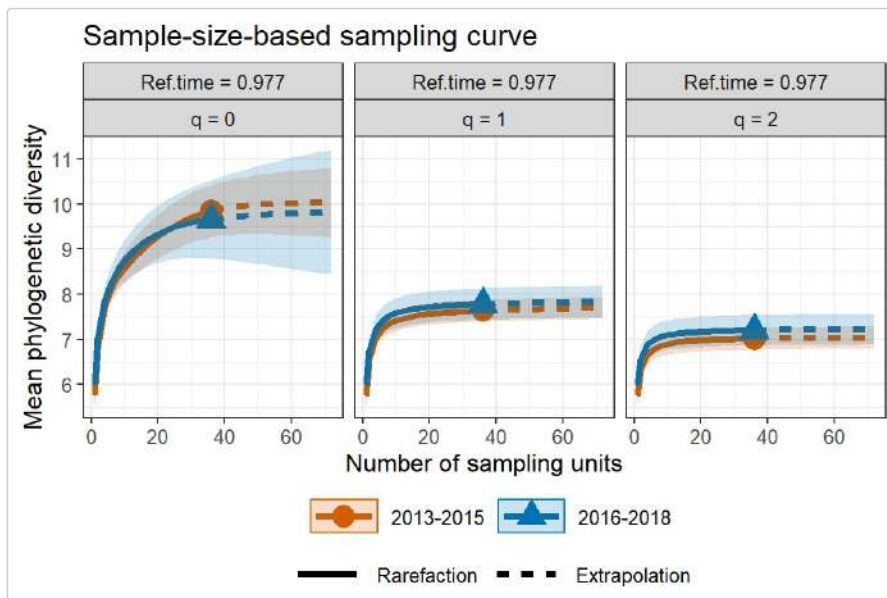
The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) is given below:

```
# PD sample-size-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_PD_inci, type = 1, facet.var = "Assemblage")
```



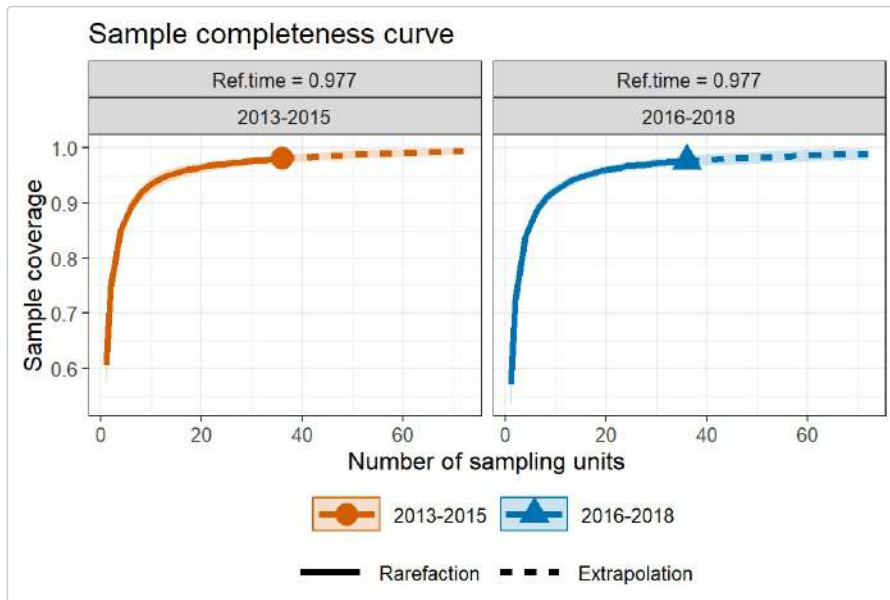
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# PD sample-size-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_PD_inci, type = 1, facet.var = "Order.q")
```



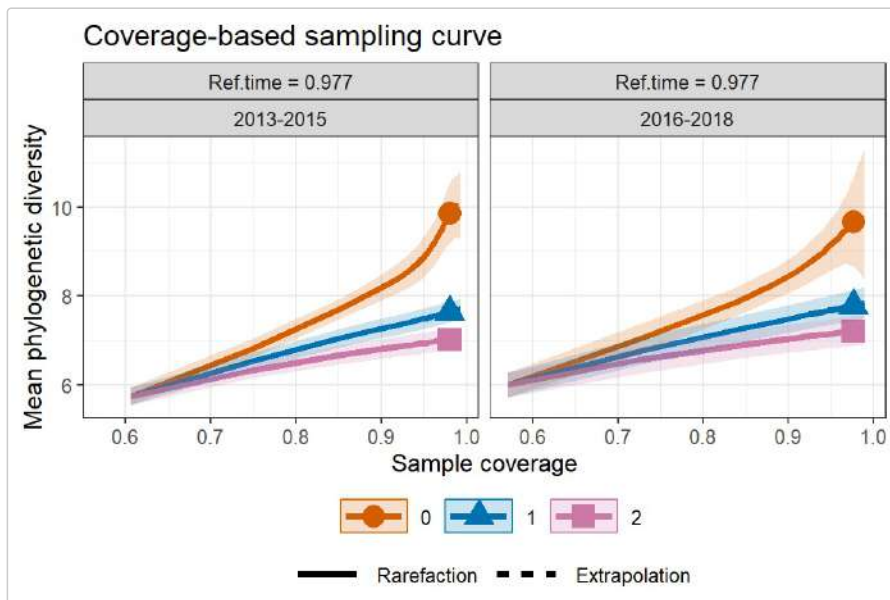
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors are used for different assemblages.

```
# Sample completeness curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_PD_inci, type = 2, color.var = "Assemblage")
```

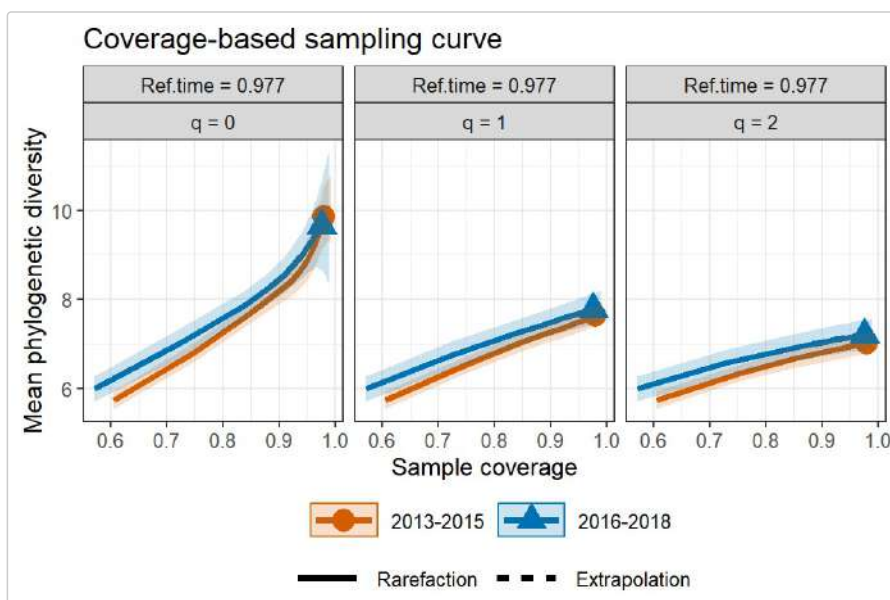


The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# PD coverage-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_PD_inci, type = 3, facet.var = "Assemblage")
```



```
# PD coverage-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_PD_inci, type = 3, facet.var = "Order.q")
```



FUNCTIONAL DIVERSITY (FD): RAREFACTION/EXTRAPOLATION VIA EXAMPLES

EXAMPLE 5: FD rarefaction/extrapolation for abundance data

Based on the dataset (`Brazil_rainforest_abun_data`) and the the distance matrix (`Brazil_rainforest_distance_matrix`) included in the package, the following commands return all numerical results for FD. The first list of the output (`$FDInfo`) returns basic data information including the name of the Assemblage, sample size (n), observed species richness (S_{obs}), sample coverage estimate of the reference sample with size n ($SC(n)$), sample coverage estimate of the extrapolated sample with size $2n$ ($SC(2n)$), and the minimum, mean, and maximum distance among all non-diagonal elements in the distance matrix (d_{min} , d_{mean} , d_{max}). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'FD'` and `datatype = "abundance"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order q between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

The required argument for performing FD analysis is `FDdistM`. For example, the distance matrix for all species (including species in both Edge and Interior habitats) is stored in `Brazil_rainforest_distance_matrix`. Then we enter the argument `FDdistM = Brazil_rainforest_distance_matrix`. 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_values"` means FD is computed under specific threshold values 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_values"` 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 data (i.e., quadratic entropy).

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_distance_matrix)
data <- Brazil_rainforest_abun_data
distM <- Brazil_rainforest_distance_matrix
output_FD_abun <- iNEXT3D(data, diversity = 'FD', datatype = "abundance", nboot = 10,
                          FDdistM = distM, FDtype = 'AUC')
output_FD_abun$FDInfo
```

```
$FDInfo
  Assemblage    n S.obs SC(n) SC(2n) dmin dmean dmax
1      Edge 1794   319 0.939  0.974   0 0.372 0.776
2    Interior 2074   356 0.941  0.973   0 0.329 0.776
```

The second list of the output (`$FDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the "Edge" assemblage, corresponding to the target sample size $m = 1, 95, 189, \dots, 1699, 1794, 1795, 1899, \dots, 3588$), which locates the reference sample size at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target sample size (m), the Method (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the size m is less than, equal to, or greater than the reference sample size), the diversity estimate of order q (q_{FD}), the lower and upper confidence limits of diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$) conditioning on the sample size, and the corresponding sample coverage estimate (SC) along with the lower and upper confidence limits of sample coverage ($SC.LCL$ and $SC.UCL$). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_FD_abun$FDiNextEst$size_based
```

	Assemblage	Order.q	m	Method	qFD	qFD.LCL	qFD.UCL	SC	SC.LCL	SC.UCL
1	Edge	0	1	Rarefaction	1.000	1.000	1.000	0.012	0.010	0.013
2	Edge	0	95	Rarefaction	10.900	10.442	11.358	0.484	0.466	0.502
3	Edge	0	189	Rarefaction	12.993	12.117	13.868	0.638	0.619	0.657
4	Edge	0	284	Rarefaction	14.129	12.888	15.371	0.718	0.702	0.735
5	Edge	0	378	Rarefaction	14.860	13.304	16.416	0.768	0.755	0.782
6	Edge	0	472	Rarefaction	15.383	13.549	17.216	0.803	0.792	0.814

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (SC), the corresponding sample size (m), the Method (`Rarefaction`, `Observed`, or `Extrapolation`, depending on whether the coverage SC is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order q (q_{FD}), and the lower and upper confidence limits of diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$) conditioning on the target sample coverage value. Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication,

leading to higher uncertainty on the resulting diversity estimate.)

```
output_FD_abun$FDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	m	Method	qFD	qFD.LCL	qFD.UCL
1	Edge	0	0.012	1	Rarefaction	1.000	1.000	1.000
2	Edge	0	0.484	95	Rarefaction	10.900	10.472	11.328
3	Edge	0	0.638	189	Rarefaction	12.993	12.328	13.657
4	Edge	0	0.718	284	Rarefaction	14.129	13.209	15.049
5	Edge	0	0.768	378	Rarefaction	14.860	13.696	16.025
6	Edge	0	0.803	472	Rarefaction	15.383	13.991	16.775

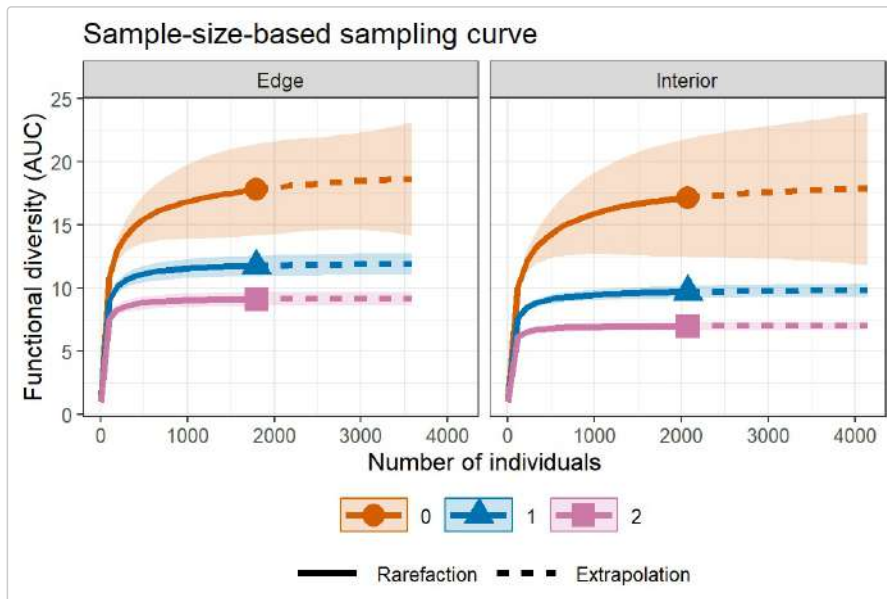
The third list of the output (`$FDAsyEst`) includes the name of the Assemblage, FD for $q = 0, 1$, and 2 (q_{FD}), the observed diversity (FD_{obs}), asymptotic diversity estimate (FD_{asy}) and its estimated bootstrap standard error (s.e.) as well as the confidence intervals for asymptotic diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$). These statistics are computed only for $q = 0, 1$ and 2 . More detailed information about asymptotic and observed diversity estimates for any order q between 0 and 2 can be obtained from function `ObsAsy3D()`. The output is shown below:

```
output_FD_abun$FDAsyEst
```

	Assemblage	qFD	FD_obs	FD_asy	s.e.	qFD.LCL	qFD.UCL
1	Edge q = 0	FD (AUC)	17.851	19.008	4.997	9.214	28.801
2	Edge q = 1	FD (AUC)	11.781	12.037	0.521	11.016	13.057
3	Edge q = 2	FD (AUC)	9.139	9.228	0.397	8.451	10.006
4	Interior q = 0	FD (AUC)	17.168	18.208	8.415	1.716	34.700
5	Interior q = 1	FD (AUC)	9.716	9.922	0.276	9.381	10.463
6	Interior q = 2	FD (AUC)	7.007	7.055	0.148	6.766	7.345

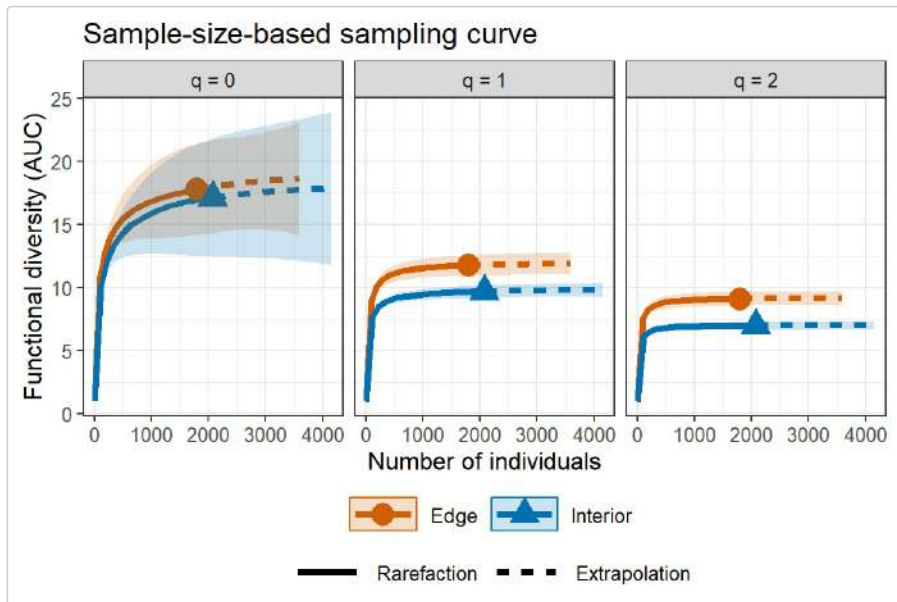
The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) is given below:

```
# FD sample-size-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_FD_abun, type = 1, facet.var = "Assemblage")
```



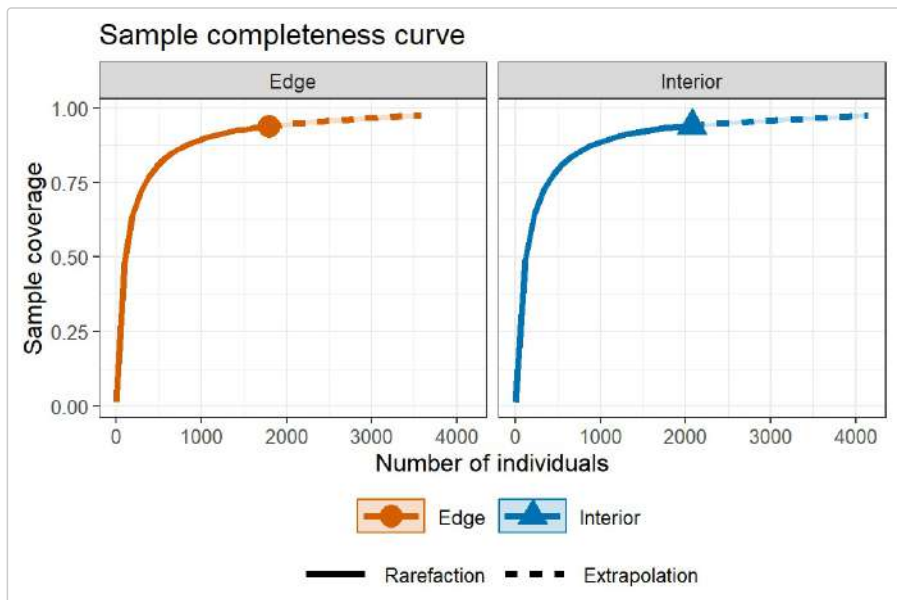
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# FD sample-size-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_FD_abun, type = 1, facet.var = "Order.q")
```



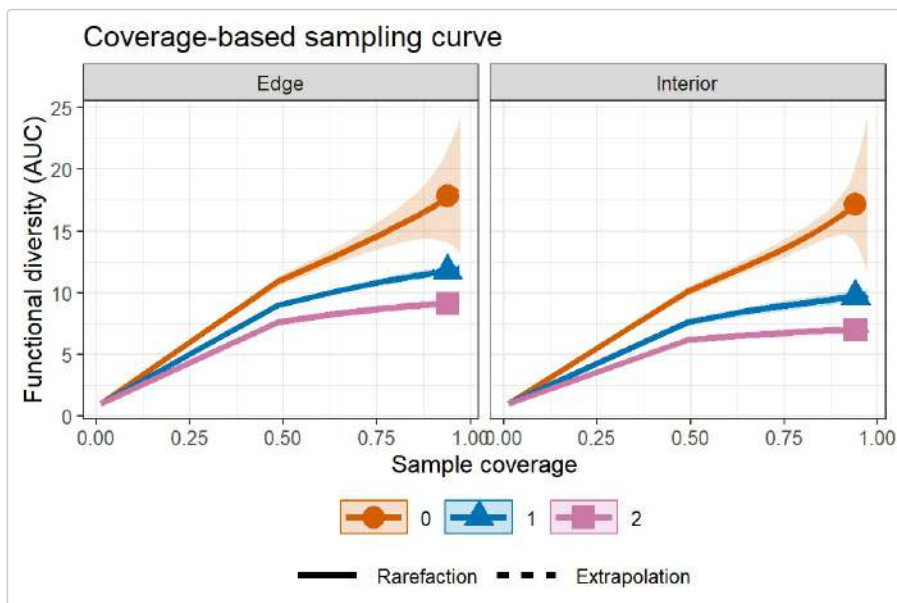
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors are used for different assemblages.

```
# Sample completeness curves for abundance data, separating by "Assemblage"
ggiNEXT3D(output_FD_abun, type = 2, color.var = "Assemblage")
```

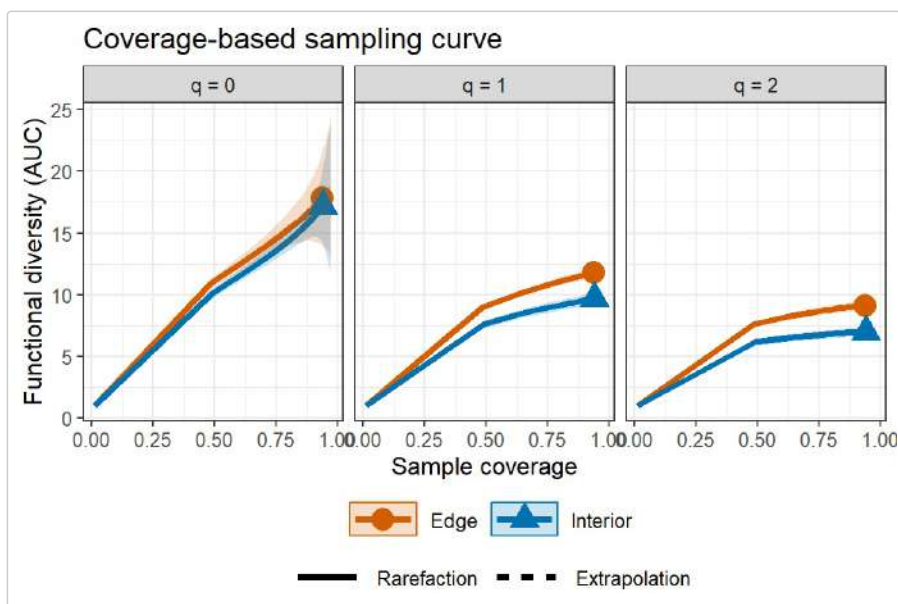


The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# FD coverage-based R/E curves, separating by "Assemblage"
ggiNEXT3D(output_FD_abun, type = 3, facet.var = "Assemblage")
```



```
# FD coverage-based R/E curves, separating by "Order.q"
ggiNEXT3D(output_FD_abun, type = 3, facet.var = "Order.q")
```



EXAMPLE 6: FD rarefaction/extrapolation for incidence data

Based on the dataset (`Fish_incidence_data`) and the the distance matrix (`Fish_distance_matrix`) included in the package, the following commands return all numerical results for FD. The first list of the output (`$FDInfo`) returns basic data information including the name of the Assemblage, number of sampling units (T), total number of incidences (v), observed species richness (S_{obs}), sample coverage estimate of the reference sample with size T ($SC(T)$), sample coverage estimate of the reference sample with size $2T$ ($SC(2T)$), and the minimum, mean, and maximum distance among all non-diagonal elements in the distance matrix (d_{min} , d_{mean} , d_{max}). The output is identical to that based on the function `DataInfo3D()` by specifying `diversity = 'FD'` and `datatype = "incidence_raw"`; see later text). Thus, if only data information is required, the simpler function `DataInfo3D()` (see later text) can be used to obtain the same output. More information about the observed diversity (for any order q between 0 and 2) can be obtained by function `ObsAsy3D()`, which will be introduced later.

The required argument for performing FD analysis is `FDdistM`. For example, the distance matrix for all species (including species in both "2013-2015" and "2016-2018" time periods) is stored in `Fish_distance_matrix`. Then we enter the argument `FDdistM = Fish_distance_matrix`. 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_values"` means FD is computed under specific threshold values 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_values"` 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 data (i.e., quadratic entropy).

```
data(Fish_incidence_data)
data(Fish_distance_matrix)
data <- Fish_incidence_data
distM <- Fish_distance_matrix
output_FD_inci <- iNEXT3D(data, diversity = 'FD', datatype = "incidence_raw", nboot = 20,
```

```
FDdistM = distM, FDtype = 'AUC')
output_FD_inci$FDInfo
```

```
$FDInfo
  Assemblage T   U S.obs SC(T) SC(2T)  dmin dmean  dmax
1  2013-2015 36 532    50 0.980  0.993 0.006 0.240 0.733
2  2016-2018 36 522    53 0.976  0.989 0.006 0.237 0.733
```

The second list of the output (`$FDiNextEst`) includes size- and coverage-based standardized diversity estimates and related statistics computed for 40 knots by default (for example in the "2013-2015" time period, corresponding to the target number of sample units $m_T = 1, 2, 4, \dots, 34, 36, 37, 38, \dots, 72$), which locates the reference sampling units at the mid-point of the selected knots. There are two data frames (`$size_based` and `$coverage_based`).

The first data frame (`$size_based`) includes the name of the Assemblage, diversity order (`Order.q`), the target number of sample units (m_T), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the target number of sample units m_T is less than, equal to, or greater than the number of sampling units in the reference sample), the diversity estimate of order q (q_{FD}), the lower and upper confidence limits of diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$) conditioning on the sample size, and the corresponding sample coverage estimate (SC) along with the lower and upper confidence limits of sample coverage ($SC.LCL$ and $SC.UCL$). These sample coverage estimates with confidence intervals are used for plotting the sample completeness curve. If the argument `nboot` is greater than zero, then a bootstrap method is applied to obtain the confidence intervals for the diversity and sample coverage estimates. Otherwise, all confidence intervals will not be computed. Here only the first six rows of the `$size_based` output are displayed:

```
output_FD_inci$FDiNextEst$size_based
```

	Assemblage	Order.q	m_T	Method	q_{FD}	$q_{FD.LCL}$	$q_{FD.UCL}$	SC	$SC.LCL$	$SC.UCL$
1	2013-2015	0	1	Rarefaction	14.778	13.862	15.694	0.606	0.575	0.637
2	2013-2015	0	2	Rarefaction	15.318	14.403	16.234	0.749	0.723	0.774
3	2013-2015	0	4	Rarefaction	15.888	14.972	16.803	0.851	0.832	0.869
4	2013-2015	0	6	Rarefaction	16.224	15.301	17.146	0.894	0.880	0.909
5	2013-2015	0	8	Rarefaction	16.463	15.530	17.396	0.919	0.906	0.931
6	2013-2015	0	10	Rarefaction	16.652	15.706	17.598	0.934	0.923	0.945

The second data frame (`$coverage_based`) includes the name of assemblage, the diversity order (`Order.q`), the target sample coverage value (SC), the corresponding number of sample units (m_T), the Method (Rarefaction, Observed, or Extrapolation, depending on whether the coverage SC is less than, equal to, or greater than the reference sample coverage), the diversity estimate of order q (q_{FD}), and the lower and upper confidence limits of diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$) conditioning on the target sample coverage value. Here only the first six rows of the `$coverage_based` output are displayed below: (Note for a fixed coverage value, the confidence interval in the `$coverage_based` table is wider than the corresponding interval in the `$size_based` table. This is because, for a given coverage value, the sample size needed to attain a fixed coverage value varies with bootstrap replication, leading to higher uncertainty on the resulting diversity estimate.)

```
output_FD_inci$FDiNextEst$coverage_based
```

	Assemblage	Order.q	SC	m_T	Method	q_{FD}	$q_{FD.LCL}$	$q_{FD.UCL}$
1	2013-2015	0	0.606	1	Rarefaction	14.778	14.179	15.376
2	2013-2015	0	0.749	2	Rarefaction	15.318	14.741	15.896
3	2013-2015	0	0.851	4	Rarefaction	15.888	15.243	16.533
4	2013-2015	0	0.894	6	Rarefaction	16.224	15.515	16.932
5	2013-2015	0	0.919	8	Rarefaction	16.463	15.699	17.226
6	2013-2015	0	0.934	10	Rarefaction	16.652	15.843	17.461

The third list of the output (`$FDAsyEst`) includes the name of the Assemblage, FD for $q = 0, 1$, and 2 (q_{FD}), the observed diversity (FD_{obs}), asymptotic diversity estimate (FD_{asy}) and its estimated bootstrap standard error (s.e.), and the confidence intervals for asymptotic diversity ($q_{FD.LCL}$ and $q_{FD.UCL}$). These statistics are computed only for $q = 0, 1$ and 2. More detailed information about asymptotic and observed diversity estimates for any order q between 0 and 2 can be obtained from function `ObsAsy3D()`. The output is shown below:

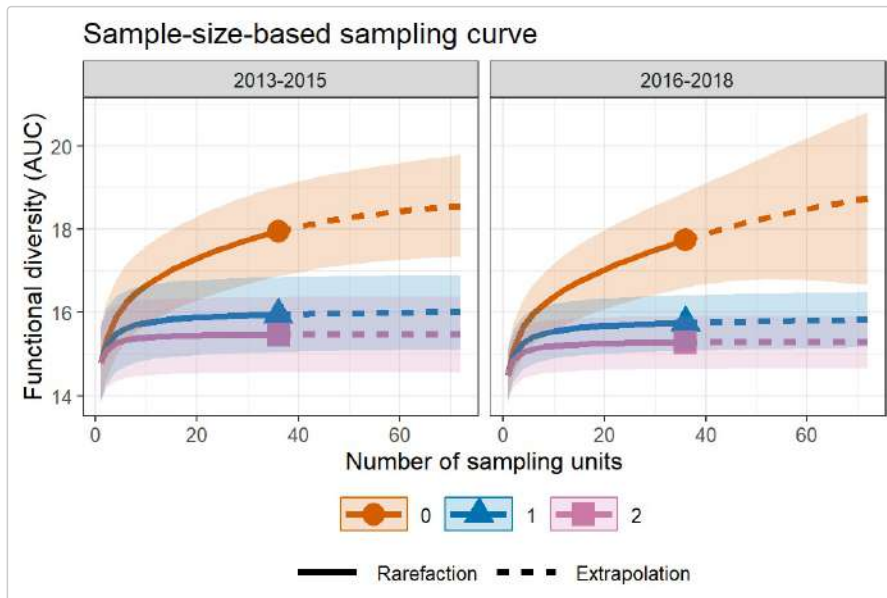
```
output_FD_inci$FDAsyEst
```

	Assemblage	q_{FD}	FD_{obs}	FD_{asy}	s.e.	$q_{FD.LCL}$	$q_{FD.UCL}$
1	2013-2015	$q = 0$	FD(AUC)	17.904	18.906	1.386	16.188 21.623
2	2013-2015	$q = 1$	FD(AUC)	15.944	16.043	0.469	15.124 16.961
3	2013-2015	$q = 2$	FD(AUC)	15.463	15.490	0.455	14.598 16.383
4	2016-2018	$q = 0$	FD(AUC)	17.739	19.770	4.931	10.106 29.434
5	2016-2018	$q = 1$	FD(AUC)	15.749	15.867	0.607	14.678 17.056
6	2016-2018	$q = 2$	FD(AUC)	15.275	15.305	0.532	14.262 16.348

The `ggiNEXT3D` function can be used to make graphical displays for rarefaction and extrapolation sampling curves. When `facet.var = "Assemblage"` is specified in the `ggiNEXT3D` function, it creates a separate plot for

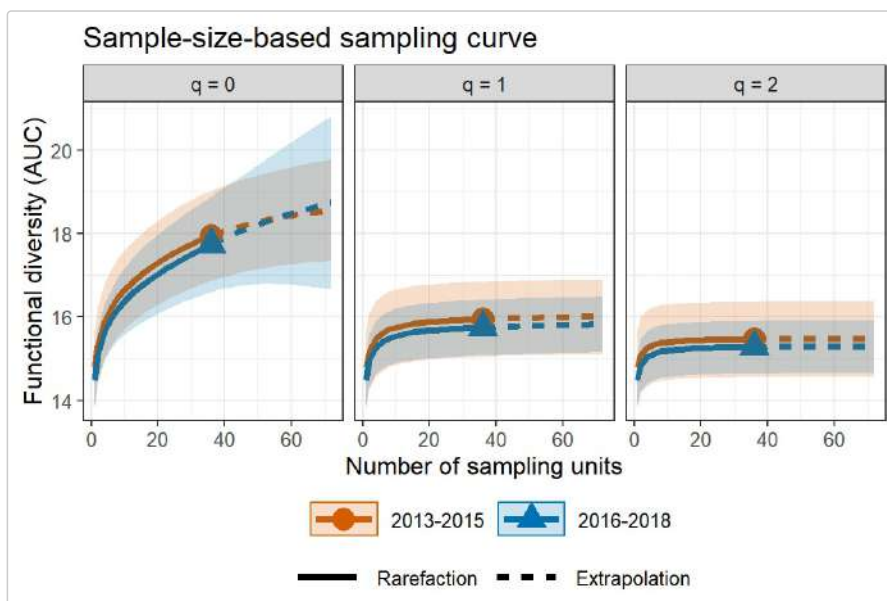
each assemblage; within each assemblage, different color curves represent diversity of different orders. An example for showing sample-size-based rarefaction/extrapolation curves (`type = 1`) is given below:

```
# FD sample-size-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_FD_inci, type = 1, facet.var = "Assemblage")
```



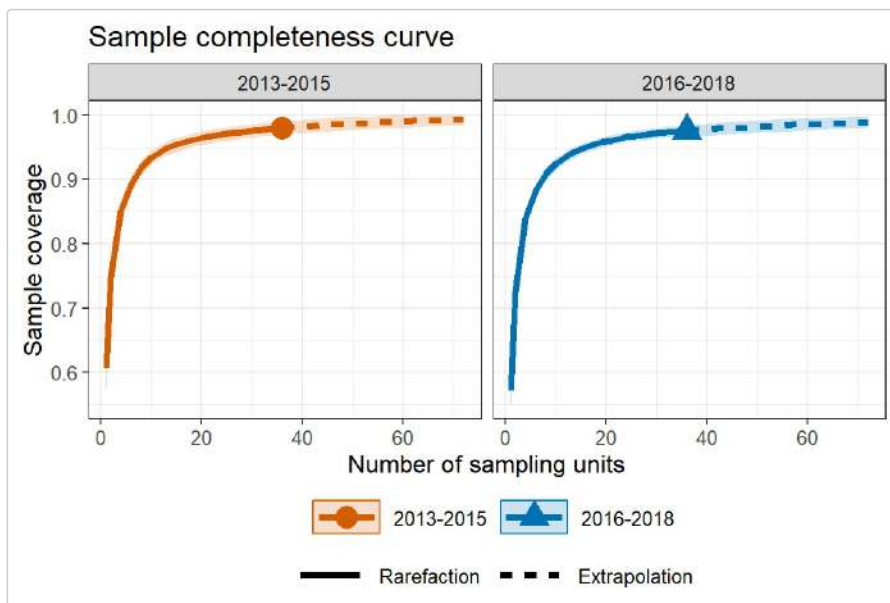
When `facet.var = "Order.q"` is specified in the `ggiNEXT3D` function, it creates a separate plot for each diversity order; within each plot, different color curves represent different assemblages. An example is shown below:

```
# FD sample-size-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_FD_inci, type = 1, facet.var = "Order.q")
```



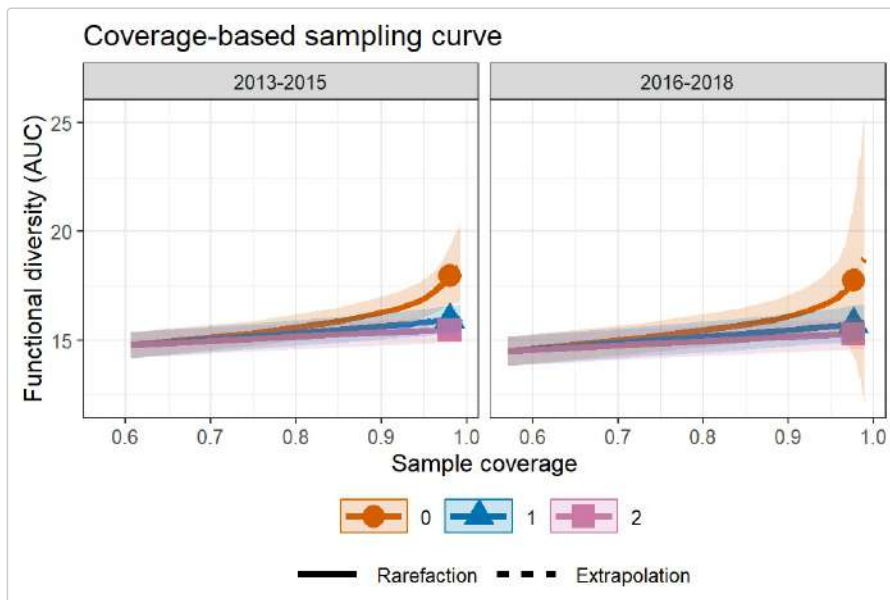
The following commands return the sample completeness (sample coverage) curve (`type = 2`) in which different colors are used for different assemblages.

```
# Sample completeness curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_FD_inci, type = 2, color.var = "Assemblage")
```

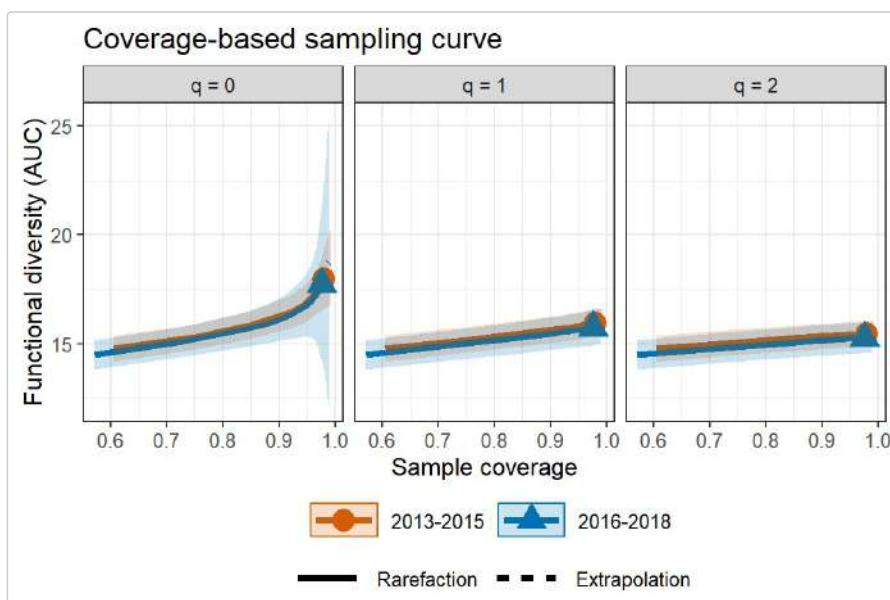



The following commands return the coverage-based rarefaction/extrapolation sampling curves in which different color curves represent three diversity orders within each assemblage (`facet.var = "Assemblage"`), or represent two assemblages within each diversity order (`facet.var = "Order.q"`), respectively.

```
# FD coverage-based R/E curves for incidence data, separating by "Assemblage"
ggiNEXT3D(output_FD_inci, type = 3, facet.var = "Assemblage")
```



```
# FD coverage-based R/E curves for incidence data, separating by "Order.q"
ggiNEXT3D(output_FD_inci, type = 3, facet.var = "Order.q")
```



FUNCTION DataInfo3D(): DATA INFORMATION

The function `DataInfo3D()` provides basic data information for the reference sample in each individual assemblage. The function `DataInfo3D()` with default arguments is shown below:

```
DataInfo3D(data, diversity = "TD", datatype = "abundance",
           nT = NULL, PDtree, PDreftime = NULL,
           FDdistM, FDtype = "AUC", FDtau = NULL)
```

All arguments in the above function are the same as those for the main function `iNEXT3D`. Running the `DataInfo3D()` 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_rainforest_abun_data` and `Fish_incidence_data` to demo the function for each dimension of diversity.

TAXONOMIC DIVERSITY (TD): Basic data information for abundance data

```
data(Brazil_rainforest_abun_data)
DataInfo3D(Brazil_rainforest_abun_data, diversity = 'TD', datatype = "abundance")
```

	Assemblage	n	S.obs	SC(n)	SC(2n)	f1	f2	f3	f4	f5
1	Edge	1794	319	0.939	0.974	110	48	38	28	13
2	Interior	2074	356	0.941	0.973	123	48	41	32	19

Output description:

- `Assemblage` = assemblage name.
- `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 with size `n`.
- `SC(2n)` = sample coverage estimate of the reference sample with size `2n`.
- `f1-f5` = the first five species abundance frequency counts in the reference sample.

TAXONOMIC DIVERSITY (TD): Basic data information for incidence data

```
data(Fish_incidence_data)
DataInfo3D(Fish_incidence_data, diversity = 'TD', datatype = "incidence_raw")
```

	Assemblage	T	U	S.obs	SC(T)	SC(2T)	Q1	Q2	Q3	Q4	Q5
1	2013-2015	36	532	50	0.980	0.993	11	6	4	1	3
2	2016-2018	36	522	53	0.976	0.989	13	5	5	2	3

Output description:

- `Assemblage` = assemblage name.
- `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 with size `T`.
- `SC(2T)` = sample coverage estimate of the reference sample with size `2T`.
- `Q1-Q5` = the first five species incidence frequency counts in the reference sample.

PHYLOGENETIC DIVERSITY (PD): Basic data information for abundance data

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_phylo_tree)
data <- Brazil_rainforest_abun_data
tree <- Brazil_rainforest_phylo_tree
DataInfo3D(data, diversity = 'PD', datatype = "abundance", PDtree = tree)
```

```
# A tibble: 2 x 11
  Assemblage      n S.obs `SC(n)` `SC(2n)` PD.obs `f1*` `f2*`      g1      g2 Reftime
  <chr>          <int> <int>  <dbl>  <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>
1 Edge          1794   319   0.939   0.974 24516  110   52  6578 2885   400
2 Interior      2074   356   0.941   0.973 27727  123   56  7065 3656   400
```

Output description:

- `Assemblage`, `n`, `S.obs`, `SC(n)` and `SC(2n)`: definitions are the same as in the TD abundance output and thus are omitted.
- `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).

PHYLOGENETIC DIVERSITY (PD): Basic data information for incidence data

```
data(Fish_incidence_data)
data(Fish_phylo_tree)
data <- Fish_incidence_data
tree <- Fish_phylo_tree
DataInfo3D(data, diversity = 'PD', datatype = "incidence_raw", PDtree = tree)
```

```
# A tibble: 2 x 12
  Assemblage T U S.obs `SC(T)` `SC(2T)` PD.obs `Q1*` `Q2*` R1 R2 Reftime
  <chr> <int> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 2013-2015 36 532 50 0.98 0.993 9.62 11 7 0.69 1.23 0.977
2 2016-2018 36 522 53 0.976 0.989 9.44 13 6 0.368 0.345 0.977
```

Output description:

- `Assemblage`, `T`, `U`, `S.obs`, `SC(T)` and `SC(2T)`: definitions are the same as in the TD incidence output and thus are omitted.
- `PD.obs` = the observed total branch length in the phylogenetic tree spanned by all observed species.
- `Q1*`, `Q2*` = the singletons/doubletons in the sample branch incidence.
- `R1`, `R2` = the total branch length of those singletons/doubletons in the sample branch incidence.
- `Reftime` = reference time.

FUNCTIONAL DIVERSITY (FD): Basic data information for abundance data

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_distance_matrix)
data <- Brazil_rainforest_abun_data
distM <- Brazil_rainforest_distance_matrix
DataInfo3D(data, diversity = 'FD', datatype = "abundance",
            FDdistM = distM, FDtype = 'AUC')
```

```
Assemblage n S.obs SC(n) SC(2n) dmin dmean dmax
1 Edge 1794 319 0.939 0.974 0 0.372 0.776
2 Interior 2074 356 0.941 0.973 0 0.329 0.776
```

Output description:

- `Assemblage`, `n`, `S.obs`, `SC(n)` and `SC(2n)`: definitions are the same as in TD abundance output 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.

FUNCTIONAL DIVERSITY (FD): Basic data information for incidence data

```
data(Fish_incidence_data)
data(Fish_distance_matrix)
data <- Fish_incidence_data
distM <- Fish_distance_matrix
DataInfo3D(data, diversity = 'FD', datatype = "incidence_raw",
            FDdistM = distM, FDtype = 'AUC')
```

```
Assemblage T U S.obs SC(T) SC(2T) dmin dmean dmax
1 2013-2015 36 532 50 0.980 0.993 0.006 0.240 0.733
2 2016-2018 36 522 53 0.976 0.989 0.006 0.237 0.733
```

Output description:

- `Assemblage`, `T`, `U`, `S.obs`, `SC(T)` and `SC(2T)`: definitions are the same as in the TD incidence output 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.

FUNCTION `estimate3D()`: POINT ESTIMATION

`estimate3D` is used to compute 3D diversity (TD, PD, FD) estimates with $q = 0, 1, 2$ under any specified levels of sample size (when `base = "size"`) and sample coverage values (when `base = "coverage"`) for abundance data (`datatype = "abundance"`) or incidence data (`datatype = "incidence_raw"`). When `base = "size"`, `level` can be specified with a particular vector of sample sizes (greater than 0); if `level = NULL`, this function computes the diversity estimates for the minimum sample size among all samples extrapolated to the double reference sizes. When `base = "coverage"`, `level` can be specified with a particular vector of sample coverage values (between 0 and 1); if `level = NULL`, this function computes the diversity estimates for the minimum sample coverage among all samples extrapolated to the double reference sizes. All arguments in the function are the same as those for the main function `iNEXT3D`.

```
estimate3D(data, diversity = "TD", q = c(0, 1, 2), datatype = "abundance",
           base = "coverage", level = NULL, nboot = 50, conf = 0.95,
           nT = NULL, PDtree, PDreftime = NULL, PDtype = "meanPD",
           FDistM, FDtype = "AUC", FDTau = NULL, FDCut_number = 50)
```

TAXONOMIC DIVERSITY (TD): point estimation

Example 7a: TD for abundance data with two target coverage values (93% and 97%)

The following commands return the TD estimates with two specified levels of sample coverage (93% and 97%) based on the `Brazil_rainforest_abun_data`.

```
data(Brazil_rainforest_abun_data)
output_est_TD_abun <- estimate3D(Brazil_rainforest_abun_data, diversity = 'TD', q = c(0,1,2),
                                datatype = "abundance", base = "coverage", level = c(0.93,
                                0.97))
output_est_TD_abun
```

	Assemblage	Order.q	SC	m	Method	qTD	s.e.	qTD.LCL	qTD.UCL
1	Edge	0	0.93	1547.562	Rarefaction	302.879	12.456	278.465	327.293
2	Edge	0	0.97	3261.971	Extrapolation	383.307	18.571	346.909	419.705
3	Edge	1	0.93	1547.562	Rarefaction	152.374	4.504	143.547	161.202
4	Edge	1	0.97	3261.971	Extrapolation	166.837	4.992	157.052	176.622
5	Edge	2	0.93	1547.562	Rarefaction	81.437	3.760	74.069	88.806
6	Edge	2	0.97	3261.971	Extrapolation	83.726	3.953	75.978	91.474
7	Interior	0	0.93	1699.021	Rarefaction	331.917	12.276	307.858	355.977
8	Interior	0	0.97	3883.447	Extrapolation	433.807	18.549	397.452	470.162
9	Interior	1	0.93	1699.021	Rarefaction	159.330	4.855	149.814	168.847
10	Interior	1	0.97	3883.447	Extrapolation	175.739	5.128	165.689	185.790
11	Interior	2	0.93	1699.021	Rarefaction	71.611	3.922	63.924	79.297
12	Interior	2	0.97	3883.447	Extrapolation	73.326	4.068	65.353	81.299

Example 7b: TD for incidence data with two target coverage values (97.5% and 99%)

The following commands return the TD estimates with two specified levels of sample coverage (97.5% and 99%) for the `Fish_incidence_data`.

```
data(Fish_incidence_data)
output_est_TD_inci <- estimate3D(Fish_incidence_data, diversity = 'TD', q = c(0, 1, 2),
                                datatype = "incidence_raw", base = "coverage",
                                level = c(0.975, 0.99))
output_est_TD_inci
```

	Assemblage	Order.q	SC	mT	Method	qTD	s.e.	qTD.LCL	qTD.UCL
1	2013-2015	0	0.975	29.169	Rarefaction	47.703	3.264	41.306	54.100
2	2013-2015	0	0.990	58.667	Extrapolation	54.914	4.665	45.771	64.057
3	2013-2015	1	0.975	29.169	Rarefaction	29.773	1.197	27.427	32.118
4	2013-2015	1	0.990	58.667	Extrapolation	30.751	1.214	28.372	33.130
5	2013-2015	2	0.975	29.169	Rarefaction	23.861	0.825	22.245	25.478
6	2013-2015	2	0.990	58.667	Extrapolation	24.126	0.840	22.479	25.773
7	2016-2018	0	0.975	34.825	Rarefaction	52.574	6.997	38.860	66.288
8	2016-2018	0	0.990	76.971	Extrapolation	62.688	14.646	33.983	91.393

9	2016-2018	1	0.975	34.825	Rarefaction	31.479	1.223	29.082	33.875
10	2016-2018	1	0.990	76.971	Extrapolation	32.721	1.186	30.397	35.046
11	2016-2018	2	0.975	34.825	Rarefaction	24.872	0.755	23.392	26.352
12	2016-2018	2	0.990	76.971	Extrapolation	25.163	0.743	23.708	26.618

PHYLOGENETIC DIVERSITY (PD): point estimation

Example 8a: PD for abundance data with two target sample sizes (1500 and 3500)

The following commands return the PD estimates with two specified levels of sample sizes (1500 and 3500) for the `Brazil_rainforest_abun_data`.

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_phylo_tree)
data <- Brazil_rainforest_abun_data
tree <- Brazil_rainforest_phylo_tree
output_est_PD_abun <- estimate3D(data, diversity = 'PD', datatype = "abundance",
                                base = "size", level = c(1500, 3500), PDtree = tree)
output_est_PD_abun
```

	Assemblage	Order.q	m	Method	SC	qPD	s.e.	qPD.LCL	qPD.UCL	Reftime	Type
1	Edge	0	1500	Rarefaction	0.928	58.370	1.007	56.396	60.344	400	meanPD
2	Edge	0	3500	Extrapolation	0.973	71.893	2.233	67.516	76.270	400	meanPD
3	Edge	1	1500	Rarefaction	0.928	5.224	0.103	5.021	5.426	400	meanPD
4	Edge	1	3500	Extrapolation	0.973	5.320	0.105	5.115	5.526	400	meanPD
5	Edge	2	1500	Rarefaction	0.928	1.797	0.024	1.749	1.844	400	meanPD
6	Edge	2	3500	Extrapolation	0.973	1.797	0.024	1.749	1.845	400	meanPD
7	Interior	0	1500	Rarefaction	0.922	63.555	0.917	61.758	65.353	400	meanPD
8	Interior	0	3500	Extrapolation	0.965	78.004	1.749	74.576	81.431	400	meanPD
9	Interior	1	1500	Rarefaction	0.922	5.675	0.113	5.454	5.896	400	meanPD
10	Interior	1	3500	Extrapolation	0.965	5.784	0.114	5.560	6.008	400	meanPD
11	Interior	2	1500	Rarefaction	0.922	1.913	0.032	1.851	1.976	400	meanPD
12	Interior	2	3500	Extrapolation	0.965	1.914	0.032	1.852	1.977	400	meanPD

Example 8b: PD for incidence data with two target coverage values (97.5% and 99%)

The following commands return the PD estimates with two specified levels of sample coverage (97.5% and 99%) for the `Fish_incidence_data`.

```
data(Fish_incidence_data)
data(Fish_phylo_tree)
data <- Fish_incidence_data
tree <- Fish_phylo_tree
output_est_PD_inci <- estimate3D(data, diversity = 'PD', datatype = "incidence_raw",
                                base = "coverage", level = c(0.975, 0.99), PDtree = tree)
output_est_PD_inci
```

	Assemblage	Order.q	SC	mT	Method	qPD	s.e.	qPD.LCL	qPD.UCL	Reftime	Type
1	2013-2015	0	0.975	29.169	Rarefaction	9.672	0.381	8.926	10.419	0.9770115	meanPD
2	2013-2015	0	0.990	58.667	Extrapolation	10.018	0.616	8.810	11.226	0.9770115	meanPD
3	2013-2015	1	0.975	29.169	Rarefaction	7.612	0.149	7.320	7.905	0.9770115	meanPD
4	2013-2015	1	0.990	58.667	Extrapolation	7.680	0.147	7.393	7.967	0.9770115	meanPD
5	2013-2015	2	0.975	29.169	Rarefaction	7.003	0.147	6.715	7.290	0.9770115	meanPD
6	2013-2015	2	0.990	58.667	Extrapolation	7.030	0.146	6.745	7.315	0.9770115	meanPD
7	2016-2018	0	0.975	34.825	Rarefaction	9.646	0.464	8.737	10.556	0.9770115	meanPD
8	2016-2018	0	0.990	76.971	Extrapolation	9.831	0.896	8.075	11.587	0.9770115	meanPD
9	2016-2018	1	0.975	34.825	Rarefaction	7.779	0.130	7.524	8.033	0.9770115	meanPD
10	2016-2018	1	0.990	76.971	Extrapolation	7.835	0.140	7.561	8.109	0.9770115	meanPD
11	2016-2018	2	0.975	34.825	Rarefaction	7.201	0.121	6.963	7.439	0.9770115	meanPD
12	2016-2018	2	0.990	76.971	Extrapolation	7.224	0.124	6.982	7.466	0.9770115	meanPD

FUNCTIONAL DIVERSITY (FD): point estimation

Example 9a: FD for abundance data with two target coverage values (93% and 97%)

The following commands return the FD estimates with two specified levels of sample coverage (93% and 97%) for the `Brazil_rainforest_abun_data`.

```
data(Brazil_rainforest_abun_data)
```

```

data(Brazil_rainforest_distance_matrix)
data <- Brazil_rainforest_abun_data
distM <- Brazil_rainforest_distance_matrix
output_est_FD_abun <- estimate3D(data, diversity = 'FD', datatype = "abundance",
                                base = "coverage", level = c(0.93, 0.97), nboot = 10,
                                FDdistM = distM, FDtype = 'AUC')
output_est_FD_abun

```

	Assemblage	Order.q	SC	m	Method	qFD	s.e.	qFD.LCL	qFD.UCL
1	Edge	0	0.93	1547.562	Rarefaction	17.590	2.069	13.534	21.645
2	Edge	0	0.97	3261.971	Extrapolation	18.578	2.740	13.207	23.949
3	Edge	1	0.93	1547.562	Rarefaction	11.732	0.311	11.123	12.341
4	Edge	1	0.97	3261.971	Extrapolation	11.920	0.313	11.307	12.534
5	Edge	2	0.93	1547.562	Rarefaction	9.120	0.261	8.609	9.632
6	Edge	2	0.97	3261.971	Extrapolation	9.183	0.264	8.665	9.701
7	Interior	0	0.93	1699.021	Rarefaction	16.890	1.820	13.324	20.457
8	Interior	0	0.97	3883.447	Extrapolation	17.839	4.980	8.079	27.599
9	Interior	1	0.93	1699.021	Rarefaction	9.668	0.258	9.161	10.175
10	Interior	1	0.97	3883.447	Extrapolation	9.834	0.275	9.294	10.374
11	Interior	2	0.93	1699.021	Rarefaction	6.994	0.160	6.680	7.308
12	Interior	2	0.97	3883.447	Extrapolation	7.033	0.162	6.716	7.350

Example 9b: FD for incidence data with two target number of sampling units (30 and 70)

The following commands return the FD estimates with two specified levels of sample sizes (30 and 70) for the `Fish_incidence_data`.

```

data(Fish_incidence_data)
data(Fish_distance_matrix)
data <- Fish_incidence_data
distM <- Fish_distance_matrix
output_est_FD_inci <- estimate3D(data, diversity = 'FD', datatype = "incidence_raw",
                                base = "size", level = c(30, 70), nboot = 10,
                                FDdistM = distM, FDtype = 'AUC')
output_est_FD_inci

```

	Assemblage	Order.q	mT	Method	SC	qFD	s.e.	qFD.LCL	qFD.UCL
1	2013-2015	0	30	Rarefaction	0.976	17.748	0.519	16.730	18.766
2	2013-2015	0	70	Extrapolation	0.993	18.550	0.696	17.186	19.914
3	2013-2015	1	30	Rarefaction	0.976	15.929	0.314	15.314	16.545
4	2013-2015	1	70	Extrapolation	0.993	16.006	0.315	15.388	16.624
5	2013-2015	2	30	Rarefaction	0.976	15.459	0.277	14.915	16.003
6	2013-2015	2	70	Extrapolation	0.993	15.477	0.278	14.932	16.022
7	2016-2018	0	30	Rarefaction	0.972	17.503	0.562	16.401	18.606
8	2016-2018	0	70	Extrapolation	0.988	18.705	1.207	16.340	21.070
9	2016-2018	1	30	Rarefaction	0.972	15.729	0.371	15.001	16.457
10	2016-2018	1	70	Extrapolation	0.988	15.816	0.364	15.103	16.530
11	2016-2018	2	30	Rarefaction	0.972	15.268	0.386	14.512	16.025
12	2016-2018	2	70	Extrapolation	0.988	15.290	0.386	14.533	16.046

FUNCTION `ObsAsy3D`: ASYMPTOTIC AND OBSERVED DIVERSITY PROFILES

```

ObsAsy3D(data, diversity = "TD", q = seq(0, 2, 0.2), datatype = "abundance",
          nboot = 50, conf = 0.95, nT = NULL,
          method = c("Asymptotic", "Observed"),
          PDtree, PDreftime = NULL, PDtype = "meanPD",
          FDdistM, FDtype = "AUC", FDtau = NULL, FDCut_number = 50
          )

```

All arguments in the above function are the same as those for the main function `iNEXT3D` (except that the default of `q` here is `seq(0, 2, 0.2)`). The function `ObsAsy3D()` computes observed and asymptotic diversity of order `q` between 0 and 2 (in increments of 0.2) for 3D diversity; these 3D values with different order `q` can be used to depict a `q`-profile in the `ggObsAsy3D` function.

It also computes observed and asymptotic PD for various reference times by specifying the argument `PDreftime`; these PD values with different reference times can be used to depict a time-profile in the `ggObsAsy3D` function.

It also computes observed and asymptotic FD for various threshold tau levels by specifying the argument `FDtau`; these FD values with different threshold levels can be used to depict a tau-profile in the `ggObsAsy3D` function.

For each dimension, by default, both the observed and asymptotic diversity estimates will be computed.

FUNCTION ggObsAsy3D(): GRAPHIC DISPLAYS OF DIVERSITY PROFILES

```
ggObsAsy3D(output, profile = "q")
```

ggObsAsy3D is a ggplot2 extension for an ObsAsy3D object to plot 3D q-profile (which depicts the observed diversity and asymptotic diversity estimate with respect to order q) for q between 0 and 2 (in increments of 0.2).

It also plots time-profile (which depicts the observed and asymptotic estimate of PD or mean PD with respect to reference times when diversity = "PD" specified in the ObsAsy3D function), and tau-profile (which depicts the observed and asymptotic estimate of FD with respect to threshold level tau when diversity = "FD" and FDtype = "tau_values" specified in the ObsAsy3D function) based on the output from the function ObsAsy3D.

In the plot of profiles, only confidence intervals of the asymptotic diversity will be shown when both the observed and asymptotic diversity estimates are computed.

TAXONOMIC DIVERSITY (TD): q-profiles

Example 10a: TD q-profiles for abundance data

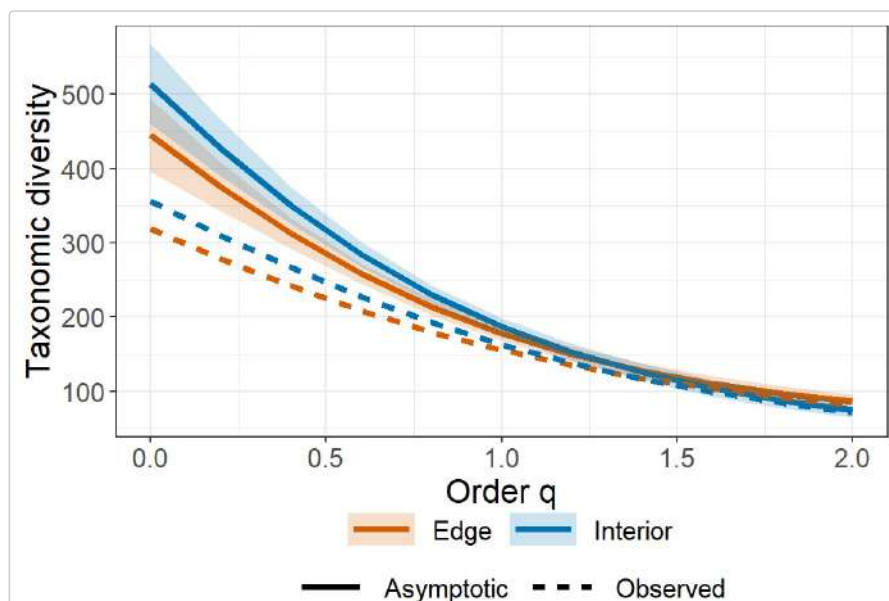
The following commands returns the observed and asymptotic taxonomic diversity ('TD') for the Brazil_rainforest_abun_data, along with its confidence interval for diversity order q between 0 to 2. Here only the first ten rows of the output are shown.

```
data(Brazil_rainforest_abun_data)
output_ObsAsy_TD_abun <- ObsAsy3D(Brazil_rainforest_abun_data, diversity = 'TD',
                                   datatype = "abundance")
output_ObsAsy_TD_abun
```

	Assemblage	Order.q	qTD	s.e.	qTD.LCL	qTD.UCL	Method
1	Edge	0.0	444.971	25.175	395.629	494.314	Asymptotic
2	Edge	0.2	375.270	16.678	342.582	407.958	Asymptotic
3	Edge	0.4	312.452	10.496	291.880	333.024	Asymptotic
4	Edge	0.6	258.379	6.878	244.900	271.859	Asymptotic
5	Edge	0.8	213.730	5.445	203.057	224.403	Asymptotic
6	Edge	1.0	178.000	5.138	167.930	188.069	Asymptotic
7	Edge	1.2	149.914	5.123	139.874	159.955	Asymptotic
8	Edge	1.4	127.945	5.135	117.879	138.010	Asymptotic
9	Edge	1.6	110.672	5.139	100.599	120.745	Asymptotic
10	Edge	1.8	96.948	5.137	86.880	107.016	Asymptotic

The following commands plot the corresponding q-profiles, along with its confidence interval for q between 0 to 2.

```
# q-profile curves
ggObsAsy3D(output_ObsAsy_TD_abun)
```



Example 10b: TD q-profiles for incidence data

The following commands return the observed and asymptotic taxonomic diversity ('TD') estimates for the

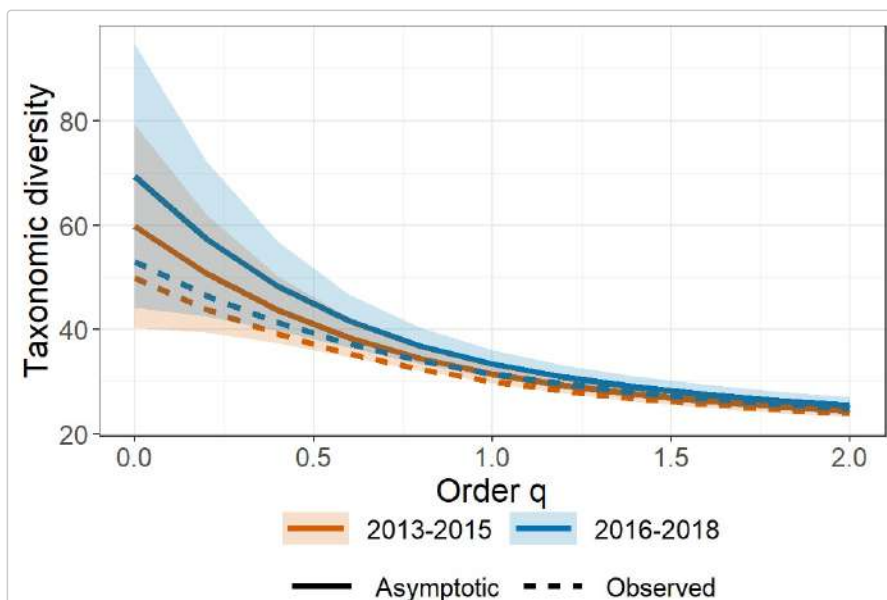
Fish_incidence_data, along with its confidence interval for diversity order q between 0 to 2. Here only the first ten rows of the output are shown.

```
data(Fish_incidence_data)
output_ObsAsy_TD_inci <- ObsAsy3D(Fish_incidence_data, diversity = 'TD',
                                  datatype = "incidence_raw")
output_ObsAsy_TD_inci
```

	Assemblage	Order.q	qTD	s.e.	qTD.LCL	qTD.UCL	Method
1	2013-2015	0.0	59.803	9.908	40.384	79.223	Asymptotic
2	2013-2015	0.2	50.828	5.806	39.449	62.207	Asymptotic
3	2013-2015	0.4	43.790	3.281	37.359	50.221	Asymptotic
4	2013-2015	0.6	38.458	1.911	34.713	42.204	Asymptotic
5	2013-2015	0.8	34.490	1.248	32.044	36.936	Asymptotic
6	2013-2015	1.0	31.542	0.947	29.685	33.398	Asymptotic
7	2013-2015	1.2	29.328	0.803	27.754	30.902	Asymptotic
8	2013-2015	1.4	27.635	0.724	26.217	29.053	Asymptotic
9	2013-2015	1.6	26.312	0.673	24.992	27.632	Asymptotic
10	2013-2015	1.8	25.255	0.639	24.002	26.509	Asymptotic

The following commands plot the corresponding q-profiles, along with its confidence interval for q between 0 to 2.

```
# q-profile curves
ggObsAsy3D(output_ObsAsy_TD_inci)
```



PHYLOGENETIC DIVERSITY (PD): time-profiles and q-profiles

Example 11a: PD time-profiles for abundance data

The following commands return the observed and asymptotic phylogenetic diversity ('PD') estimates for the Brazil_rainforest_abun_data, along with its confidence interval for diversity order q = 0, 1, 2 under reference times from 0.01 to 400 (tree height). Here only the first ten rows of the output are shown.

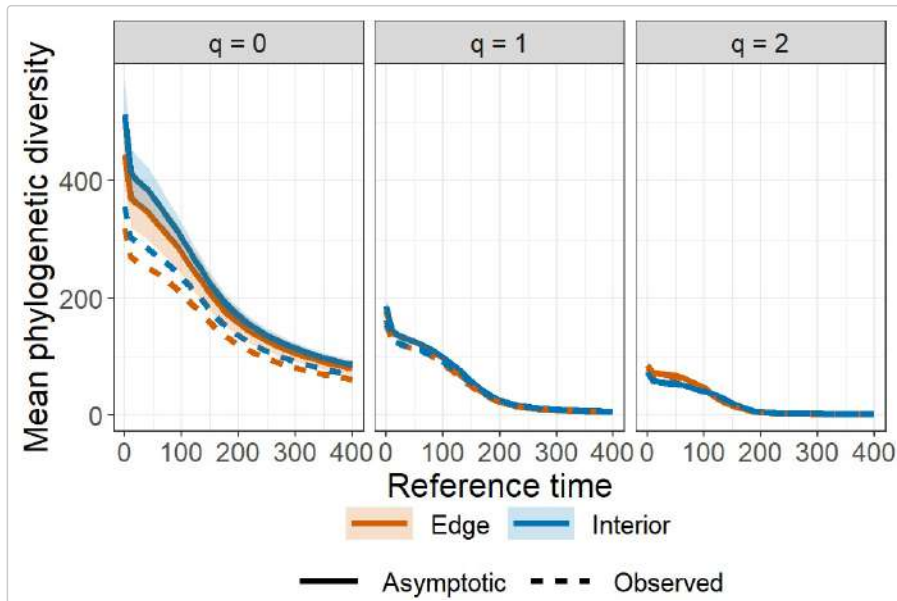
```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_phylo_tree)
data <- Brazil_rainforest_abun_data
tree <- Brazil_rainforest_phylo_tree
output_ObsAsy_PD_abun <- ObsAsy3D(data, diversity = 'PD', q = c(0, 1, 2),
                                   PDreftime = seq(0.01, 400, length.out = 20),
                                   datatype = "abundance", nboot = 20, PDtree = tree)
output_ObsAsy_PD_abun
```

	Assemblage	Order.q	qPD	s.e.	qPD.LCL	qPD.UCL	Method	Reftime	Type
1	Edge	0	444.971	29.001	388.130	501.812	Asymptotic	0.100	meanPD
2	Edge	1	178.000	5.074	168.055	187.944	Asymptotic	0.100	meanPD
3	Edge	2	85.905	4.149	77.773	94.038	Asymptotic	0.100	meanPD
4	Interior	0	513.518	29.215	456.256	570.779	Asymptotic	0.100	meanPD
5	Interior	1	186.983	5.190	176.812	197.154	Asymptotic	0.100	meanPD
6	Interior	2	74.718	4.210	66.466	82.969	Asymptotic	0.100	meanPD
7	Edge	0	371.100	25.520	321.082	421.117	Asymptotic	10.354	meanPD
8	Edge	1	141.418	3.841	133.891	148.946	Asymptotic	10.354	meanPD

9	Edge	2	72.848	3.260	66.458	79.238	Asymptotic	10.354	meanPD
10	Interior	0	413.568	22.401	369.663	457.472	Asymptotic	10.354	meanPD

The argument `profile = "time"` in the `ggObsAsy3D` function creates a separate plot for each diversity order $q = 0, 1,$ and 2 with x-axis being "Reference time". Different assemblages will be represented by different color lines.

```
# time-profile curves
ggObsAsy3D(output_ObsAsy_PD_abun, profile = "time")
```



Example 11b: PD q-profiles for incidence data

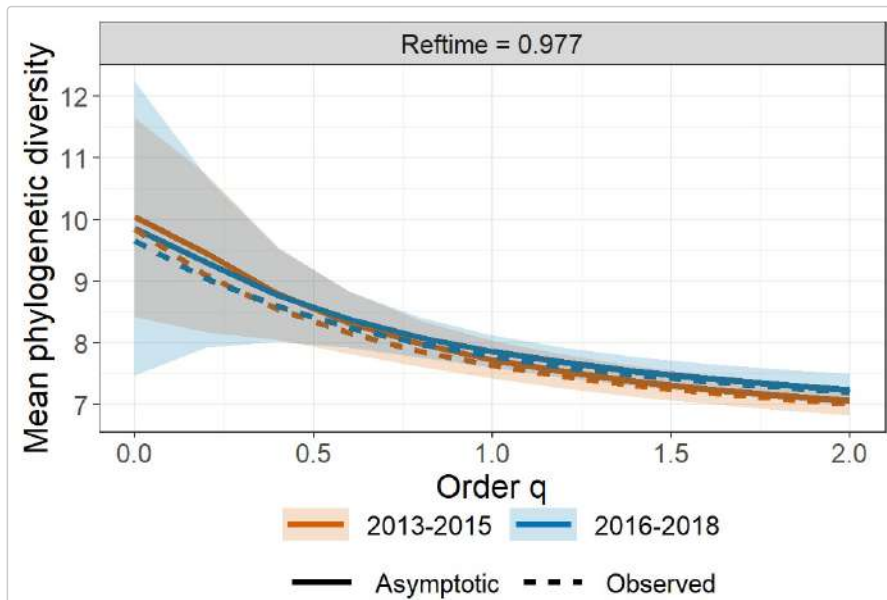
The following commands return the observed and asymptotic taxonomic diversity ('PD') estimates for the `Fish_incidence_data`, along with its confidence interval for diversity order q between 0 to 2. Here only the first ten rows of the output are shown.

```
data(Fish_incidence_data)
data(Fish_phylo_tree)
data <- Fish_incidence_data
tree <- Fish_phylo_tree
output_ObsAsy_PD_inci <- ObsAsy3D(data, diversity = 'PD', q = seq(0, 2, 0.2),
                                datatype = "incidence_raw", nboot = 20, PDtree = tree,
                                PDreftime = NULL)
output_ObsAsy_PD_inci
```

	Assemblage	Order.q	qPD	s.e.	qPD.LCL	qPD.UCL	Method	Reftime	Type
1	2013-2015	0.0	10.039	0.823	8.426	11.653	Asymptotic	0.977	meanPD
2	2013-2015	0.2	9.462	0.656	8.177	10.748	Asymptotic	0.977	meanPD
3	2013-2015	0.4	8.802	0.387	8.043	9.561	Asymptotic	0.977	meanPD
4	2013-2015	0.6	8.329	0.257	7.825	8.833	Asymptotic	0.977	meanPD
5	2013-2015	0.8	7.985	0.192	7.608	8.362	Asymptotic	0.977	meanPD
6	2013-2015	1.0	7.729	0.158	7.419	8.039	Asymptotic	0.977	meanPD
7	2013-2015	1.2	7.533	0.139	7.260	7.805	Asymptotic	0.977	meanPD
8	2013-2015	1.4	7.378	0.128	7.126	7.629	Asymptotic	0.977	meanPD
9	2013-2015	1.6	7.252	0.122	7.012	7.492	Asymptotic	0.977	meanPD
10	2013-2015	1.8	7.147	0.119	6.913	7.381	Asymptotic	0.977	meanPD

The following commands plot the corresponding q-profiles, along with its confidence interval for q between 0 to 2, for the default reference time = 0.977 (the tree depth).

```
# q-profile curves
ggObsAsy3D(output_ObsAsy_PD_inci, profile = "q")
```



FUNCTIONAL DIVERSITY (FD): tau-profiles and q-profiles

Example 12a: FD tau-profiles for abundance data

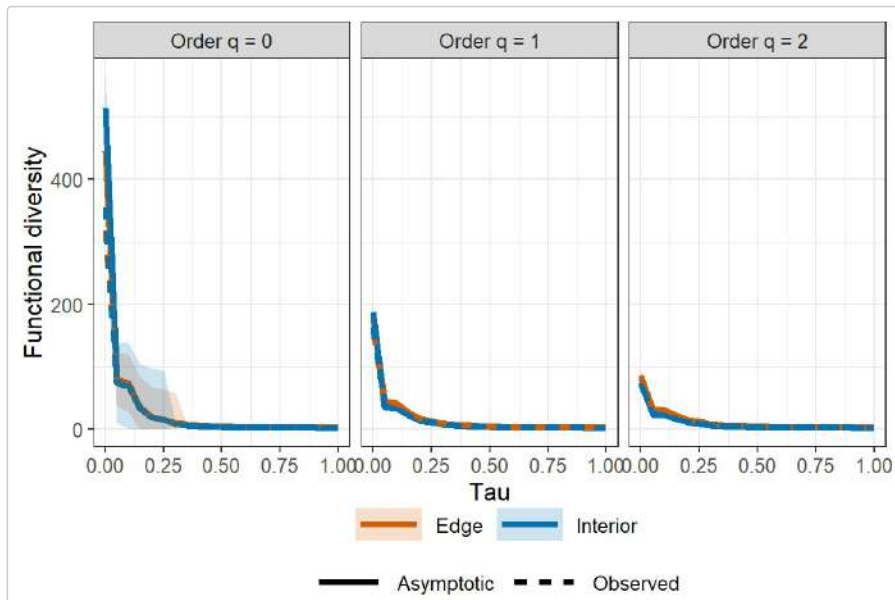
The following commands returns observed and asymptotic functional diversity ('FD') for `Brazil_rainforest_abun_data`, along with its confidence interval at diversity order $q = 0, 1, 2$ under tau values from 0 to 1. Here only the first ten rows of the output are shown.

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_distance_matrix)
data <- Brazil_rainforest_abun_data
distM <- Brazil_rainforest_distance_matrix
output_ObsAsy_FD_abun_tau <- ObsAsy3D(data, diversity = 'FD', q = c(0, 1, 2),
                                     datatype = "abundance", nboot = 10, FDdistM = distM,
                                     FDtype = 'tau_values', FDtau = seq(0, 1, 0.05))
output_ObsAsy_FD_abun_tau
```

	Assemblage	Order.q	qFD	s.e.	qFD.LCL	qFD.UCL	Method	Tau
1	Edge	0	444.971	22.481	400.909	489.034	Asymptotic	0.00
2	Edge	1	178.000	5.377	167.461	188.538	Asymptotic	0.00
3	Edge	2	85.905	4.471	77.143	94.668	Asymptotic	0.00
4	Edge	0	79.904	22.161	36.468	123.340	Asymptotic	0.05
5	Edge	1	45.187	1.216	42.804	47.569	Asymptotic	0.05
6	Edge	2	32.092	0.799	30.526	33.658	Asymptotic	0.05
7	Edge	0	73.276	23.497	27.223	119.328	Asymptotic	0.10
8	Edge	1	42.200	1.137	39.972	44.427	Asymptotic	0.10
9	Edge	2	30.182	0.683	28.843	31.521	Asymptotic	0.10
10	Edge	0	35.372	24.511	0.000	83.413	Asymptotic	0.15

The following commands plot the corresponding tau-profiles, along with its confidence interval for diversity order $q = 0, 1, 2$.

```
# tau-profile curves
ggObsAsy3D(output_ObsAsy_FD_abun_tau, profile = "tau")
```



Example 12b: FD q-profiles for abundance data

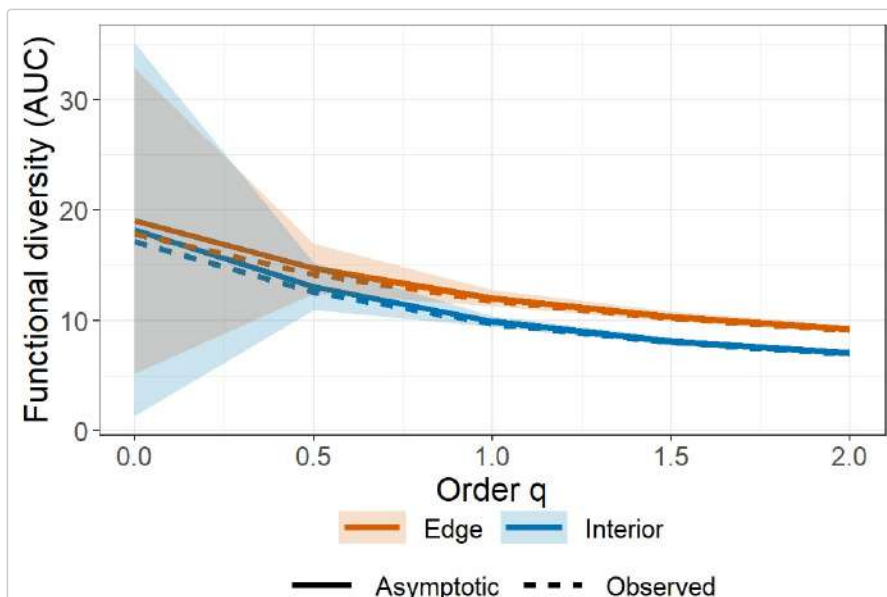
The following commands returns the observed and asymptotic taxonomic diversity ('FD') for the `Brazil_rainforest_abun_data`, along with its confidence interval for diversity order q between 0 to 2 with `FDtype = 'AUC'`. Here only the first ten rows of the output are shown.

```
data(Brazil_rainforest_abun_data)
data(Brazil_rainforest_distance_matrix)
data <- Brazil_rainforest_abun_data
distM <- Brazil_rainforest_distance_matrix
output_ObsAsy_FD_abun <- ObsAsy3D(data, diversity = 'FD', q = seq(0, 2, 0.5),
                                   datatype = "abundance", nboot = 10,
                                   FDdistM = distM, FDtype = 'AUC')
output_ObsAsy_FD_abun
```

	Assemblage	Order.q	qFD	s.e.	qFD.LCL	qFD.UCL	Method
1	Edge	0.0	19.008	7.049	5.191	32.824	Asymptotic
2	Edge	0.5	14.698	1.144	12.456	16.941	Asymptotic
3	Edge	1.0	12.037	0.362	11.328	12.746	Asymptotic
4	Edge	1.5	10.345	0.233	9.889	10.802	Asymptotic
5	Edge	2.0	9.228	0.189	8.857	9.600	Asymptotic
6	Interior	0.0	18.208	8.615	1.322	35.094	Asymptotic
7	Interior	0.5	13.071	1.076	10.963	15.179	Asymptotic
8	Interior	1.0	9.922	0.249	9.434	10.410	Asymptotic
9	Interior	1.5	8.103	0.167	7.776	8.430	Asymptotic
10	Interior	2.0	7.055	0.143	6.776	7.335	Asymptotic

The following commands plot the corresponding q-profiles, along with its confidence interval for q between 0 to 2.

```
# q-profile curves
ggObsAsy3D(output_ObsAsy_FD_abun, profile = "q")
```



Example 12c: FD q-profiles for incidence data

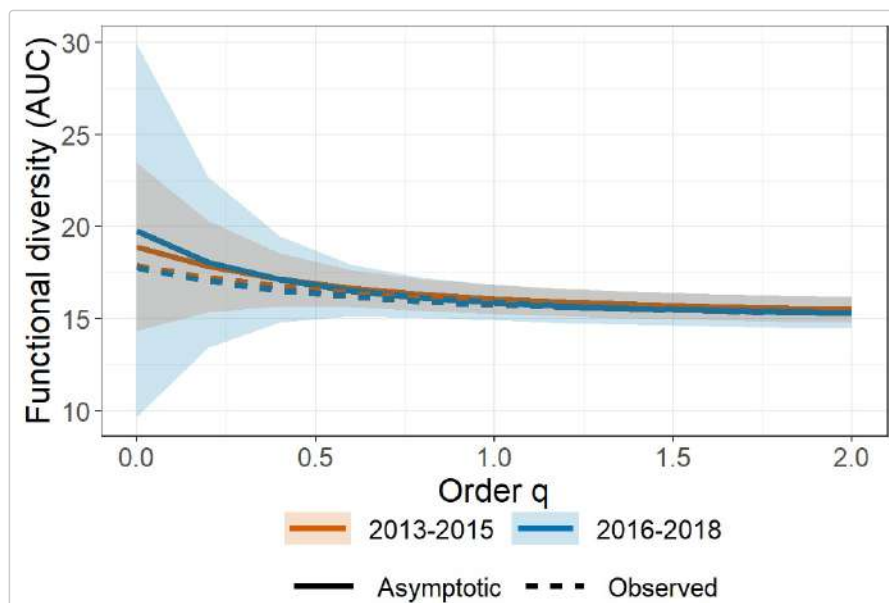
The following commands returns observed and asymptotic functional diversity ('FD') for `Fish_incidence_data`, along with its confidence interval at diversity order q from 0 to 2. Here only the first ten rows of the output are shown.

```
data(Fish_incidence_data)
data(Fish_distance_matrix)
data <- Fish_incidence_data
distM <- Fish_distance_matrix
output_ObsAsy_FD_inci <- ObsAsy3D(data, diversity = 'FD', datatype = "incidence_raw",
                                   nboot = 20, FDdistM = distM, FDtype = 'AUC')
output_ObsAsy_FD_inci
```

	Assemblage	Order.q	qFD	s.e.	qFD.LCL	qFD.UCL	Method
1	2013-2015	0.0	18.906	2.329	14.341	23.470	Asymptotic
2	2013-2015	0.2	17.826	1.264	15.348	20.303	Asymptotic
3	2013-2015	0.4	17.115	0.736	15.673	18.557	Asymptotic
4	2013-2015	0.6	16.624	0.518	15.609	17.639	Asymptotic
5	2013-2015	0.8	16.284	0.435	15.430	17.137	Asymptotic
6	2013-2015	1.0	16.043	0.401	15.257	16.828	Asymptotic
7	2013-2015	1.2	15.868	0.383	15.117	16.618	Asymptotic
8	2013-2015	1.4	15.736	0.372	15.007	16.466	Asymptotic
9	2013-2015	1.6	15.635	0.365	14.919	16.351	Asymptotic
10	2013-2015	1.8	15.555	0.360	14.849	16.262	Asymptotic

The following commands plot the corresponding q-profiles, along with its confidence interval for q between 0 to 2.

```
# q-profile curves
ggObsAsy3D(output_ObsAsy_FD_inci, profile = "q")
```



License

The `iNEXT.3D` package is licensed under the GPLV3. To help refine `iNEXT.3D`, your comments or feedback would be welcome (please send them to Anne Chao or report an issue on the `iNEXT.3D` github [iNEXT.3D github](#)).

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.
- Hsieh, T. C., Ma, K-H, and Chao, A. (2016). `iNEXT`: An R package for rarefaction and extrapolation of species diversity (Hill numbers). *Methods in Ecology and Evolution*, 7, 1451-1456.