

# Package ‘iNEXT.meta’

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**Type** Package

**Title** Meta-analysis of the Difference Between Two Treatments in iNterpolation and EXTrapola-  
tion for Beta Diversity Across Three Dimensions

**Version** 1.0.0

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**Description** Provides functions to compute the difference between two treatments in taxonomic, phy-  
logenetic, or functional diversity (3D) at a standardized sample coverage across al-  
pha, beta, and gamma diversity levels, as well as dissimilarity and turnover indices. This pack-  
age also includes tools to conduct meta-analysis and generate forest plots for visualizing the re-  
sults.

**License** GPL(>=3)

**Imports** dplyr, forestplot, grid, gridExtra, iNEXT.3D, iN-  
EXT.beta3D, knitr, magrittr, metafor, purrr, rmarkdown, stringr, tibble, tidyr

**Suggests** tidyverse

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**Depends** R (>= 4.0)

**RoxygenNote** 7.3.2

## R topics documented:

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iNEXT.meta-package	<i>Meta-analysis of the difference between two treatments in interpolation and extrapolation for beta diversity across three dimensions</i>
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### Description

iNEXT.meta (Meta-analysis of the difference between two treatments in interpolation and extrapolation for beta diversity across three dimensions) is an R package that extends the concepts of iNEXT.beta3D (Chao et al., 2023) to meta-analysis (fixed-effect model).

iNEXT.meta is primarily designed to integrate results comparing diversity differences between two treatments across multiple studies. It enables the calculation of three dimensions (3D) of diversity: taxonomic diversity (TD), phylogenetic diversity (PD) and functional diversity (FD), at a specified level of sample coverage.

This package provides three main functions:

1. DataInfobeta3Dmeta provides basic data information in each combination of site and treatment for (1) the gamma reference sample in the pooled assemblage, and (2) the alpha reference sample in the joint assemblage.
2. iNEXTbeta3Dmeta estimates the difference of standardized 3D diversity with common sample coverage (for alpha, beta, gamma diversity, and four classes of dissimilarity measures) between two treatments, and fit a fixed-effect model to perform meta-analysis.
3. ggiNEXTmeta visualizes the output from the function iNEXTbeta3Dmeta by providing forest plot of the difference between two treatments of standardized 3D diversity in each study/site and meta-analysis.

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Beetle_abundance_data	<i>Beetle abundance data (datatype = "abundance" for TD, PD, and FD)</i>
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### Description

This dataset includes beetle species abundance data in eleven sites (B04, B05, B06, B07, H09, L11, P08, S10, U01, U02, U03) with two treatments (Control and Enhanced).

### Usage

```
data("Beetle_abundance_data")
```

### Format

Beetle\_abundance\_data is a matrix where:

- The first two columns represent Site, Treatment.
- The remaining 1308 columns correspond to species names.

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Beetle_distM	<i>Species pairwise distance matrix for beetle species</i>
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**Description**

This dataset includes a beetle species pairwise symmetric distance matrix for 199 species listed in the Beetle\_abundance\_data dataset. Each element in the matrix represents a Gower distance between two species computed from species traits.

**Usage**

```
data("Beetle_distM")
```

**Format**

Beetle\_distM is a 1308 x 1308 (species by species) symmetric data.frame. Each element of the data.frame is between zero (for species pairs with identical traits) and one.

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Beetle_tree	<i>Phylogenetic tree for beetle abundance data</i>
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**Description**

This dataset includes a phylogenetic tree spanned by 1308 species listed in the Beetle\_abundance\_data dataset.

**Usage**

```
data("Beetle_tree")
```

**Format**

Beetle\_tree is a list (phylo tree) with the following phylogenetic information:

A list of 4:

\$ edge : int [1:1720, 1:2] 1309 1310 1311 1312 1313 1310 1311 ...

\$ edge.length: num [1:1720] 0.1091 0.4511 0.2800 0.0349 0.1000 0.0160 ...

\$ Nnode : int 413

\$ tip.label : chr [1:1308] "Otiorynchus\_porcatus" "Otiorynchus\_crataegi" "Otiorynchus\_pupillatus"

...

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Bird\_distM

*Species pairwise distance matrix for bird species*


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### Description

This dataset includes a bird species pairwise symmetric distance matrix for 72 species listed in the Bird\_incidence\_data dataset. Each element in the matrix represents a Gower distance between two species computed from species traits.

### Usage

```
data("Bird_distM")
```

### Format

Bird\_distM is a 72 x 72 (species by species) symmetric data.frame. Each element of the data.frame is between zero (for species pairs with identical traits) and one.

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Bird\_incidence\_data

*Bird incidence raw data (datatype = "incidence\_raw" for TD, PD, and FD)*


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### Description

This dataset includes bird species incidence data in eleven sites (B04, B05, B06, B07, H09, L11, P08, S10, U01, U02, U03) with two treatments (Control and Enhanced). In each combinations of eleven sites and two treatments (B04C, B04E, B05C, B05E, ...), there are 84, 84, 49, 69, 75, 84, 71, 57, 62, 77, 48, 78, 84, 84, 64, 83, 77, 69, 84, 55, 84, 51 sampling units.

### Usage

```
data("Bird_incidence_data")
```

### Format

Bird\_incidence\_data is a matrix where:

- The first three columns represent Site, Treatment, and Patch.
- The remaining 72 columns correspond to species names.

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Bird\_tree

*Phylogenetic tree for bird incidence data*


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### Description

This dataset includes a phylogenetic tree spanned by 72 species listed in the Bird\_incidence\_data dataset.

### Usage

```
data("Bird_tree")
```

### Format

Bird\_tree is a list (phylo tree) with the following phylogenetic information:

A list with 4 elements:

\$ edge : int [1:135, 1:2] 73 74 75 75 74 73 1 2 3 76 ...

\$ edge.length: num [1:30] 19.1 68.5 15.8 84.3 16.5 ...

\$ Nnode : int 64

\$ tip.label : chr [1:16] "Bonasa\_bonasia" "Tetrao\_urogallus" "Bucephala\_clangula" ...

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DataInfobeta3Dmeta

*Data information for reference samples*


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### Description

DataInfobeta3Dmeta provides basic data information for each combination of site and treatment for (1) the gamma reference sample in the pooled assemblage, and (2) the alpha reference sample in the joint assemblage.

### Usage

```
DataInfobeta3Dmeta(
  data,
  diversity = "TD",
  datatype = "abundance",
  PDtree = NULL,
  PDreftime = NULL,
  FDdistM = NULL,
  FDtype = "AUC",
  FDtau = NULL
)
```

**Arguments**

data	(a) For datatype = "abundance", a data.frame whose first two columns are study/site and treatment, followed by species columns (an assemblage = site $\times$ treatment). (b) For datatype = "incidence_raw", a data.frame whose first three columns are study/site, treatment, and patch, followed by species columns with entries in {0,1}.
diversity	Diversity type: 'TD' (Taxonomic), 'PD' (Phylogenetic), or 'FD' (Functional).
datatype	"abundance" for individual-based data, or "incidence_raw" for incidence-by-sampling-units data (0/1).
PDtree	(required for diversity = "PD") a phylogenetic tree in Newick format for all observed species in the pooled data.
PDreftime	(required only for diversity = "PD") a numeric reference time; default NULL uses the root age of PDtree.
FDdistM	(required for diversity = "FD") a species pairwise distance matrix for the pooled data.
FDtype	(required for diversity = "FD") either "tau_value" for a specified threshold or "AUC" (default) for the area under the tau-profile.
FDtau	(required for diversity = "FD" and FDtype = "tau_value") a value in [0,1] specifying the threshold. If FDtau = NULL (default), the threshold is set to the mean pairwise distance (quadratic entropy).

**Value**

A data.frame with basic information restricted to the pooled and joint assemblages. Columns follow `iNEXT.beta3D::DataInfobeta3D` output.

**Examples**

```
## (Data Information) Taxonomic diversity for abundance data
data("Beetle_abundance_data")
info_TD_abu <- DataInfobeta3Dmeta(data = Beetle_abundance_data,
                                diversity = 'TD',
                                datatype = 'abundance')

info_TD_abu

## (Data Information) Taxonomic diversity for incidence data (Bird)
data("Bird_incidence_data")
info_TD_inc <- DataInfobeta3Dmeta(data = Bird_incidence_data,
                                diversity = 'TD',
                                datatype = 'incidence_raw')

info_TD_inc

## (Data Information) Mean phylogenetic diversity for abundance data
data("Beetle_abundance_data")
data("Beetle_tree")
info_PD_abu <- DataInfobeta3Dmeta(data = Beetle_abundance_data,
                                diversity = 'PD',
                                datatype = 'abundance',
                                PDtree = Beetle_tree, PDreftime = NULL)

info_PD_abu
```

```

## (Data Information) Mean phylogenetic diversity for incidence data (Bird)
data("Bird_incidence_data")
data("Bird_tree")
info_PD_inc <- DataInfobeta3Dmeta(data = Bird_incidence_data,
                                diversity = 'PD',
                                datatype = 'incidence_raw',
                                PDtree = Bird_tree,
                                PDreftime = NULL)

info_PD_inc

## (Data Information) Functional diversity for abundance data (tau-value)
data("Beetle_abundance_data")
data("Beetle_distM")
info_FDtau_abu <- DataInfobeta3Dmeta(data = Beetle_abundance_data,
                                    diversity = 'FD',
                                    datatype = 'abundance',
                                    FDdistM = Beetle_distM,
                                    FDtype = "tau_value", FDtau = NULL)

info_FDtau_abu

## (Data Information) Functional diversity for abundance data (AUC)
data("Beetle_abundance_data")
data("Beetle_distM")
info_FDAUC_abu <- DataInfobeta3Dmeta(data = Beetle_abundance_data,
                                     diversity = 'FD',
                                     datatype = 'abundance',
                                     FDdistM = Beetle_distM,
                                     FDtype = "AUC", FDtau = NULL)

info_FDAUC_abu

## (Data Information) Functional diversity for incidence data (Bird)
data("Bird_incidence_data")
data("Bird_distM")
info_FDtau_inc <- DataInfobeta3Dmeta(data = Bird_incidence_data,
                                    diversity = 'FD',
                                    datatype = 'incidence_raw',
                                    FDdistM = Bird_distM,
                                    FDtype = "tau_value", FDtau = NULL)

info_FDtau_inc

```

ggiNEXTmeta

*Forest plot of the standardized 3D diversity difference (fixed effect)***Description**

ggiNEXTmeta draws a forest plot for the difference of standardized 3D diversity between two treatments, summarized using a fixed-effect model.

**Usage**

```
ggiNEXTmeta(output, q, num_round = 3, range, type = NULL, level = NULL)
```

**Arguments**

output	The output from iNEXTbeta3Dmeta.
q	A value of Order.q present in output.
num_round	Number of decimal places shown.
range	Optional lower/upper bounds to clip CIs (pass to forestplot's clip; commented out by default).
type	One of "Gamma", "Alpha", "Beta", "1-C", "1-U", "1-V", or "1-S".
level	Optional sample coverage (in percent) to annotate in the title; if NULL, no annotation is added.

**Value**

A forest plot showing site-level differences and the fixed-effect combined estimate.

**Examples**

```
data("Beetle_abundance_data")
out <- iNEXTbeta3Dmeta(Beetle_abundance_data, diversity = "TD",
  order.q = c(0,1,2), datatype = "abundance",
  level = NULL, nboot = 10,
  treatment_order = c("Enhanced", "Control"))
ggiNEXTmeta(out, q = 0, num_round = 3, range = c(-20,15), type = "Gamma", level = NULL)
```

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iNEXTbeta3Dmeta	<i>Difference of standardized 3D diversity (fixed-effect meta-analysis)</i>
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**Description**

iNEXTbeta3Dmeta estimates the difference of standardized 3D (taxonomic, phylogenetic, functional) diversity between two treatments (e.g., Enhanced vs. Control) and synthesizes results across sites using a fixed-effect model.

**Usage**

```
iNEXTbeta3Dmeta(
  data,
  diversity = "TD",
  order.q = 0,
  datatype = "abundance",
  level = NULL,
  nboot = 10,
  treatment_order,
  conf = 0.95,
  PDtree,
  PDreftime = NULL,
  PDtype = "meanPD",
  FDdistM,
  FDtype = "AUC",
  FDtau = NULL,
  FDcut_number = 30
)
```



**Arguments**

<code>data</code>	Same structure as <code>iNEXT.beta3D</code> ; for <code>datatype = "abundance"</code> , the first two columns are site and treatment; for <code>datatype = "incidence_raw"</code> , the first three columns are site, treatment, and patch.
<code>diversity</code>	'TD', 'PD', or 'FD'.
<code>order.q</code>	Numeric vector of diversity orders (e.g., <code>c(0, 1, 2)</code> ).
<code>datatype</code>	"abundance" or "incidence_raw".
<code>level</code>	Sample-coverage level in [0,1]. If NULL, the function uses the minimum coverage achieved at double the reference sample size across all site $\times$ treatment combinations.
<code>nboot</code>	Number of bootstrap replications for uncertainty.
<code>treatment_order</code>	Character vector of length 2 specifying the treatment order; differences are computed as <code>treatment_order[1] - treatment_order[2]</code> .
<code>conf</code>	Confidence level (default 0.95).
<code>PDtree</code> , <code>PDreftime</code> , <code>PDtype</code> , <code>FDdistM</code> , <code>FDtype</code> , <code>FDtau</code> , <code>FDcut_number</code>	As in <code>iNEXT.beta3D</code> .

**Value**

A list with seven components: `Summary_Gamma`, `Summary_Alpha`, `Summary_Beta`, `Summary_1-C`, `Summary_1-U`, `Summary_1-V`, and `Summary_1-S`. Each component contains: (1) a data frame of site-level differences (with SE, CI, weights) plus a fixed-effect combined row, and (2) a one-row meta summary with Cochran's Q (`Q_val`), degrees of freedom (`df_val`), p-value (`p_val`), and heterogeneity percentage (`I2_val`).

**Examples**

```
## TD / abundance (Beetle), coverage-standardized, fixed effect
data("Beetle_abundance_data")
out_TD_abu <- iNEXTbeta3Dmeta(data = Beetle_abundance_data, diversity = "TD",
                             order.q = c(0,1,2), datatype = "abundance", level = NULL,
                             nboot = 10, treatment_order = c("Enhanced", "Control"), conf = 0.95)

out_TD_abu

## PD / abundance (Beetle) - requires Beetle_tree
data("Beetle_abundance_data"); data("Beetle_tree")
out_PD_abu <- iNEXTbeta3Dmeta(data = Beetle_abundance_data, diversity = "PD",
                             order.q = c(0,1,2), datatype = "abundance", level = NULL,
                             nboot = 10, treatment_order = c("Enhanced", "Control"), conf = 0.95,
                             PDtree = Beetle_tree, PDreftime = NULL, PDtype = "meanPD")

out_PD_abu

## FD / abundance (Beetle) - requires Beetle_distM
data("Beetle_abundance_data"); data("Beetle_distM")
out_FD_abu <- iNEXTbeta3Dmeta(data = Beetle_abundance_data, diversity = "FD",
                             order.q = c(0,1,2), datatype = "abundance", level = NULL,
                             nboot = 10, treatment_order = c("Enhanced", "Control"), conf = 0.95,
                             FDdistM = Beetle_distM, FDtype = "AUC", FDcut_number = 30)

out_FD_abu

## TD / incidence_raw (Bird)
```

```
data("Bird_incidence_data")
out_TD_inc <- iNEXTbeta3Dmeta(data = Bird_incidence_data, diversity = "TD",
                             order.q = c(0,1,2), datatype = "incidence_raw", level = NULL,
                             nboot = 10, treatment_order = c("Enhanced", "Control"), conf = 0.95)
out_TD_inc
```

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