# Package 'iNEXT.UniFrac'

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**Type** Package

**Title** Interpolation and Extrapolation for UniFrac based on dissimilarity measure

**Version** 0.1.0

**Author** YaYun Teng

**Maintainer** YaYun Teng <jewel860911@gmail.com>

**Description** iNEXT.UniFrac provides the function to calculate UniFrac for multiple assemblages.

**Depends** R (>= 4.0)

**Imports** tidyverse,
magrittr,
tidyr,
ggplot2,
abind,
ape,
ade4,
phytools,
phyclust,
tidytree,
colorRamps,
future.apply,
iNEXT.3D,
iNEXT.beta3D

**Remotes** AnneChao/iNEXT.beta3D

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

## R topics documented:


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## ggiNEXTUniFrac *ggplot2 extension for an iNEXT.UniFrac object*

### Description

ggiNEXTUniFrac: the ggplot extension for iNEXTUniFrac object to plot coverage-based rarefaction/extrapolation curves for UniFrac.

### Usage

```
ggiNEXTUniFrac(output, scale = "fixed", transp = 0.4)
```

### Arguments

| | |
|---|---|
| output | the output from iNEXTUniFrac |
| scale | Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")? |
| transp | a value between 0 and 1 for controlling transparency. transp = 0 is completely transparent, default is 0.4. |

### Value

a figure for two types of UniFrac based on dissimilarity measure.

### Examples

```
data("tongue_cheek")
data("tongue_cheek_tree")
output <- iNEXTUniFrac(tongue_cheek, q=c(0,1,2), nboot = 0, PDtree = tongue_cheek_tree)
ggiNEXTUniFrac(output, scale = 'free', transp = 0.4)
```

## iNEXTUniFrac *function to calculate UniFrac distance based on dissimilarity measure*

### Description

iNEXTUniFrac: function to calculate UniFrac distance based on Sørensen- and Jaccard-type dissimilarity measure

### Usage

```
iNEXTUniFrac(
  data,
  q = c(0, 1, 2),
  level = NULL,
  nboot = 10,
  conf = 0.95,
  PDtree = NULL,
  PDreftime = NULL
)
```

### Arguments

| | |
|---|---|
| data | OTU data can be input as a matrix/data.frame (species by assemblages), or a list of matrices/data.frames, each matrix represents species-by-assemblages abundance matrix. |
| q | a numerical vector specifying the diversity orders. Default is c(0, 1, 2). |
| level | A numerical vector specifying the particular value of sample coverage (between 0 and 1). level = 1 means complete coverage (the corresponding UniFrac represents asymptotic UniFrac distance).<br>If level = NULL, this function computes the gamma and alpha diversity estimates up to one (for q>0) or up to the coverage of double the reference sample size (for q = 0); the corresponding beta diversity and UniFrac distance is computed up to the same maximum coverage as the alpha diversity. |
| nboot | a positive integer specifying the number of bootstrap replications when assessing sampling uncertainty and constructing confidence intervals. Bootstrap replications are generally time consuming. Enter 0 to skip the bootstrap procedures. Default is 10. |
| conf | a positive number < 1 specifying the level of confidence interval. Default is 0.95. |
| PDtree | a phylogenetic tree in Newick format for all observed species in the pooled assemblage. |
| PDreftime | a numerical value specifying reference time for PD. Default is NULL (i.e., the age of the root of PDtree). |

### Value

a list of two data frames with two types dissimilarity measure for UniFrac distance.

### Examples

```
data("tongue_cheek")
data("tongue_cheek_tree")
output <- iNEXTUniFrac(tongue_cheek, q=c(0,1,2),
                       level = seq(0.5, 1, 0.05), nboot = 10,
                       conf = 0.95, PDtree = tongue_cheek_tree, PDreftime = NULL)
```

---

## tongue_cheek *tongue and cheek OTU count data*

---

### Usage

```
data("tongue_cheek")
```

### Format

A data frame with 2549 observations on the following 2 variables.

Cheek a numeric vector

Tongue a numeric vector

## Examples

```
data(tongue_cheek)
```

---

`tongue_cheek_tree` *phylogenetic for tongue and cheek data*

---

## Usage

```
data("tongue_cheek_tree")
```

## Format

The format is: List of 4 $ edge : int [1:25400, 1:2] 12702 12703 12704 12704 12705 12706 12706 12707 12707 12705 ... $ edge.length: num [1:25400] 2.20e-03 9.91e-01 6.61e-03 7.87e-05 6.38e-03 ... $ Nnode : int 12700 $ tip.label : chr [1:12701] "OTU_97.15099" "OTU_97.13686" "OTU_97.30326" "OTU_97.26112" ... - attr(*, "class")= chr "phylo" - attr(*, "order")= chr "cladewise"

## Examples

```
data(tongue_cheek_tree)
```

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