

Package: lirrr (via r-universe)

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Type Package

Title Functions collected/wrote by Daijiang Li

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Description To keep all my functions in one place, and to use them more easily.

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Encoding UTF-8

LazyData yes

Depends R (>= 3.5)

RoxygenNote 7.2.1

Imports plyr, dplyr, purrr, stringr, tibble, tidyr, reshape2, rotl, vegan, ape, picante, phylocomr, PhyloMeasures, tidytree, ggtree

Suggests testthat, betapart

Additional_repositories <https://ropensci.r-universe.dev>

Remotes cran/PhyloMeasures

Repository <https://daijiang.r-universe.dev>

RemoteUrl <https://github.com/daijiang/lirrr>

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Contents

cap_first_letter	2
comm_a	2
comm_b	3
dist_to_df	3
get_n_polytomy	4
get_pd_alpha	4
highlight_subset_sp_in_phylogeny	6

logit_tran	6
mvpd	7
panel.cor	7
panel.hist	7
pd2	8
phylo_betapart	8
rand_test	9
rm_site_noobs	9
rm_sp_noobs	10
tnrs_match_names_2	10
tree	11
unifrac2	11
var_to_rownames	12

Index **13**

cap_first_letter *Make the first letter upper case*

Description

Make the first letter to be upper case.

Usage

cap_first_letter(x)

Arguments

x A vector of species names.

Value

A vector.

comm_a *Example community data*

Description

A data frame with site names as row names, species names as column names, cells are the abundance of each species at each site

Usage

comm_a

Format

a data frame with 15 sites and 15 species

```
comm_b          #' Example community data
```

Description

A data frame with site names as row names, species names as column names, cells are the abundance of each species at each site

Usage

```
comm_b
```

Format

a data frame with 15 sites and 9 species

```
dist_to_df      Change a distance matrix or a matrix to a data frame
```

Description

Convert a distance class object or a matrix to a data frame.

Usage

```
dist_to_df(x)
```

Arguments

x An object of class 'dist' or a matrix.

Value

A data frame with three columns: Var1, Var2, distance.

get_n_polytomy	<i>Calculate number of polytomies</i>
----------------	---------------------------------------

Description

Calculate the number of polytomies a phylogeny has.

Usage

```
get_n_polytomy(tree)
```

Arguments

tree A phylogeny with 'phylo' as class.

Value

A data frame with number of polytomies as columns.

Examples

```
library(lirrr)
get_n_polytomy(tree)
```

get_pd_alpha	<i>Calculate alpha phylogenetic diversity</i>
--------------	---

Description

A function to calculate a bunch of phylo diversity: Faith's PD, MPD, VPD (variance of pairwise distance), MNTD, PSV/PSE. Results of MPD/MNTD from PhyloMeasures are equal with those from Phylocom/Picante with abundance.weight = FALSE Results of PD from PhyloMeasures are unrooted; PD from Phylocom are rooted.

Usage

```
get_pd_alpha(
  samp_wide,
  tree,
  samp_long,
  null.model.pd.root = FALSE,
  null.model.phylomeasures = TRUE,
  null.model.phylocom = FALSE,
  null.type.phylomeasures = "uniform",
  null.type.phylocom = 0,
```

```

    null.type.picante = "taxa.labels",
    n.item = 999,
    abund.weight = FALSE,
    verbose = TRUE,
    vpd = FALSE,
    ...
)

```

Arguments

samp_wide	Wide version of samp_long, row.names are sites, colnames are species.
tree	A phylogeny with class of 'phylo'.
samp_long	A 3-column data frame, site, freq, sp.
null.model.pd.root	Whether to run null models for rooted PD?
null.model.phylomeasures	Whether to run null models using PhyloMeasures package?
null.model.phylocom	Whether to run null models using phylocomr package?
null.type.phylomeasures	If null.model is TRUE, which null model to use for PhyloMeasure?
null.type.phylocom	If null.model is TRUE, which null model to use for Phylocom? - 0: phylogeny shuffle. - 1: maintain site richness and draw from species actually observed in sites. - 2: maintain site richness and draw from the phylogeny - 3: independent swap. See ?phylocomr::ph_comstruct for details
null.type.picante	If null.model is TRUE, which null model to use for Picante? Not used yet.
n.item	The number of randomization.
abund.weight	Should abundance information used when calculating pd with Phylocom/Picante? Default is FALSE.
verbose	Do you want to see relevant information?
vpd	To calculate vpd (variance of pairwise distance) or not?
...	Additional arguments.

Value

A data frame.

highlight_subset_sp_in_phylogeny

Highlight all branches linking a subset of species in a phylogeny

Description

Highlight all branches linking a subset of species in a phylogeny

Usage

```
highlight_subset_sp_in_phylogeny(phy, subset_sp, highlight_color = "red")
```

Arguments

phy The large phylogeny to plot.
subset_sp A vector of species names to be highlighted on the plot of phylogeny.
highlight_color The color to highlight the branches, the default is red.

Value

A 'ggplot2' object.

logit_tran

Logit transformation

Description

Conduct logit-transformation for proportion data.

Usage

```
logit_tran(x, add_num = 0.01)
```

Arguments

x A vector of proportions (either in form of 0.20 or 20).
add_num The number to add for 0s, the default is 0.01.

Value

A vector has been logit transformed.

mvpd	<i>MPD and VPD (mean and variance of pairwise distance)</i>
------	---

Description

Calculate MPD and VPD. The distance matrix can be from functional traits or phylogeny. This function is the same as `'picante::mpd'` when `'abundance.weighted = FALSE'`; it is, however, different when `'abundance.weighted = TRUE'` because this function does not include the diagonal values while `'picante::mpd'` does, which is actually equal to Rao's Q instead of MPD (de Bello et al, 2016, *Oecologia*).

Usage

```
mvpd(samp, dis, abundance.weighted = FALSE)
```

Arguments

<code>samp</code>	A site by species data frame, site names as row names.
<code>dis</code>	A distance matrix.
<code>abundance.weighted</code>	Whether to weight by species abundance? Default is <code>'FALSE'</code> .

Value

A data frame with three columns: `site`, `mpd`, and `vpd`.

<code>panel.cor</code>	<i>panel.cor to plot absolute value of correlations</i>
------------------------	---

Description

`panel.cor` to plot absolute value of correlations

Usage

```
panel.cor(x, y, digits = 2, prefix = "", cex.cor, color.threshold = 0.5, ...)
```

<code>panel.hist</code>	<i>panel.hist to plot absolute value of correlations</i>
-------------------------	--

Description

`panel.hist` to plot absolute value of correlations

Usage

```
panel.hist(x, ...)
```

pd2 *Faith's PD*

Description

Calculate faith's pd, this is a wrapper of 'phylocomr::ph_pd' and 'picante::pd'.

Usage

```
pd2(comm, tree, include.root = TRUE, comm_long)
```

Arguments

comm	A site by species data frame, site names as row names, only works for presence/absence data.
tree	A phylogeny of class "phylo".
include.root	Whether include root in picante::pd; phylocomr::ph_pd always include root.
comm_long	Long format of comm, 3-columns: site, freq, sp; optional.

Value

A data frame of PD for each site.

phylo_betapart *Phylogenetic beta diversity partition*

Description

Calculate Phylogenetic beta diversity and its partition, adapted from betapart::phylo.belt.xx(). Since the pairwise and multisie version share the same core computation process, it makes more sense to return both. Then we can choose which one to use.

Usage

```
phylo_betapart(comm = dat_1, tree)
```

Arguments

comm	A site by species data frame, site names as row names.
tree	A phylogeny of class "phylo".

Value

A list of four: pairwise beta of jaccard and sorensen; and multisite beta of jaccard and sorensen. Pairwise beta has three distance matrix. For jaccard, phylo.beta.jtu is the turnover-fraction of Jaccard, phylo.beta.jne is the nestedness-fraction. For sorensen, phylo.beta.sim is the turnover part measured as Simpson derived pairwise dissimilarity, phylo.beta.sne is the nestedness-fraction. Similarly for the multisite version.

 rand_test

Randomization tests

Description

Perform randomization test between two vectors.

Usage

```
rand_test(x, y, n = 1000)
```

Arguments

x	A numeric vector.
y	A numeric vector.
n	The number of randomization, default is 1000.

Value

a data frame with mean, rank, p.value, etc.

 rm_site_noobs

Remove site that has no observations (site by sp matrix)

Description

Remove site that has no observations of any species.

Usage

```
rm_site_noobs(df)
```

Arguments

df	A data frame in wide form, i.e. site by species data frame, with site names as row name.
----	--

Value

A data frame.

`rm_sp_noobs`*Remove sp that not observed at any site (site by sp matrix)*

Description

Remove species that not observed in any site.

Usage

```
rm_sp_noobs(df)
```

Arguments

`df` A data frame in wide form, i.e. site by species data frame, with site names as row name.

Value

A data frame.

`tnrs_match_names_2`*Match taxa names with the Open Tree of Life*

Description

This function will try to do batch match based on `rotl::tnrs_match_names()`, which only allows \leq 250 species each time.

Usage

```
tnrs_match_names_2(taxa, n_per_req = 20, ...)
```

Arguments

`taxa` A vector of species names to match.
`n_per_req` Number of species to match per requery, must be \leq 250.

Value

A data frame.

```
tree          #' Example phylogeny
```

Description

A phylogeny with more species than the community data

Usage

```
tree
```

Format

Newick format

```
unifrac2      unifrac
```

Description

calculate unifrac of pairwise site. This is based on picante::unifrac, but with phylocomr::ph_pd to calculate pd, which can improve speed dramatically.

Usage

```
unifrac2(comm, tree, comm_long)
```

Arguments

comm	A site by sp data frame, row names are site names.
tree	A phylogeny with 'phylo' class.
comm_long	A long format of comm, can be missing.

Value

A site by site distance object.

var_to_rownames	<i>Function to add a column as row names, and remove it from columns</i>
-----------------	--

Description

Convert a column of a data frame to be its row name.

Usage

```
var_to_rownames(df, var = "site")
```

Arguments

df	A data frame.
var	The column name (as character) you want to put as row name.

Value

A data frame.

Index

* datasets

comm_a, 2

comm_b, 3

tree, 11

cap_first_letter, 2

comm_a, 2

comm_b, 3

dist_to_df, 3

get_n_polytomy, 4

get_pd_alpha, 4

highlight_subset_sp_in_phylogeny, 6

logit_tran, 6

mvpd, 7

panel.cor, 7

panel.hist, 7

pd2, 8

phylo_betapart, 8

rand_test, 9

rm_site_noobs, 9

rm_sp_noobs, 10

tnrs_match_names_2, 10

tree, 11

unifrac2, 11

var_to_rownames, 12