

Package: fddimensionality (via r-universe)

September 5, 2024

Title Test Effect of Traits of FD-Environment Relationship

Version 0.0.0.9000

Description Companion code for paper XXX <doi:xxx> on FD-Environment relationship, which tests to what extent we can expect FD-Environment trait relationship in function of number of traits included and type of environmental filtering.

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ByteCompile true

Encoding UTF-8

LazyData true

Imports ape, broom, bookdown, cowplot, dplyr, drake (>= 7.3.0), ecolottery, funrar, FD, geometry, ggplot2, purrr, rmarkdown, rlang, tibble, Weighted.Desc.Stat

Suggests forcats, narray, purrr, tidyr, vegan

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

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

RemoteUrl https://github.com/Rekyt/fddimensionality_ms

RemoteRef HEAD

RemoteSha dc480a52b7a0ce89487658e2b0cc983336268cce

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compute_dissim_di *Compute Functional Diversity Using All Dissimilarities*

Description

Compute Functional Diversity Using All Dissimilarities

Usage

```
compute_dissim_di(trait_dissim_list, site_sp_df, trait_comb_df)
```

Arguments

trait_dissim_list	[list(list(matrix(1+)))] a list containing list of dissimilarity matrices with their names
site_sp_df	[data.frame()] a tidy species data.frame with a row defining a species in a site with its abundance
trait_comb_df	[data.frame()] a data.frame with the list of trait combinations considered as well as the number of traits included

compute_other_fd *Compute FD indices without abundances*

Description

Wrapper around [FD::dbFD\(\)](#)

Usage

```
compute_other_fd(site_sp_df, trait_comb, trait_df, var_type = "env")
```

Arguments

site_sp_df	[data.frame()] a tidy species data.frame with a row defining a species in a site with its abundance
trait_comb	[list(character(1+))] a list containing combinations of trait combinations
trait_df	[data.frame()] a trait data.frame with species as rows and traits as columns
var_type	[character(1)] a string giving the column on which site_sp_df should be spread

compute_trait_dissim *Compute Trait Dissimilarities*

Description

For each provided trait combination in a list, returns a list of dissimilarity matrices computed using funrar. This function computes euclidean dissimilarity matrices

Usage

```
compute_trait_dissim(trait_comb_list, trait_df)
```

Arguments

trait_comb_list	[list(character(1+))] a list of character vectors containing the trait combination on which dissimilarity should be computed
trait_df	[data.frame()] a trait data.frame with species as rows and traits as columns

Value

a list of dissimilarity matrices with concatenated names from trait combinations

generate_traits *Generate uncorrelated traits*

Description

Generate uncorrelated traits

Usage

```
generate_traits(n_species, n_traits)
```

Arguments

n_species	[integer(1)] the number of species
n_traits	[integer(1)] the number of traits

Value

a matrix with `n_species` rows and `n_traits` column with uniform uncorrelated traits between 0 and 1

Examples

```
generate_traits(3, 2)
```

<code>global_workflow</code>	<i>Contains Local vs. Global drake workflow</i>
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Description

Contains Local vs. Global drake workflow

Usage

```
global_workflow()
```

<code>plot_env_fd_obs_ses_two</code>	<i>Figure of FD vs. Environment Comparing Observed and SES values</i>
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Description

Figure of FD vs. Environment Comparing Observed and SES values

Usage

```
plot_env_fd_obs_ses_two(full_fd_df)
```

Arguments

<code>full_fd_df</code>	[<code>data.frame()</code>] data.frame containing both observed and SES values of functional diversity
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scale_zero_one	<i>Scale Vector between Zero and One</i>
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Description

With a numeric vector scale between zero and one.

Usage

```
scale_zero_one(vec)
```

Arguments

vec a numeric vector

Examples

```
vec = stats::rnorm(1000)

zero_one = scale_zero_one(vec)

range(vec)
range(zero_one)
```

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