

Package ‘TAD’

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Title Realize the Trait Abundance Distribution

Version 1.0.1

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Description The “TAD” package compiled an analytical framework based on an analysis of the shape of the trait abundance distributions to better understand community assembly processes, and predict community dynamics under environmental changes. This framework mobilized a study of the relationship between the moments describing the shape of the distributions: the skewness and the kurtosis (SKR). The SKR allows the identification of commonalities in the shape of trait distributions across contrasting communities. Derived from the SKR, we developed mathematical parameters that summarise the complex pattern of distributions by assessing (i) the R^2 , (ii) the Y-intercept, (iii) the slope, (iv) the functional stability of community (TADstab), and, (v) the distance from specific distribution families (i.e., the distance from the skew-uniform family a limit to the highest degree of evenness: TADeve).

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CONSTANTS

The CONSTANTS constant

Description

Provides a set of constants to prevent typo and provide some defaults values to functions in the TAD. Among those constants are:

- SKEW_UNIFORM_SLOPE_DISTANCE

- SKEW_UNIFORM_INTERCEPT_DISTANCE
- DEFAULT_SIGNIFICATIVITY_THRESHOLD
- DEFAULT_LIN_MOD
- DEFAULT_SLOPE_DISTANCE
- DEFAULT_INTERCEPT_DISTANCE

Usage

CONSTANTS

Format

An object of class list of length 6.

`generate_random_matrix`
Generate random matrix

Description

Generate and save random matrix

Usage

```
generate_random_matrix(  
  weights,  
  aggregation_factor = NULL,  
  randomization_number,  
  seed = NULL  
)
```

Arguments

<code>weights</code>	the dataframe of weights, one row correspond to a series of observation
<code>aggregation_factor</code>	the dataframe of factor to take into account for the randomization
<code>randomization_number</code>	the number of random abundance matrix to generate
<code>seed</code>	the seed of the pseudo random number generator

Value

a data.frame of `randomization_number` observations

Examples

```

aggregation_factor_name <- c("Year", "Bloc")
weights_factor = TAD::AB[, c("Year", "Plot", "Treatment", "Bloc")]
aggregation_factor <- as.data.frame(
  weights_factor[, aggregation_factor_name]
)
random_matrix <- TAD::generate_random_matrix(
  weights = TAD::AB[, 5:102],
  aggregation_factor = aggregation_factor,
  randomization_number = 100,
  seed = 1312
)
head(random_matrix)

```

launch_analysis_tad *Launch the analysis*

Description

Launch distribution analysis

Usage

```

launch_analysis_tad(
  weights,
  weights_factor,
  trait_data,
  randomization_number,
  aggregation_factor_name = NULL,
  statistics_factor_name = NULL,
  seed = NULL,
  abundance_file = NULL,
  weighted_moments_file = NULL,
  stat_per_obs_file = NULL,
  stat_per_rand_file = NULL,
  stat_skr_param_file = NULL,
  regenerate_abundance_df = FALSE,
  regenerate_weighted_moments_df = FALSE,
  regenerate_stat_per_obs_df = FALSE,
  regenerate_stat_per_rand_df = FALSE,
  regenerate_stat_skr_df = FALSE,
  significativity_threshold = CONSTANTS$DEFAULT_SIGNIFICATIVITY_THRESHOLD,
  lin_mod = CONSTANTS$DEFAULT_LIN_MOD,
  slope_distance = CONSTANTS$DEFAULT_SLOPE_DISTANCE,
  intercept_distance = CONSTANTS$DEFAULT_INTERCEPT_DISTANCE,
  csv_tsv_load_parameters = list()
)

```

Arguments

weights	the dataframe of weights, one row correspond to a series of observation
weights_factor	the dataframe which contains the different factor linked to the weights
trait_data	a vector of the data linked to the different factor
randomization_number	the number of random abundance matrix to generate
aggregation_factor_name	vector of factor name for the generation of random matrix
statistics_factor_name	vector of factor name for the computation of statistics for each generated matrix
seed	the seed of the pseudo random number generator
abundance_file	the path and name of the RDS file to load/save the dataframe which contains the observed data and the generated matrix
weighted_moments_file	the path and name of the RDS file to load/save the dataframe which contains the calculated moments
stat_per_obs_file	the path and name of the RDS file to load/save the dataframe which contains the statistics for each observed row regarding the random ones
stat_per_rand_file	the path and name of the RDS file to load/save the dataframe which contains the statistics for each random matrix generated
stat_skr_param_file	default=NULL You can provide the output to write the SKR statistics results to.
regenerate_abundance_df	boolean to specify if the abundance dataframe is computed again
regenerate_weighted_moments_df	boolean to specify if the weighted moments dataframe is computed again
regenerate_stat_per_obs_df	boolean to specify if the statistics per observation dataframe is computed again
regenerate_stat_per_rand_df	boolean to specify if the statistics per random matrix dataframe is computed again
regenerate_stat_skr_df	boolean to specify if the stats SKR dataframe is computed again
significativity_threshold	the significance threshold to consider that the observed value is in the randomized value
lin_mod	Indicates the type of linear model to use for (SKR): choose "lm" or "mblm"
slope_distance	slope of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform distribution family)
intercept_distance	intercept of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform distribution family)

csv_tsv_load_parameters

a list of parameters for each data structure we want to load. Each element must be named after the data structure we want to load.

Value

A list of the 9 following named elements:

- raw_abundance_df
- filtered_weights
- filtered_weights_factor
- filtered_trait_data
- abundance_df
- weighted_moments
- statistics_per_observation
- stat_per_rand
- ses_skr

Examples

```
output_path <- file.path(tempdir(), "outputs")
dir.create(output_path)
results <- TAD::launch_analysis_tad(
  weights = TAD::AB[, 5:102],
  weights_factor = TAD::AB[, c("Year", "Plot", "Treatment", "Bloc")],
  trait_data = log(TAD::trait[["SLA"]]),
  aggregation_factor_name = c("Year", "Bloc"),
  statistics_factor_name = (statistics_factor_name <- c("Treatment")),
  regenerate_abundance_df = TRUE,
  regenerate_weighted_moments_df = TRUE,
  regenerate_stat_per_obs_df = TRUE,
  regenerate_stat_per_rand_df = TRUE,
  weighted_moments_file = file.path(output_path, "weighted_moments.csv"),
  stat_per_obs_file = file.path(output_path, "stat_per_obs.csv"),
  stat_per_rand_file = file.path(output_path, "stat_per_rand.csv"),
  stat_skr_param_file = file.path(output_path, "stat_skr_param.csv"),
  randomization_number = 20,
  seed = 1312,
  significativity_threshold = c(0.05, 0.95),
  lin_mod = "lm",
  slope_distance = (
    slope_distance <- TAD::CONSTANTS$SKEW_UNIFORM_SLOPE_DISTANCE
  ),
  intercept_distance = (
    intercept_distance <- TAD::CONSTANTS$SKEW_UNIFORM_INTERCEPT_DISTANCE
  )
)
moments_graph <- TAD::moments_graph(
  moments_df = results$weighted_moments,
  statistics_per_observation = results$statistics_per_observation,
```

```

    statistics_factor_name = statistics_factor_name,
    statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
    statistics_factor_name_col = c("#1A85FF", "#D41159"),
    output_path = file.path(output_path, "moments_graph.jpeg"),
    dpi = 100
  )
skr_graph <- TAD::skr_graph(
  moments_df = results$weighted_moments,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  output_path = file.path(output_path, "skr_graph.jpeg"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance,
  dpi = 100
)
skr_param_graph <- TAD::skr_param_graph(
  skr_param = results$ses_skr,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance,
  save_skr_param_graph = file.path(output_path, "skr_param_graph.jpeg"),
  dpi = 100
)

unlink(output_path, recursive = TRUE, force = TRUE)

```

load_abundance_dataframe

load_abundance_dataframe

Description

load_abundance_dataframe

Usage

load_abundance_dataframe(path, ...)

Arguments

path	the path to the file to load
...	a set of parameters provided to load_dependent_on_format may contain some operations to apply to format/cast CSV or TSV data which are almost typeless by default

Value

an abundance dataframe, with the column number casted into integers and rownames casted into integers.

```
load_statistics_per_obs
      load_statistics_per_obs
```

Description

load_statistics_per_obs

Usage

```
load_statistics_per_obs(path, ...)
```

Arguments

path	the path to the file to load
...	a set of parameters provided to <code>load_dependent_on_format</code> may contain some operations to apply to format/cast CSV or TSV data which are almost typeless by default

Value

a stats par observations dataframe with rownames casted into integers.

```
load_statistics_per_random
      load_statistics_per_random
```

Description

load_statistics_per_random

Usage

```
load_statistics_per_random(path, ...)
```

Arguments

path	the path to the file to load
...	a set of parameters provided to <code>load_dependent_on_format</code> may contain some operations to apply to format/cast CSV or TSV data which are almost typeless by default

Value

a stats per randon dataframe with distance_to_family and cv_distance_to_family casted into doubles and with rownames casted into integers.

load_stat_skr_param *load_stat_skr_param*

Description

load_stat_skr_param

Usage

load_stat_skr_param(path, ...)

Arguments

path	the path to the file to load
...	a set of parameters provided to load_dependent_on_format may contain some operations to apply to format/cast CSV or TSV data which are almost typeless by default

Value

a stats SKR parameters dataframe with distance_to_family_ses and cv_distance_to_family_ses casted into doubles and with rownames casted into integers.

load_weighted_moments *load_weighted_moments*

Description

load_weighted_moments

Usage

load_weighted_moments(path, ...)

Arguments

path	the path to the file to load
...	a set of parameters provided to load_dependent_on_format may contain some operations to apply to format/cast CSV or TSV data which are almost typeless by default

Value

a weighted moments dataframe with the column number casted into integers and rownames casted into integers.

moments_graph	<i>moments_graph</i>
---------------	----------------------

Description

Graph of the distributions' moments (mean, variance, skewness and kurtosis) compared to null model

Usage

```
moments_graph(
  moments_df,
  statistics_per_observation,
  statistics_factor_name,
  statistics_factor_name_breaks = NULL,
  statistics_factor_name_col = NULL,
  output_path = NULL,
  dpi = 600
)
```

Arguments

`moments_df` Moments data frame (mean, variance, skewness, kurtosis)

`statistics_per_observation` SES of the Moments data frame and significance compared to null model

`statistics_factor_name` column of data use for colors discrimination

`statistics_factor_name_breaks` vector of factor levels of the `statistics_factor_name`, same dimension than `statistics_factor_name_col`

`statistics_factor_name_col` vector of colors, same dimension than `statistics_factor_name_breaks`

`output_path` The path to save the graph

`dpi` The dpi number to use when we generate png/jpg graph

Value

A graph instance

Examples

```

results <- TAD::launch_analysis_tad(
  weights = TAD::AB[, 5:102],
  weights_factor = TAD::AB[, c("Year", "Plot", "Treatment", "Bloc")],
  trait_data = log(TAD::trait[["SLA"]]),
  aggregation_factor_name = c("Year", "Bloc"),
  statistics_factor_name = (statistics_factor_name <- c("Treatment")),
  randomization_number = 100
)

# if you want to display the graph
graph <- TAD::moments_graph(
  moments_df = results$weighted_moments,
  statistics_per_observation = results$statistics_per_observation,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159")
)

plot(graph)

# if you want to save the graph as a file
# either jpg, jpeg, png or svg are
output_path <- file.path(tempdir(), "outputs")
dir.create(output_path)
TAD::moments_graph(
  moments_df = results$weighted_moments,
  statistics_per_observation = results$statistics_per_observation,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  output_path = file.path(output_path, "moment_graph.png")
)

unlink(output_path, recursive = TRUE, force = TRUE)

```

null_model_distribution_stats

Compare a value to random values

Description

Compute different statistics (standardized by the distribution of random values).

Usage

```
null_model_distribution_stats(  
  observed_value,  
  random_values,  
  significance_threshold = c(0.05, 0.95),  
  remove_nas = TRUE  
)
```

Arguments

`observed_value` the observed value
`random_values` the random Values
`significance_threshold`
the array of values used to compute the quantile (c(0.025, 0.975) by default)
`remove_nas` boolean - tells whether to remove NAs or not

Value

a list corresponding to :

- the observed value
- quantile values (minimum significance threshold)
- quantile values (maximum significance threshold)
- significance (observed value not in quantile values)

Examples

```
null_model_distribution_stats(  
  observed_value = 2,  
  random_values = c(1, 4, 5, 6, 8),  
  significance_threshold = c(0.025, 0.975)  
)
```

save_abundance_dataframe

save_abundance_dataframe

Description

This function provides a secured way to save `abundance_dataframe` dataframe. The more generic function provided by TAD `saveDependingOnFormat` expects saves object using their name, but saves nothing if the provided name is not correct, or may even save an unwanted object. This function provides a way to verify the object you want to save, and so, it is more secured.

Usage

```
save_abundance_dataframe(path, object = NULL)
```

Arguments

path	the path of the file to load
object	the object to save

Value

NULL - called for side effects

save_statistics_per_obs
save_statistics_per_obs

Description

This function provides a secured way to save statistics_per_obs dataframe. The more generic function provided by TAD `saveDependingOnFormat` expects saves object using their name, but saves nothing if the provided name is not correct, or mya even save an unwanted object. This function provides a way to verify the object you want to save, and so, it is more secured.

Usage

```
save_statistics_per_obs(path, object = NULL)
```

Arguments

path	the path of the file to load
object	the object to save

Value

NULL - called for side effects

```
save_statistics_per_random
    save_statistics_per_random
```

Description

This function provides a secured way to save `statistics_per_random` dataframe. The more generic function provided by TAD `saveDependingOnFormat` expects saves object using their name, but saves nothing if the provided name is not correct, or mya even save an unwanted object. This function provides a way to verify the object you want to save, and so, it is more secured.

Usage

```
save_statistics_per_random(path, object = NULL)
```

Arguments

<code>path</code>	the path of the file to load
<code>object</code>	the object to save

Value

NULL - called for side effects

```
save_stat_skr_param    save_stat_skr_param
```

Description

This function provides a secured way to save `stat_skr_param` dataframe. The more generic function provided by TAD `saveDependingOnFormat` expects saves object using their name, but saves nothing if the provided name is not correct, or mya even save an unwanted object. This function provides a way to verify the object you want to save, and so, it is more secured.

Usage

```
save_stat_skr_param(path, object = NULL)
```

Arguments

<code>path</code>	the path of the file to load
<code>object</code>	the object to save

Value

NULL - called for side effects

save_weighted_moments *save_weighted_moments*

Description

This function provides a secured way to save weighted_moments dataframe. The more generic function provided by TAD saveDependingOnFormat expects saves object using their name, but saves nothing if the provided name is not correct, or mya even save an unwanted object. This function provides a way to verify the object you want to save, and so, it is more secured.

Usage

```
save_weighted_moments(path, object = NULL)
```

Arguments

path	the path of the file to load
object	the object to save

Value

NULL - called for side effects

skr_graph *skr_graph*

Description

Graph of the SKR, compared to null model

Usage

```
skr_graph(
  moments_df,
  statistics_factor_name,
  statistics_factor_name_breaks = NULL,
  statistics_factor_name_col = NULL,
  slope_distance = CONSTANTS$SKEW_UNIFORM_SLOPE_DISTANCE,
  intercept_distance = CONSTANTS$SKEW_UNIFORM_INTERCEPT_DISTANCE,
  output_path = NULL,
  dpi = 600
)
```

Arguments

moments_df moments data frame (mean, variance, skewness, kurtosis)
statistics_factor_name
 column of data use for colors discrimination
statistics_factor_name_breaks
 vector of factor levels of the statistics_factor_name, same dimension than statistics_factor_name_col
statistics_factor_name_col
 vector of colors, same dimension than statistics_factor_name_breaks
slope_distance slope of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform)
intercept_distance
 intercept of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform)
output_path The path to save the graph
dpi The dpi number to use when we generate png/jpg graph

Value

A graph instance

Examples

```

results <- TAD::launch_analysis_tad(
  weights = TAD::AB[, 5:102],
  weights_factor = TAD::AB[, c("Year", "Plot", "Treatment", "Bloc")],
  trait_data = log(TAD::trait[["SLA"]]),
  aggregation_factor_name = c("Year", "Bloc"),
  statistics_factor_name = (statistics_factor_name <- c("Treatment")),
  randomization_number = 100,
  slope_distance = (
    slope_distance <- TAD::CONSTANTS$SKEW_UNIFORM_SLOPE_DISTANCE
  ),
  intercept_distance = (
    intercept_distance <- TAD::CONSTANTS$SKEW_UNIFORM_INTERCEPT_DISTANCE
  )
)

graph <- TAD::skr_graph(
  moments_df = results$weighted_moments,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance
)

```

```

plot(graph)

output_path <- file.path(tempdir(), "outputs")
dir.create(output_path)
TAD::skr_graph(
  moments_df = results$weighted_moments,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance,
  dpi = 200,
  output_path = file.path(output_path, "moment_graph.png")
)

unlink(output_path, recursive = TRUE, force = TRUE)

```

```

skr_param_graph      skr_param_graph

```

Description

Graph of the parameters computed from the SKR, compared to null model

Usage

```

skr_param_graph(
  skr_param,
  statistics_factor_name,
  statistics_factor_name_breaks = NULL,
  statistics_factor_name_col = NULL,
  slope_distance = CONSTANTS$SKEW_UNIFORM_SLOPE_DISTANCE,
  intercept_distance = CONSTANTS$SKEW_UNIFORM_INTERCEPT_DISTANCE,
  save_skr_param_graph = NULL,
  dpi = 600
)

```

Arguments

```

skr_param      SES of SKR parameters data frame (SES and Significance)
statistics_factor_name
                column of data use for colors discrimination
statistics_factor_name_breaks
                vector of factor levels of the statistics_factor_name, same dimension than statistics_factor_name_col

```

statistics_factor_name_col
 vector of colors, same dimension than **statistics_factor_name_breaks**

slope_distance slope of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform distribution family)

intercept_distance
 intercept of the theoretical distribution law (default: slope = 1 intercept = 1.86 skew-uniform distribution family)

save_skr_param_graph
 The path to save the graph

dpi The dpi number to use when we generate png/jpg graph

Value

A graph instance

Examples

```

results <- TAD::launch_analysis_tad(
  weights = TAD::AB[, 5:102],
  weights_factor = TAD::AB[, c("Year", "Plot", "Treatment", "Bloc")],
  trait_data = log(TAD::trait[["SLA"]]),
  aggregation_factor_name = c("Year", "Bloc"),
  statistics_factor_name = (statistics_factor_name <- c("Treatment")),
  randomization_number = 100,
  slope_distance = (
    slope_distance <- TAD::CONSTANTS$SKEW_UNIFORM_SLOPE_DISTANCE
  ),
  intercept_distance = (
    intercept_distance <- TAD::CONSTANTS$SKEW_UNIFORM_INTERCEPT_DISTANCE
  )
)

# if you want to display the graph
graph <- TAD::skr_param_graph(
  skr_param = results$ses_skr,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance
)

plot(graph)

output_path <- file.path(tempdir(), "outputs")
dir.create(output_path)

# if you want to save the graph as a file
# either jpg, jpeg, png or svg are

```

```

TAD::skr_param_graph(
  skr_param = results$ses_skr,
  statistics_factor_name = statistics_factor_name,
  statistics_factor_name_breaks = c("Mown_Unfertilized", "Mown_NPK"),
  statistics_factor_name_col = c("#1A85FF", "#D41159"),
  slope_distance = slope_distance,
  intercept_distance = intercept_distance,
  save_skr_param_graph = file.path(output_path, "skr_param_graph.jpeg"),
  dpi = 300
)

unlink(output_path, recursive = TRUE, force = TRUE)

```

weighted_mvsk

Compute the weighted mean, variance, skewness and kurtosis

Description

Compute the weighted mean, variance, skewness and kurtosis of data with given weights

Usage

```
weighted_mvsk(data, weights)
```

Arguments

data	the data
weights	the vector or matrix of weights corresponding to the data (each row corresponding to an iteration of data)

Value

the list of weighted mean, variance, skewness and kurtosis of the data

Examples

```

weighted_mvsk(
  data = c(1, 2, 3),
  weights = matrix(data = c(1, 1, 1, 2, 1, 3), nrow = 2, ncol = 3)
)

```

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