

Package ‘nichetools’

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Type Package

Title Complementary Package to 'nicheROVER' and 'SIBER'

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Description Provides functions complementary to packages 'nicheROVER' and 'SIBER' allowing the user to extract Bayesian estimates from data objects created by the packages 'nicheROVER' and 'SIBER'. Please see the following publications for detailed methods on 'nicheROVER' and 'SIBER' Hansen et al. (2015) <[doi:10.1890/14-0235.1](https://doi.org/10.1890/14-0235.1)>, Jackson et al. (2011) <[doi:10.1111/j.1365-2656.2011.01806.x](https://doi.org/10.1111/j.1365-2656.2011.01806.x)>, and Layman et al. (2007) <[doi:10.1890/0012-9658\(2007\)88\[42:CSIRPF\]2.0.CO;2](https://doi.org/10.1890/0012-9658(2007)88[42:CSIRPF]2.0.CO;2)>, respectfully.

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create_comparisons	<i>create comparisons</i>
--------------------	---------------------------

Description

Creates a list with all of the comparisons needed to create Bayesian and maximum-likelihood estimates for proportion of niche similarities.

Usage

```
create_comparisons(data, comparison = c("within", "among"))
```

Arguments

data	a data.frame that is the names of the community and group names
comparison	a character that is either "within" or "among" indicating whether the comparisons are within a community and between groups or among communities for the same groups.

Examples

```
# ---- load siber ----
library(SIBER)

# ---- create community names data frame ----
# uncomment to use
# str(demo.siber.data.2)

demo.siber.data.2$group_name <- as.factor(demo.siber.data.2$group)
```

```

demo.siber.data.2$group <- as.numeric(demo.siber.data.2$group_name) |>
as.character()

demo.siber.data.2$community_names <- as.factor(demo.siber.data.2$community)

demo.siber.data.2$community <- as.numeric(demo.siber.data.2$community_names) |>
as.character()

cg_names <- demo.siber.data.2 |>
dplyr::distinct(community, group, community_names, group_name)

# ---- create comparisons ----
create_comparisons(cg_names,
                   comparison = "within")

```

extract_group_metrics *extract maximum-likelihood estimates for group metrics*

Description

Extract group metrics within each community from a matrix object that is produced by `groupMetricsML()` function from **SIBER**. These metrics are the following the convex hull total area (TA), Standard Ellipse Area (SEA), and the corresponding small sample size corrected version SEAc based on the maximum likelihood estimates of the means and covariance matrices of each group.

Usage

```
extract_group_metrics(data = NULL, community_df = NULL, data_format = NULL)
```

Arguments

<code>data</code>	a matrix produced by the function <code>groupMetricsML()</code> in the package SIBER .
<code>community_df</code>	a four column data frame. One of the columns has to be named <code>community</code> and the data in the column will be numeric as a character string (e.g., "1", "2", "3"). This is the order of the community names and will be used to join the actual community names to the correct data. These are the same class and values required by the function, <code>createSiberObject()</code> from SIBER . The second column will be the names of the groups that are needed to supply required by the function, <code>createSiberObject()</code> from SIBER . The third and fourth columns contains the actual names of the communities and groups the user is working with (e.g., "region", "common_name").
<code>data_format</code>	a character string that decides whether the returned object is in long or wide format. Default is "long", with the alternative supplied being "wide".

Value

A tibble containing four rows when `data_format` is set to its default which is long. These four rows are the following, `community`, `the_name_of_the_communities`, `metric` and `post_est`.

Examples

```

library(SIBER)

# ---- create community names data frame ----
# uncomment to use
# str(demo.siber.data.2)

demo.siber.data.2$group_name <- as.factor(demo.siber.data.2$group)

demo.siber.data.2$group <- as.numeric(demo.siber.data.2$group_name) |>
as.character()

demo.siber.data.2$community_name <- as.factor(demo.siber.data.2$community)

demo.siber.data.2$community <- as.numeric(demo.siber.data.2$community_name) |>
as.character()

cg_name <- demo.siber.data.2 |>
dplyr::distinct(community, group, community_name, group_name)

# ---- create comparisons ----

demo.siber.data.2 <- demo.siber.data.2[,1:4]

siber_example <- createSiberObject(demo.siber.data.2)

# extract group metrics
group_ml <- groupMetricsML(siber_example)

group_convert <- extract_group_metrics(data = group_ml,
                                       community_df = cg_name)

```

extract_layman

extract Layman metrics

Description

Extract Bayesian estimates for the following six layman metrics, $\delta^{13}\text{C}$ range, $\delta^{15}\text{N}$ range, total area (TA), distance to centroid (CD), distance to the nearest neighbour (NND), and the standard deviation of the distance to the nearest neighbour (SDNND) from data objects created by **SIBER**. To learn more about the following metrics please review [Layman et al. \(2008\)](#).

Usage

```

extract_layman(
  data,
  type = NULL,
  community_df = NULL,
  data_format = NULL,

```

```

    isotope_x = NULL,
    isotope_y = NULL,
    element_x = NULL,
    element_y = NULL
  )

```

Arguments

data	a list created by the function <code>bayesianLayman()</code> from the package SIBER .
type	a character that is either "bay" or "ml" which indicates whether the community metrics to be extracted are from a Bayesian analysis or a maximum-likelihood.
community_df	a two column data frame. One of the columns has to be named <code>community</code> and the data in the column will be numerics as a character string (e.g., "1", "2", "3"). This is the order of the community names and will be used to join the actual community names to the correct data. These are the same class and values required by the function, <code>createSiberObject()</code> from SIBER . The second column contains the actual names of the communities that the user is working with (e.g., "region").
data_format	a character string that decides whether the returned object is in long or wide format. Default is "long", with the alternative supplied being "wide".
isotope_x	a numeric that will be used in the labeling processes for the range of the x. Default is 13 (e.g., $\delta^{13}\text{C}$). This will create a column called <code>labels</code> , that will only be created when <code>data_format</code> is set to long.
isotope_y	a numeric that will be used in the labeling processes for the range of the y isotope. Default is 15 (e.g., $\delta^{15}\text{N}$). #' This will create a column called <code>labels</code> , that will only be created when <code>data_format</code> is set to long.
element_x	a character that will be used in the labeling process for the range of the x isotope. Default is C (e.g., $\delta^{13}\text{C}$). This will create a column called <code>labels</code> , that will only be created when <code>data_format</code> is set to long.
element_y	a character that will be used in the labeling process for the range of the y isotope. Default is N (e.g., $\delta^{13}\text{N}$). #' This will create a column called <code>labels</code> , that will only be created when <code>data_format</code> is set to long.

Value

A tibble containing four rows when `data_format` is set to its default which is long. These four rows are the following, `community`, `the_name_of_the_communities`, `metric` and `post_est`.

See Also

[SIBER::bayesianLayman\(\)](#) and [SIBER::createSiberObject\(\)](#)

Examples

```
library(SIBER)
```

```

# ---- bring in SIBER demo data ----
# uncomment to use
# str(demo.siber.data)

# ---- create community names data frame ----
# uncomment to use
# str(demo.siber.data.2)

demo.siber.data.2$community_names <- as.factor(demo.siber.data.2$community)

demo.siber.data.2$community <- as.numeric(demo.siber.data.2$community_names) |>
as.character()
c_names <- demo.siber.data.2 |>
dplyr::distinct(community, community_names)

# ---- create the siber object ----
siber.example <- createSiberObject(demo.siber.data)

# ---- view Bayesian estimates of mu and sigma produced by SIBER ---
# uncomment to use
# str(post_sam_siber)

# ---- extract posterior estimates of mu -----
mu_post <- extractPosteriorMeans(siber.example, post_sam_siber)

# ---- Bayesian estimates of layman metrics using SIBER ----
layman_b <- bayesianLayman(mu.post = mu_post)

# ---- use nichetools to extract Bayesian estimates of Layman metrics ----
layman_be <- extract_layman(layman_b, community_df = c_names)

layman_be

```

extract_mu

extract μ

Description

Extract Bayesian estimates of μ from data objects created by **nicheROVER** or **SIBER**.

Usage

```

extract_mu(
  data,
  pkg = NULL,
  isotope_a = NULL,

```

```

    isotope_b = NULL,
    data_format = NULL
  )

```

Arguments

data	a list created by the function <code>niw.post()</code> or <code>siberMVN()</code> in the package nicheROVER or SIBER , respectively.
pkg	a character string that is the name of the package that you're using. Defaults to "nicheROVER". Alternatively the user can supply the argument with "SIBER".
isotope_a	a character string to change the column name of the first isotope used in the analysis. Defaults to "d13c".
isotope_b	a character string to change the name of second isotope used in the analysis. Defaults to "d15n".
data_format	a character string that decides whether the returned object is in long or wide format. Default is "long", with the alternative supplied being "wide".

Value

Returns a tibble of extracted estimates of μ created by the function `niw.post()` or `siberMVN()` in the packages **nicheROVER** and **SIBER**.

The tibble will contain five columns in the following order, `metric`, `sample_name`, `sample_number`, and the names of the isotope columns supplied to `niw.post()` or `siberMVN()` (e.g., `d13c` and `d15n`).

See Also

[nicheROVER::niw.post\(\)](#) and [SIBER::siberMVN\(\)](#)

Examples

```

extract_mu(
  data = niw_fish_post
)
extract_mu(
  data = post_sam_siber,
  pkg = "SIBER"
)

```

extract_niche_size *extract niche size*

Description

Extract niche size based on elliptical niche region of Bayesian estimates of sigma created by function `niw.post()` or `siberEllipses()` in the package **nicheROVER** or **SIBER**, respectively. For **nicheROVER** this function is a wrapper around `nicheROVER::niche.size`.

Usage

```
extract_niche_size(
  data,
  pkg = NULL,
  name = NULL,
  prob = NULL,
  community_df = NULL
)
```

Arguments

data	a list or matrix created by the function <code>niw.post()</code> or <code>siberEllipses()</code> in the package nicheROVER or SIBER , respectfully.
pkg	a character string that is the name of the package that you're using. Defaults to "nicheROVER". Alternatively the user can supply the argument with "SIBER".
name	a character string that will be assigned as the column name for groups. Default is <code>sample_name</code> . Only to be used when <code>pkg</code> is set to "nicheROVER".
prob	a numeric bound by 0 and 1 indicating the probabilistic niche size. Default is 0.95. Only to be used when <code>pkg</code> is set to "nicheROVER".
community_df	a four column data frame. One of the columns has to be named <code>community</code> and the data in the column will be numeric as a character string (e.g., "1", "2", "3"). This is the order of the community names and will be used to join the actual community names to the correct data. These are the same class and values required by the function, <code>createSiberObject()</code> from SIBER . The second column will be the names of the groups that are needed to supply required by the function, <code>createSiberObject()</code> from SIBER . The third and fourth columns contains the actual names of the communities and groups the user is working with (e.g., "region", "common_name").

Value

if `pkg` is set to "nicheROVER" then a tibble containing three rows, `sample_name`, `id`, and `niche_size` is returned.

See Also

[nicheROVER::niche.size\(\)](#), [nicheROVER::niw.post\(\)](#), [SIBER::siberEllipses\(\)](#), and [SIBER::createSiberObject\(\)](#)

Examples

```
extract_niche_size(data = niw_fish_post)
```

extract_overlap	<i>extract overlap</i>
-----------------	------------------------

Description

Extract Bayesian estimates of similarities among groups produced by the following function `overlap()` in the package **nicheROVER**.

Usage

```
extract_overlap(data, name_a = NULL, name_b = NULL)
```

Arguments

<code>data</code>	a array object containing matrices created by the function <code>overlap()</code> in the package nicheROVER .
<code>name_a</code>	character string to supply for the first <code>sample_name</code> used in <code>overlap()</code> . Defaults to "sample_name_a".
<code>name_b</code>	character string to supply for the second <code>sample_name</code> used in <code>overlap()</code> . Defaults to "sample_name_b".

Value

A tibble containing five rows, `sample_name_a`, `id`, `sample_name_b`, `sample_number`, and `niche_overlap`.

See Also

[nicheROVER::overlap\(\)](#)

Examples

```
extract_overlap(data = over_stat)
```

extract_sigma	<i>extract Σ</i>
---------------	------------------------------------

Description

Extract Bayesian estimates of Σ from data objects created by **nicheROVER** or **SIBER**.

Usage

```
extract_sigma(
  data,
  pkg = NULL,
  isotope_a = NULL,
  isotope_b = NULL,
  data_format = NULL
)
```

Arguments

data	a list created by the function <code>niw.post()</code> or <code>siberMVN()</code> in the package nicheROVER or SIBER , respectfully.
pkg	a character string that is the name of the package that you're using. Defaults to "nicheROVER". Alternatively the user can supply the argument with "SIBER".
isotope_a	a character string to change the column name of the first isotope used in the analysis. Defaults to "d13c".
isotope_b	a character string to change the name of second isotope used in the analysis. Defaults to "d15n".
data_format	a character string that decides whether the returned object is in long or wide format. Default is "wide", with the alternative supplied being "long".

Value

Returns a tibble of extracted estimates of Σ created by the function `niw.post()` or `siberMVN()` in the packages **nicheROVER**. and **SIBER**.

The returned object will contain five columns in the following order when `data_format` is set to "wide", `metric`, `id`, `sample_name`, `isotope`, `sample_number`, and the posterior sample for Σ (e.g., `d13c` and `d15n`).

See Also

[nicheROVER::niw.post\(\)](#) and [SIBER::siberMVN\(\)](#)

Examples

```
extract_sigma(
  data = niw_fish_post
)

extract_sigma(
  data = post_sam_siber,
  pkg = "SIBER"
)
```

 extract_similarities *extract similarities*

Description

Extract niche similarities from objects created by {SIBER}.

Usage

```
extract_similarities(data, type = c("bay", "ml"), community_df = NULL)
```

Arguments

data	a list of results from either <code>maxLikOverlap()</code> or <code>bayesianOverlap()</code> .
type	description
community_df	a four column data frame. One of the columns has to be named <code>community</code> and the data in the column will be numeric as a character string (e.g., "1", "2", "3"). This is the order of the community names and will be used to join the actual community names to the correct data. These are the same class and values required by the function, <code>createSiberObject()</code> from SIBER . The second column will be the names of the groups that are needed to supply required by the function, <code>createSiberObject()</code> from SIBER . The third and fourth columns contains the actual names of the communities and groups the user is working with (e.g., "region", "common_name").

Examples

```
library(purrr)
library(SIBER)

# ---- create community names data frame ----
# uncomment to use
# str(demo.siber.data.2)

demo.siber.data.2$group_name <- as.factor(demo.siber.data.2$group)

demo.siber.data.2$group <- as.numeric(demo.siber.data.2$group_name) |>
as.character()

demo.siber.data.2$community_name <- as.factor(demo.siber.data.2$community)

demo.siber.data.2$community <- as.numeric(demo.siber.data.2$community_name) |>
as.character()

cg_name <- demo.siber.data.2 |>
dplyr::distinct(community, group, community_name, group_name)

# ---- create comparisons ----
```

```

cg_names_within_c <- create_comparisons(cg_name,
                                       comparison = "within")

demo.siber.data.2 <- demo.siber.data.2[,1:4]

siber_example <- createSiberObject(demo.siber.data.2)

ml_within_overlap <- cg_names_within_c |>
  map(~ maxLikOverlap(.x$cg_1, .x$cg_2, siber_example,
                    p.interval = NULL, n = 100), .progress = TRUE)

ml_95_within_com <- extract_similarities(ml_within_overlap, type = "ml",
                                       community_df = cg_name)

```

mu_est_long	A data.frame containing posterior estimates of μ
-------------	--

Description

Posterior estimates of μ using fish data set from **nicheROVER**, using Normal-Inverse-Wishart (NIW) priors.

Usage

```
mu_est_long
```

Format

data.frame containing 8,000 rows and 7 variables

metric name of the metric extracted from niw.post()

species species abbreviation

sample_number sample number from 1-1000

isotope column with isotope name

mu_est estimate of mu produced from niw.post()

element isotopic element used in labelling

neutron neutron number used in labelling

niche_ellipse *Create ellipses based on Bayesian estimates of μ and Σ*

Description

This function allows the user to supply Bayesian estimates of μ and Σ to create estimated Bayesian ellipse for niche region.

Usage

```
niche_ellipse(
  dat_mu,
  dat_sigma,
  isotope_a = NULL,
  isotope_b = NULL,
  p_ell = NULL,
  random = NULL,
  set_seed = NULL,
  n = NULL,
  message = TRUE
)
```

Arguments

dat_mu	a data.frame containing μ Bayesian estimates. This data.frame needs to be in long format with each μ estimate for each isotope stacked on top of each other. This can be produced using <code>extract_mu()</code> .
dat_sigma	a data.frame containing Σ Bayesian estimates. This data.frame needs be in wide format, that is Σ (covariance) matrices stacked on top of each other. See example of how to convert to wide format. This can be produced using <code>extract_sigma()</code> .
isotope_a	character string that is the column name of the first isotope used in <code>dat_sigma</code> . Defaults to "d13c".
isotope_b	character string that is the column name of the second isotope used in <code>dat_sigma</code> . Defaults to "d15n".
p_ell	is the confidence interval of each ellipse estimate. Default is 0.95 (i.e., 95% confidence interval). This value is bound by 0 and 1 and has to be a numeric.
random	logical value indicating whether or not to randomly sample posterior distributions for μ and Σ to create a sub-sample of ellipse. Default is TRUE.
set_seed	numerical value to set seed for random sampling. Default is a random value. To consistently sample the same subsample, please supply a numerical value (e.g., 4). It is highly suggested to use <code>set_seed</code> to make the function results when randomly sampling reproducible.
n	numerical value that controls the number of random samples. Default is 10.
message	control whether the time processing is displayed after the end of the function. Default is TRUE.

Value

A tibble containing, `sample_name`, `sample_number`, and the isotopes that were used in the estimation of ellipse (i.e., `d13c` and `d15n`).

See Also

`nicheROVER::niw.post()`, `SIBER::siberMVN()`, `extract_mu()`, and `extract_sigma()`

Examples

```
niche_ellipse(dat_mu = mu_est_long,
              dat_sigma = sigma_est_wide)
```

<code>niw_fish_post</code>	<i>A list of the posterior estimates of μ and Σ from {nicheROVER}</i>
----------------------------	--

Description

Posterior estimates of μ and Σ using the fish data set from **nicheROVER**, using Normal-Inverse-Wishart (NIW) priors. This list is produced using the function `niw.post()` from **nicheROVER**.

Usage

```
niw_fish_post
```

Format

A list with elements μ and Σ of sizes `c(nsamples, length(lambda))` and `c(dim(Psi))`.

<code>over_stat</code>	<i>A data.frame containing the estimates of percentage of overlap among groups</i>
------------------------	--

Description

Estimates of the percentage of overlap among example species used in **nicheROVER**.

Usage

```
over_stat
```

Format

A arraycontaining matrices of the percent overlap for each group used in Bayesian estimates of μ and Σ using Normal-Inverse-Wishart (NIW) priors calculated in `niw.post()`.

post_sam_siber	<i>A list of the posterior estimates of μ and Σ from {SIBER}</i>
----------------	---

Description

Posterior estimates of μ and Σ using the demo.siber.data data set from **SIBER**. This list is produced using the function siberMVN() from **SIBER**.

Usage

```
post_sam_siber
```

Format

A list with estimates of μ and Σ for each species and group.

sigma_est_wide	<i>A data.frame containing posterior estimates of Σ</i>
----------------	---

Description

Posterior estimates of Σ using fish data set from **nicheROVER**, using Normal-Inverse-Wishart (NIW) priors

Usage

```
sigma_est_wide
```

Format

data.frame containing 8,000 rows and 6 variables

metric name of the metric extracted from niw.post()

species species abbreviation

isotope column with isotope name

sample_number sample number from 1-1000

d15n estimate of Σ for d15n produced from niw.post()

d13c estimate of Σ for d13c produced from niw.post()

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