

Package ‘nichetools’

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Type Package

Title Complementary Package to 'nicheROVER' and 'SIBER'

Version 0.2.0

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)> and 'SIBER', Jackson et al. (2011) <[doi:10.1111/j.1365-2656.2011.01806.x](https://doi.org/10.1111/j.1365-2656.2011.01806.x)>, respectfully.

Depends R (>= 2.10)

Imports cli, dplyr, ellipse, lifecycle, nicheROVER, purrr, rlang, tibble, tidyr

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LazyData true

RoxygenNote 7.3.1

URL <https://benjaminhlina.github.io/nichetools/>

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extract_mu	<i>extract μ</i>
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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 , 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 "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"  
)
```

<code>extract_niche_size</code>	<i>extract niche size</i>
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Description

Extract niche size based on elliptical niche region of Bayesian estimates of sigma created by function `niw.post()` in the package **nicheROVER**. This function is a wrapper around `nicheROVER::niche.size`.

Usage

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

Arguments

<code>data</code>	a list created by the function <code>niw.post()</code> in the package nicheROVER .
<code>name</code>	a character string that will be assigned as the column name for groups. Default is <code>sample_name</code> .
<code>prob</code>	a numeric bound by 0 and 1 indicating the probabilistic niche size. Default is 0.95.

Value

a tibble containing three rows, `sample_name`, `id`, and `niche_size`.

See Also

[nicheROVER::niche.size\(\)](#) and [nicheROVER::niw.post\(\)](#)

Examples

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

extract_overlap	<i>extract overlap</i>
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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

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

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