Package: sohungry (via r-universe)

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Type Package

Title Southern Ocean Diet and Energetics Data

Version 0.9.3

Description Provides access to data from the SCAR Southern Ocean Diet and Energetics Database.

URL https://github.com/SCAR/sohungry

BugReports https://github.com/SCAR/sohungry/issues

Depends R (>= 3.3.0)

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Encoding UTF-8

Roxygen list(markdown = TRUE)

Imports assertthat, curl, dplyr, jsonlite, lubridate, rappdirs, readr, rlang

Suggests covr, ggplot2, knitr, rmarkdown, tidyr, testthat

RoxygenNote 7.2.3

VignetteBuilder knitr

Repository https://scar.r-universe.dev

RemoteUrl https://github.com/SCAR/sohungry

RemoteRef HEAD

RemoteSha 91558e3fb5173dfe3c6fe0574c2d92d3d658d2f8

Contents

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diet_summary	*Diet summaries from the SCAR Southern Ocean Diet and Energetics Database*

Description

Given a diet data.frame, the prey or predators are aggregated to group level and dietary importance values reported. Note that dietary importance values are currently calculated by unweighted averaging across studies (so that e.g. a study of 100 individuals will carry the same weight as a study of one individual).

Usage

```
diet_summary(
  x,
  summary_type = "prey",
  minimum_importance = 0,
  treat_trace_values_as = 0
)
```

Arguments

x   data.frame: diet data, as returned by so_diet

summary_type   string: either "predators" (report the predators in the data) or "prey" (report the prey items)

minimum_importance

                  numeric: ignore records with dietary importance less than this threshold

treat_trace_values_as

                  numeric: what numeric value to use for a dietary item recorded as "trace"

Value

data.frame with columns:

- N_fraction_diet_by_weight - number of diet observations where fraction of diet by weight was quantified
- fraction_diet_by_weight - mean fraction of diet by weight
- N_fraction_occurrence - number of diet observations where fraction of occurrence quantified
- fraction_occurrence - mean fraction of occurrence
- N_fraction_diet_by_prey_items - number of diet observations where fraction of diet by number of prey items was quantified
- fraction_diet_by_prey_items - mean fraction of diet by number of prey items

Examples

```
## Not run:
  x <- so_diet()

  ## summary of what Electrona carlsbergi eats
  x %>% filter_by_predator_name("Electrona carlsbergi") %>%
  diet_summary(summary_type = "prey")

  ## summary of what eats Electrona carlsbergi
  x %>% filter_by_prey_name("Electrona carlsbergi") %>%
  diet_summary(summary_type = "predators")

## End(Not run)
```

---

filter_by_importance   *Filter out diet data below a given importance threshold*

Description

A diet record is retained if any of the importance measures are above the threshold. Records with all-NA importance values will be removed.

Usage

```
filter_by_importance(x, threshold, which_measures = "any")
```

Arguments

x	data.frame: diet data, as returned by so_diet
threshold	numeric: remove entries below this threshold
which_measures	string: one or more of "fraction_diet_by_weight", "fraction_diet_by_prey_items", "fraction_occurrence", or "any" (shorthand for all three)

Value

data.frame

See Also

so_diet, replace_by_importance

Examples

```
## Not run:
  x <- so_diet()
  x %>% filter_by_importance(0.1)

## End(Not run)
```

---

filter_by_name   *Filter data by predator, prey, or taxon name*

Description

A convenience function that matches on the species and/or group names. `filter_by_predator_name` is a convenience shorthand for `filter_by_name(...,name_type="predator")` `filter_by_prey_name` is a convenience shorthand for `filter_by_name(...,name_type="prey")`

Usage

```
filter_by_name(x, name, name_type)

filter_by_predator_name(x, name)

filter_by_prey_name(x, name)
```

Arguments

x	data.frame: diet data as returned by e.g. `so_diet` or `so_isotopes`
name	character: vector of one or more names to match on
name_type	string: one of "predator", "prey", "predatorprey" (to match on either predator names or prey names), or "taxon". If missing will default to predator names for diet data, and taxon names for isotope data

Value

data.frame

See Also

[so_diet](#), [so_isotopes](#)

Examples

```
## Not run:
  x <- so_isotopes()
  x %>% filter_by_name(c("Electrona", "Gymnoscopelus"), "taxon")

  x <- so_diet()
  x %>% filter_by_name("Electrona carlsbergi", name_type = "predator")
  ## equivalent to
  x %>% filter_by_predator_name("Electrona carlsbergi")

## End(Not run)
```

replace_by_importance *Replace diet data entries below a given importance threshold*

Description

Replace diet data entries below a given importance threshold

Usage

```
replace_by_importance(x, threshold, replace_with = NA, which_measures = "all")
```

Arguments

x	data.frame: diet data, as returned by so_diet
threshold	numeric: replace entries below this threshold
replace_with	numeric: value to replace with
which_measures	string: one or more of "fraction_diet_by_weight", "fraction_diet_by_prey_items", "fraction_occurrence", or "all" (shorthand for all three)

Value

data.frame

See Also

[so_diet](#) [filter_by_importance](#)

Examples

```
## Not run:
  x <- so_diet()
  ## discard entries representing less than 10% of diet
  x <- x %>% replace_by_importance(0.1)

## End(Not run)
```

---

replace_trace_values   *Replace "trace" values in diet data*

Description

Some diet studies record small amounts of a prey item as "trace". These are encoded in the diet database using the value -999. This function replaces those entries with the nominated numeric value.

Usage

```
replace_trace_values(x, replace_with = 0)
```

Arguments

x	data.frame: diet data, as returned by so_diet
replace_with	numeric: value to use as a replacement for "trace" values

Value

data.frame

See Also

[so_diet](#)

Examples

```
## Not run:
  x <- so_diet() %>% replace_trace_values()

## End(Not run)
```

---

sohungry   **sohungry**

Description

Provides access to data from the SCAR Southern Ocean Diet and Energetics Database.

References

<https://scar.org/resources/southern-ocean-diet-energetics/>

so_diet	*Load data from the SCAR Southern Ocean Diet and Energetics database*

Description

Load data from the SCAR Southern Ocean Diet and Energetics database. Data will be fetched from the remote server and optionally cached locally, or fetched from the local cache, depending on the arguments passed.

Usage

```
so_diet(
  method = "get",
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE
)

so_dna_diet(
  method = "get",
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE
)

so_isotopes(
  method = "get",
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE,
  format = "mv"
)

so_energetics(
  method = "get",
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE
)

so_lipids(
  method = "get",
```

```
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE
)

so_sources(
  method = "get",
  cache_directory = "session",
  refresh_cache = FALSE,
  public_only = TRUE,
  verbose = FALSE
)
```

Arguments

`method`	string: "get" (fetch the data via a web GET call)
`cache_directory`	
	string: (optional) cache the data locally in this directory, so that they can be used offline later. Values can be "session" (a per-session temporary directory will be used, default), "persistent" (the directory returned by rappdirs::user_cache_dir() will be used), or a string giving the path to the directory to use. Use NULL for no caching. An attempt will be made to create the cache directory if it does not exist. A warning will be given if a cached copy of the data file exists and is more than 30 days old. Use refresh_cache = TRUE to refresh the cached data if necessary
`refresh_cache`	logical: if TRUE, and data already exist in the cache_directory, they will be refreshed. If FALSE, the cached data will be used
`public_only`	logical: ignored, here for historical reasons
`verbose`	logical: show progress messages?
`format`	string: ignored, kept for historical purposes only

Details

The `format` parameter was introduced to the `so_isotopes` function in package version 0.4.0. The previous default `format` was "wide" (the data were formatted with one row per record and multiple measurements (of different isotopes) per row). With `format` "mv", the data were in measurement-value (long) format with multiple rows per original record, split so that each different isotope measurement appeared in its own row. As of package version 0.9.0, "wide" has been hard-deprecated and "mv" is the only option.

Value

data.frame

Examples

```
## Not run:
```

```
## conventional diet data
x <- so_diet()
subset(x, predator_name == "Electrona antarctica")

## DNA diet data
x <- so_dna_diet()
subset(x, predator_name == "Thalassarche melanophris")

## stable isotopes
x <- so_isotopes()

## energetics data
x <- so_energetics()

## lipids data
x <- so_lipids()

## End(Not run)
```

---

so_doi   *Return the DOI of the SCAR Diet and Energetics Database being used*

Description

Return the DOI of the SCAR Diet and Energetics Database being used

Usage

```
so_doi(cache_directory, ...)
```

Arguments

cache_directory

> string: (optional) the local cache directory containing the data. If no valid DOI is found in that directory, the return value will be NA_character_. If cache_directory is not supplied, the DOI of the data last accessed in this session will be returned (and if no data has yet been accessed, the most recent known DOI will be returned)

...   : additional parameters passed to so_diet etc

Value

string

See Also

[so_diet](), [so_dna_diet](), [so_isotopes](), [so_energetics](), [so_lipids]()

Examples

```
## Not run:
  xd <- so_diet(cache_directory = "session")
  ## the DOI of the data just read
  so_doi()

  ## the DOI of the data in a particular cache directory
  so_doi(cache_directory = "c:/my/cache/dir")

## End(Not run)
```

---

so_isotope_adjust   *Stable isotope corrections*

Description

Apply stable isotope corrections following various published methods.

Usage

```
so_isotope_adjust(
  d13c = NULL,
  d15n = NULL,
  cn_ratio = NULL,
  method,
  cn_ratio_type = "mass"
)
```

Arguments

d13c	numeric: d13C values
d15n	numeric: d15n values
cn_ratio	numeric: C:N ratio values
method	string: one of "Weldrick 2019", "Kiljunen 2006", "Kiljunen 2006 atomic" "Post 2007" "Smyntek 2007" "Smyntek 2007 atomic" "Logan 2008" "Syvaranta 2010" (see Details)
cn_ratio_type	string: the basis of the C:N ratio (either "mass" or "atomic")

Details

Methods:

- "Weldrick 2019": lipid normalization of d13C values following Weldrick CK et al. (2019) Can lipid removal affect interpretation of resource partitioning from stable isotopes in Southern Ocean pteropods? Rapid Communications in Mass Spectrometry. https://doi.org/10.1002/rcm.8384

- "Kiljunen 2006": lipid normalization of d13C values following Kiljunen M et al. (2006) A revised model for lipid-normalizing d13C values from aquatic organisms, with implications for isotope mixing models. Journal of Applied Ecology. https://doi.org/10.1111/j.1365-2664.2006.01224.x

- "Kiljunen 2006 atomic": as for Kiljunen 2006 but using atomic C:N ratio

- "Post 2007": lipid normalization of d13C values followingPost DM et al. (2007) Getting to the fat of the matter: Models, methods and assumptions for dealing with lipids in stable isotope analyses. Oecologia. https://doi.org/10.1007/s00442-006-0630-x

- "Smyntek 2007": lipid normalization of d13C values following Smyntek PM et al. (2007) A standard protocol for stable isotope analysis of zooplankton in aquatic food web research using mass balance correction models. Limnol. Oceanogr. https://doi.org/10.4319/lo.2007.52.5.2135

- "Smyntek 2007 atomic": as for Smyntek 2007 but using atomic C:N ratio

- "Logan 2008": lipid normalization of d13C values following Logan JM et al. (2008) Lipid corrections in carbon and nitrogen stable isotope analyses: comparison of chemical extraction and modelling methods. Journal of Animal Ecology. https://doi.org/10.1111/j.1365-2656.2008.01394.x

- "Syvaranta 2010": lipid normalization of d13C values following Syväranta J and Rautio M (2010) Zooplankton, lipids and stable isotopes: Importance of seasonal, latitudinal, and taxonomic differences. Canadian Journal of Fisheries and Aquatic Science. https://doi.org/10.1139/F10-091

Value

A data.frame with corrected values, comprising one or more of the columns "d13c", "d15n", "cn_ratio" depending on the method.

See Also

so_isotopes

Examples

```
## lipid normalization of bulk d13C following Weldrick et al. 2019
so_isotope_adjust(d13c = -26.816, cn_ratio = 3.7014, cn_ratio_type = "mass",
                  method = "Weldrick 2019")
```

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