

Package ‘spidR’

October 14, 2022

Title Spider Knowledge Online

Version 1.0.2

Date 2021-10-18

Description Allows the user to connect with the World Spider Catalogue (WSC; <<https://wsc.nmbe.ch/>>) and the World Spider Trait (WST; <<https://spidertraits.sci.muni.cz/>>) databases. Also performs several basic functions such as checking names validity, retrieving coordinate data from the Global Biodiversity Information Facility (GBIF; <<https://www.gbif.org/>>), and mapping.

Depends R (>= 3.5.0)

Imports graphics, httr, jsonlite, rgbif, rworldmap, rworldxtra, stats, utils

Encoding UTF-8

License GPL-3

LazyData true

RoxygenNote 7.1.2

NeedsCompilation no

Author Pedro Cardoso [aut, cre]

Maintainer Pedro Cardoso <pedro.cardoso@helsinki.fi>

Repository CRAN

Date/Publication 2021-10-18 07:20:02 UTC

R topics documented:

authors	2
checknames	3
distribution	4
lsid	5
map	6
records	7
species	8

taxonomy	9
traits	10
wsc	11
wscmap	12
Index	13

authors	<i>Get species authors from WSC.</i>
---------	--------------------------------------

Description

Get species authority from the World Spider Catalogue.

Usage

```
authors(tax, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
order	Order taxa alphabetically or keep as in tax.

Details

This function will get species authorities from the World Spider Catalogue (2021). Higher taxa will be converted to species names.

Value

A data.frame with species and authority names.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:
authors("Amphiledorus")
authors(tax = c("Iberesia machadoi", "Nemesia bacelarae", "Amphiledorus ungoliantae"), order = TRUE)

## End(Not run)
```

checknames	<i>Check taxa names in WSC.</i>
------------	---------------------------------

Description

Check taxa names against the World Spider Catalogue.

Usage

```
checknames(tax, full = FALSE, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
full	returns the full list of names.
order	Order taxa alphabetically or keep as in tax.

Details

This function will check if all species, genera and family names in tax are updated according to the World Spider Catalogue (2021). If not, it returns a matrix with valid synonym or possible misspellings using fuzzy matching (Levenshtein edit distance).

Value

If any mismatches, a matrix with taxa not found in WSC or, if full = TRUE, the full list of names.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:  
tax = c("Nemesis", "Nemesia brauni", "Iberesia machadoi", "Nemesia bacelari")  
checknames(tax)  
checknames(tax, full = TRUE, order = TRUE)  
  
## End(Not run)
```

distribution	<i>Get species distributions from WSC.</i>
--------------	--

Description

Get species distribution from the World Spider Catalogue.

Usage

```
distribution(tax, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
order	Order taxa alphabetically or keep as in tax.

Details

This function will get species distributions from the World Spider Catalogue (2021).

Value

A data.frame with species and distribution. Family and genera names will be converted to species.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:  
distribution("Nemesia")  
distribution(tax = c("Iberesia machadoi", "Amphiledorus ungoliantae"), order = TRUE)  
  
## End(Not run)
```

lsid	<i>Get species LSID from WSC.</i>
------	-----------------------------------

Description

Get species LSID from the World Spider Catalogue.

Usage

```
lsid(tax, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
order	Order taxa names alphabetically or keep as in tax.

Details

This function will get species LSID from the World Spider Catalogue (2021). Family and genera names will be converted to species.

Value

A data.frame with species and LSID.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:  
lsid("Anapistula")  
lsid(tax = c("Iberesia machadoi", "Nemesia bacelarae", "Amphiledorus ungoliantae"), order = TRUE)  
  
## End(Not run)
```

 map

Map species ranges.

Description

Maps species range according to the World Spider Catalogue and records according to GBIF and the World Spider Trait database.

Usage

```
map(
  tax,
  countries = TRUE,
  records = TRUE,
  hires = FALSE,
  zoom = FALSE,
  order = FALSE
)
```

Arguments

tax	A taxon name or vector with taxa names.
countries	Maps countries according to WSC.
records	Maps records according to GBIF and WST.
hires	Provides high resolution maps. Beware it might take longer to render.
zoom	If records is TRUE, the map will be zoomed to the region with records.
order	Order taxa names alphabetically or keep as in tax.

Details

Countries based on the interpretation of the textual descriptions available at the World Spider Catalogue (2021). These might be only approximations to country level and should be taken with caution.

Value

A world map with countries and records highlighted.

References

Pekar, S., Cernečka, L., Wolff, J., Mammola, S., Cardoso, P., Lowe, E., Fukushima, C.S., Birkhofer, K. & Herberstein, M.E. (2021). The world spider trait database. Masaryk University, Brno, URL: <https://spidertraits.sci.muni.cz>

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:
map(c("Pardosa hyperborea"))
map("Amphiledorus", zoom = TRUE)
map(c("Pardosa hyperborea", "Iberesia machadoi"), countries = FALSE, hires = TRUE, zoom = TRUE)

## End(Not run)
```

records *Get coordinate data from GBIF and WST.*

Description

Downloads coordinate data from records in GBIF and the World Spider Trait database.

Usage

```
records(tax, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
order	Order taxa names alphabetically or keep as in tax.

Details

Outputs non-duplicate records with geographical (long, lat) coordinates. As always when using data from multiple sources the user should be careful and check if records "make sense" before using them.

Value

A data.frame with species name, longitude, latitude, source database and reference.

References

Pekar, S., Cernecka, L., Wolff, J., Mammola, S., Cardoso, P., Lowe, E., Fukushima, C.S., Birkhofer, K. & Herberstein, M.E. (2021). The world spider trait database. Masaryk University, Brno, URL: <https://spidertraits.sci.muni.cz>

Examples

```
## Not run:
records("Pardosa hyperborea")
records(tax = c("Pardosa hyperborea", "Anapistula"), order = TRUE)

## End(Not run)
```

species	<i>Get species from higher taxa.</i>
---------	--------------------------------------

Description

Get species within given families or genera from the World Spider Catalogue.

Usage

```
species(tax, order = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names.
order	Order species names alphabetically.

Details

This function will get all species currently listed for given families or genera from the World Spider Catalogue (2021).

Value

A vector with species names.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:  
species("Amphiledorus")  
species(tax = c("Amphiledorus", "Nemesiidae"), order = TRUE)  
  
## End(Not run)
```

`taxonomy`*Get taxonomy from species.*

Description

Get species sub/infraorder, family and genus from the World Spider Catalogue.

Usage

```
taxonomy(tax, check = FALSE, aut = FALSE, id = FALSE, order = FALSE)
```

Arguments

<code>tax</code>	A taxon name or vector with taxa names.
<code>check</code>	species names should be replaced by possible matches in the WSC if outdated.
<code>aut</code>	add species authorities.
<code>id</code>	the lsid should be returned.
<code>order</code>	Order taxa names alphabetically or keep as in tax.

Details

This function will get species sub/infraorder, family and genus from the World Spider Catalogue (2021). Optionally, it will correct the species names (using function `checknames`) and provide the lsid and authors from the WSC (using functions `lsid` and `authors`).

Value

A data.frame with species and taxonomy.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:
taxonomy("Symphytognathidae", order = TRUE)
taxonomy(c("Nemesia machadoi", "Nemesia bacelari"), check = TRUE, aut = TRUE, id = TRUE)

## End(Not run)
```

traits	<i>Get trait data from WST.</i>
--------	---------------------------------

Description

Downloads the most recent data from the World Spider Trait database.

Usage

```
traits(
  tax,
  trait = NULL,
  sex = NULL,
  life = NULL,
  country = NULL,
  habitat = NULL,
  user = "",
  key = "",
  order = FALSE
)
```

Arguments

tax	A taxon name or vector with taxa names.
trait	A vector with required trait(s) as abbreviations. Valid values can be found at: https://spidertraits.sci.muni.cz/traits
sex	A vector with required sex(es).
life	A vector with required life stage(s).
country	A vector with required country(ies) ISO3 code(s).
habitat	A vector with required habitat(s).
user	To obtain restricted data get a user name from https://spidertraits.sci.muni.cz/api .
key	To obtain restricted data get an api key from https://spidertraits.sci.muni.cz/api .
order	Order taxa names alphabetically or keep as in tax.

Details

The World Spider Trait database (Pekar et al. 2021) has been designed to contain trait data in a broad sense, from morphological traits to ecological characteristics, ecophysiology, behavioural habits, and more (Lowe et al. 2020). This function will download everything available for the taxa given, possibly filtered to the traits given in parameter trait. Some data might be restricted access, in which case a user name and api key are needed (<https://spidertraits.sci.muni.cz/api>), otherwise the value will show as NA.

Value

A matrix with trait data.

References

Lowe, E., Wolff, J.O., Aceves-Aparicio, A., Birkhofer, K., Branco, V.V., Cardoso, P., Chichorro, F., Fukushima, C.S., Goncalves-Souza, T., Haddad, C.R., Isaia, M., Krehenwinkel, H., Audisio, T.L., Macias-Hernandez, N., Malumbres-Olarte, J., Mammola, S., McLean, D.J., Michalko, R., Nentwig, W., Pekar, S., Petillon, J., Privet, K., Scott, C., Uhl, G., Urbano-Tenorio, F., Wong, B.H. & Herbestein, M.E. (2020). Towards establishment of a centralized spider traits database. *Journal of Arachnology*, 48: 103-109. <https://doi.org/10.1636/0161-8202-48.2.103>

Pekar, S., Cernecka, L., Wolff, J., Mammola, S., Cardoso, P., Lowe, E., Fukushima, C.S., Birkhofer, K. & Herberstein, M.E. (2021). The world spider trait database. Masaryk University, Brno, URL: <https://spidertraits.sci.muni.cz>

Examples

```
## Not run:
traits("Atypus affinis")
traits("Atypus", order = TRUE)
traits("Atypidae", country = c("PRT", "CZE"), order = TRUE)
traits(c("Zodarion costapratae", "Zodarion alacre"))
traits(c("Iberesia machadoi", "Zodarion costapratae"), trait = c("balo", "bole"))

## End(Not run)
```

wsc

Downloads WSC data.

Description

Downloads the most recent data from the World Spider Catalogue.

Usage

```
wsc()
```

Details

The World Spider Catalog (2021) lists all currently valid species of spiders, from Clerck to date. Updated daily.

Value

A matrix with all current species names and distribution. This should be used for other functions using wsc data.

References

World Spider Catalog (2021). World Spider Catalog. Version 22.0. Natural History Museum Bern, online at <http://wsc.nmbe.ch>. doi: 10.24436/2.

Examples

```
## Not run:  
wsc()  
  
## End(Not run)
```

wscmap

Matrix matching WSC and ISO3 country codes.

Description

A dataset that links species distribution descriptions with the map using the ISO3 code

Usage

```
data(wscmap)
```

Format

A matrix with regions and corresponding ISO3 codes.

Index

* **datasets**

wscmap, [12](#)

authors, [2](#)

checknames, [3](#)

distribution, [4](#)

lsid, [5](#)

map, [6](#)

records, [7](#)

species, [8](#)

taxonomy, [9](#)

traits, [10](#)

wsc, [11](#)

wscmap, [12](#)