Package ‘arakno’

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Title ARAcnhiDN KNowledge Online
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Description Allows the user to connect with the World Spider Cata-
logue (WSC; <https://wsc.nmbe.ch/>) and the World Spi-
der Trait (WST; <https://spidertraits.sci.muni.cz/>) databases. Also performs sev-
eral basic functions such as checking names validity, retrieving coordi-
nate data from the Global Biodiversity Information Facil-
ity (GBIF; <https://www.gbif.org/>), and mapping.

Depends R (>= 3.5.0)
Imports graphics, httr, jsonlite, rgbif, rworldmap, rworldxtra, stats,
utils

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Author Pedro Cardoso [aut, cre]
Maintainer Pedro Cardoso <pedro.cardoso@helsinki.fi>
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get species authors from WSC.

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 (2022). Higher taxa will be converted to species names.

Value
A data.frame with species and authority names.

References

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

## End(Not run)
checknames

Check taxa names in WSC.

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 (2022). If not, it returns a matrix with nomenclature changes, valid synonyms 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


Examples

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

## End(Not run)
countries

Get taxon countries from WSC.

Description

Get countries of taxa from the World Spider Catalogue textual descriptions.

Usage

countries(tax)

Arguments

tax A taxon name or vector with taxa names.

Details

Countries based on the interpretation of the textual descriptions available at the World Spider Catalogue (2022). These might be only approximations to country level and should be taken with caution.

Value

A vector with country ISO codes. Family and genera names will be converted to species.

References


Examples

## Not run:
countries("Iberesia machadoi")
countries(c("Iberesia machadoi", "Nemesia"))

## End(Not run)
distribution  

Get species distributions from WSC.

---

**Description**

Get species distribution from the World Spider Catalogue.

**Usage**

```r
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 (2022).

**Value**

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

**References**


**Examples**

```r
## Not run:
distribution("Nemesia")
distribution(tax = c("Iberesia machadoi", "Amphileorus ungoliantea"), order = TRUE)
## End(Not run)
```
endemics

Get country endemics from WSC.

Description

Get endemic species in any country or region from the World Spider Catalogue textual descriptions.

Usage

endemics(country)

Arguments

country  The country/region name or ISO3 code.

Details

Species list based on the interpretation of the textual descriptions available at the World Spider Catalogue (2022). These might be only approximations to country level and should be taken with caution.

Value

A vector with species names.

References


Examples

## Not run:
endemics("Portugal")
endemics("Azores")
endemics("FIN")

## End(Not run)
lsid

Get species LSID from WSC.

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 (2022). Family and genera names will be converted to species.

Value

A data.frame with species and LSID.

References


Examples

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

## End(Not run)
**Description**

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

**Usage**

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

**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.
- `verbose`: Display information as data are retrieved.

**Details**

Countries based on the interpretation of the textual descriptions available at the World Spider Catalogue (2022). These might be only approximations to country level and should be taken with caution.

**Value**

A world map with countries and records highlighted.

**References**


records

Examples

```r
## Not run:
map(c("Pardosa hyperborea"))
map("Amphiledorus", zoom = TRUE, hires = 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, verbose = TRUE)`

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>tax</code></td>
<td>A taxon name or vector with taxa names.</td>
</tr>
<tr>
<td><code>order</code></td>
<td>Order taxa names alphabetically or keep as in tax.</td>
</tr>
<tr>
<td><code>verbose</code></td>
<td>Display information as data are retrieved.</td>
</tr>
</tbody>
</table>

**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**


**Examples**

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

## End(Not run)
```
species

Get species from higher taxa.

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 (2022).

Value

A vector with species names.

References


Examples

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

## End(Not run)
**taxon**:y

*Get taxonomy from species.*

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

This function will get species sub/infraorder, family and genus from the World Spider Catalogue (2022). 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**


**Examples**

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

Get trait data from WST.

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,
  verbose = TRUE
)

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.
verbose Display information as data are retrieved.

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


Examples

```r
## 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)
```

Description

Downloads WSC data.

Usage

`wsc()`

Details

The World Spider Catalog (2022) 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


Examples

```r
## 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

```r
data(wscmap)
```

Format

A matrix with regions and corresponding ISO3 codes.
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