Package 'arakno'

October 23, 2026

Title ARAchnid KNowledge Online

Version 1.4.0

Date 2026-10-23

Description Allows the user to connect with the World Spider Catalogue (WSC; <https://wsc.nmbe.ch/>) and the World Spider Trait (WST; <https://arachnidatraits.sci.muni.cz/araneae/) 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 (>= 4.0.0)

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

Encoding UTF-8

License GPL-3

LazyData true

Config/roxygen2/version 8.1.1

NeedsCompilation no

Author Pedro Cardoso [aut, cre]

Maintainer Pedro Cardoso <pmcardoso@ciencias.ulisboa.pt>

Repository CRAN

Date/Publication 2026-10-23 16:50:02 UTC

Contents

authors 2
buildTree 3
checkNames 4
continents 5
countries 6
distribution 7
endemics 8

globalTree 9
lsid 9
map 10
records 11
species 12
taxonomy 13
traits 14
wsc 15
wscCont 16
wscMap 16

Index **17**

`authors` *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 (2026). Higher taxa will be converted to species names.

Value

A data.frame with species and authority names.

References

World Spider Catalog (2026). World Spider Catalog. Version 27. 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)
```

buildTree *Create phylogenetic tree.*

Description

Create a phylogenetic tree based on the backbone from Macias-Hernandez et al. (2020) and the species taxonomical hierarchy.

Usage

```
buildTree(tax, update = FALSE)
```

Arguments

tax	A taxon name or vector with taxa names. Should be in the general form "Family_sp" or "Genus speciesname", with family or genus name plus anything to uniquely identify the species separated by "_" or " ".
update	Whether to update the taxonomy of the backbone tree according to the WSC (2026).

Details

Based on the backbone phylogeny of Macias-Hernandez et al. (2020). All species in tax present in the backbone are included in the output tree. If the species is not in the backbone, or if only family or genus are known, species are inserted at the level of the most recent common ancestor of confamiliar or congenerics respectively. If only one congeneric or confamiliar are in the backbone, the species is inserted at half the length of the corresponding edge.

Value

A phylo object with a phylogenetic tree for the community.

References

Macías-Hernández et al. (2020). Building-up of a robust, densely sampled spider tree of life for assessing phylogenetic diversity at the community level. Diversity, 12: 288. https://doi.org/10.3390/d12080288

World Spider Catalog (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

Examples

```
## Not run:
spp = c("Atypus affinis", "Tenuiphantes tenuis", "Zodarion sp1", "Araneus diadematus")
spp = c(spp, "Zodarion sp2", "Atypus_nsp", "Nemesia ungoliant", "Linyphiidae sp1")
spp = c(spp, "Zoropsis spinimana", "Pardosa sp1", "Pardosa acorensis", "Liphistius nsp")
tree = buildTree(spp)
plot(tree)

## 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 (2026). 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

World Spider Catalog (2026). World Spider Catalog. Version 27. 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", "Dysdera vandeli")
checkNames(tax)
checkNames(tax, full = TRUE, order = TRUE)

## End(Not run)
```

`continents` *Get taxon continents from WSC.*

Description

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

Usage

```
continents(tax)
```

Arguments

`tax`	A taxon name or vector with taxa names.

Details

Continents based on the interpretation of the textual descriptions available at the World Spider Catalogue (2026). These might be only approximations and should be taken with caution.

Value

A vector with continent names. Family and genera names will be converted to species.

References

World Spider Catalog (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

Examples

```
## Not run:
continents("Iberesia machadoi")
continents(c("Iberesia machadoi", "Nemesia"))
continents("Melopoeus lividus")

## 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 (2026). 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

World Spider Catalog (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

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

```
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 (2026).

Value

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

References

World Spider Catalog (2026). World Spider Catalog. Version 27. 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)
```

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 ISO3 code (preferred to avoid ambiguity) or country/region name. Note that ISO3 codes will only identify countries while names will also identify many regions (e.g., islands of a larger country).

Details

Species list based on the interpretation of the textual descriptions available at the World Spider Catalogue (2026). These might be only approximations to country level and should be taken with caution.

Value

A vector with species names.

References

World Spider Catalog (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

Examples

```
## Not run:
endemics("PRT")
endemics("Madeira")
endemics("Finland")

## End(Not run)
```

globalTree *Global spider backbone tree.*

Description

From Macias-Hernandez et al. (2020) with nomenclature updated.

Usage

```
data(globalTree)
```

Format

A phylo object with 132 families and 800+ genera, 1400+ species.

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 (2026). Family and genera names will be converted to species.

Value

A data.frame with species and LSID.

References

World Spider Catalog (2026). World Spider Catalog. Version 27. 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,
  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 (2026). 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 et al. (2021). The World Spider Trait database: a centralized global open repository for curated data on spider traits. Database, 2021: baab064. https://doi.org/10.1093/database/baab064

World Spider Catalog (2026). World Spider Catalog. Version 27. 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, 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

tax	A taxon name or vector with taxa names.
order	Order taxa names alphabetically or keep as in tax.
verbose	Display information as data are retrieved.

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 et al. (2021). The World Spider Trait database: a centralized global open repository for curated data on spider traits. Database, 2021: baab064. https://doi.org/10.1093/database/baab064

Examples

```
## 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 (2026).

Value

A vector with species names.

References

World Spider Catalog (2026). World Spider Catalog. Version 27. 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 suborder, family and genus from the World Spider Catalogue.

Usage

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

Arguments

`tax`	A taxon name or vector with taxa names.
`aut`	add species authorities.
`id`	the lsid should be returned.
`order`	Order taxa names alphabetically or keep as in tax.

Details

This function will get species suborder, family and genus from the World Spider Catalogue (2026). 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 (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

Examples

```
## Not run:
taxonomy("Symphytognathidae", order = TRUE)
taxonomy(c("Iberesia machadoi", "Nemesia bacelarae"), 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

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 et al. (2021). The World Spider Trait database: a centralized global open repository for curated data on spider traits. Database, 2021: baab064. https://doi.org/10.1093/database/baab064

Examples

```
## Not run:
traits("Zodarion costapratae")
traits("Zodarion costapratae", country = c("PRT"), 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 (2026) 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 (2026). World Spider Catalog. Version 27. Natural History Museum Bern, online at http://wsc.nmbe.ch. doi: 10.24436/2.

Examples

```
## Not run:
wsc()

## End(Not run)
```

`wscCont` *Matrix matching WSC and continents.*

Description

A dataset that links species distribution descriptions with continents.

Usage

```
data(wscCont)
```

Format

A matrix with regions and corresponding continents.

`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**
globalTree, 9
wscCont, 16
wscMap, 16

authors, 2

buildTree, 3

checkNames, 4
continents, 5
countries, 6

distribution, 7

endemics, 8

globalTree, 9

lsid, 9

map, 10

records, 11

species, 12

taxonomy, 13
traits, 14

wsc, 15
wscCont, 16
wscMap, 16