

Package ‘rSymbiota’

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Type Package

Title Interface to 'Symbiota' Portals for Accessing Multi-Organismal Biodiversity Data

Version 1.0.0

Description Interface to the web data portals of 'Symbiota'. Allows to query taxon natural history collections (herbarium specimens, etc.) from 41 portals including plants, animals and fungi. See the 'Symbiota' main page <<http://symbiota.org/docs/>> for more information.

License GPL (>= 2)

Encoding UTF-8

LazyData true

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URL <http://symbiota.org/docs/>

Imports RSelenium, httr, rworldmap, ggplot2, maps, rvest, XML, xml2, stringr, treemap, magick, Hmisc, crayon, dplyr, sf, mapview, sp, methods, RCurl, sys, knitr

Collate 'details.R' 'download.R' 'getCollections.R'
'is_onclick_next_page.R' 'is_table_button.R' 'nr_pages.R'
'plot_datamap.R' 'plot_distmap.R' 'plot_recordstreemap.R'
'portals.R' 'records-class.R' 'records.R' 'recordsTable.R'
'remote_table.R' 'retry.R' 'start_stop_docker.R' 'symbiota.R'

Suggests rmarkdown

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Author Franz-Sebastian Krah [aut, cre],
McCabe Lindsie [aut]

Maintainer Franz-Sebastian Krah <f.krah@mailbox.org>

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details	<i>Retrieve images and meta-data for a specific record (specimen)</i>
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Description

Retrieve images and meta-data for a specific record (specimen)

Usage

```
details(x, id)
```

Arguments

x	object of S4 class records (output of symbiota)
id,	as found in output of records

Author(s)

Franz-Sebastian KraH

Examples

```
## Not run:
# use function records to download records; then use one of the IDs:
spec.dist <- symbiota(taxon = "Amanita muscaria", db = "mycoportal", wait = 4)
pic <- details(spec.dist, id = 2136920)
# Look at one of the images in more detail
print(image_read(pic$urls[1])) # a rather orangeish specimen
library(magick)
par(mfrow = c(1,3))
plot(image_read(pic$urls[1]))
```

```
plot(image_read(pic$urls[2]))
plot(image_read(pic$urls[3]))
# Look at meta data
pic$meta

## End(Not run)
```

`getCollections` *List of available collections*

Description

List of available collections

Usage

```
getCollections(db)
```

Arguments

`db` portal name, for an overview see [portals](#)

Details

Get list of available collections from the MyCoPortal. For details also see <http://mycoportal.org/portal/collections/index.php>

Author(s)

Franz-Sebastian KraH

Examples

```
## Not run:
getCollections(db = "SCAN")

## End(Not run)
```

plot_datamap

Plot data heatmap on geographic map

Description

Plot data heatmap on geographic map

Usage

```
plot_datamap(x, mapdatabase = "world", area = NULL, index = "rich",
  plot = TRUE, trans = "log10", gazetter = TRUE)
```

Arguments

x	an object of class records, see symbiota
mapdatabase	The map database to use in mapping, see plot_distmap
area	list with four elements. Currently mapdatabase does not contain areas such as Europe, however, this may be manually chosen like this: area = list(min_long = -10, max_long = 24, min_lat = 14, max_lat = 70)
index	character string, either "rec" (number of records) or "rich" (number of species)
plot	logical
trans	transformation of the data, default = log10
gazetter	logical if Gazetter should be used to add long lat for USA counties where coordinates are missing; default = TRUE

Author(s)

Franz-Sebastian Krah

References

Gazetter: <https://www.census.gov/geo/maps-data/data/gazetteer2017.html>

Examples

```
## Not run:
am.dist <- symbiota(taxon = "Amanita muscaria", db = "MyCoPortal")
head(recordsTable(am.dist))
plot_datamap(am.dist, mapdatabase = "state")

## End(Not run)
```

plot_distmap	<i>Plot distribution data on map</i>
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Description

Plot distribution data on map

Usage

```
plot_distmap(x, mapdatabase = "world", region = ".", legend = FALSE,
  panel = FALSE, interactive = TRUE, jitter = position_jitter(width =
  0, height = 0), plot = TRUE, gazetter = TRUE)
```

Arguments

x	an object of class "records", see symbiota
mapdatabase	The map database to use in mapping. What you choose here determines what you can choose in the region parameter. One of: county, state, usa, world, world2, france, italy, or nz.
region	The region of the world to map. From the maps package, run <code>sort(unique(map_data("world")\$region))</code> to see region names for the world database layer, or e.g., <code>sort(unique(map_data("state")\$region))</code> for the state layer.
legend	logical
panel	plots panels for each species for species above threshold supplied to panel, e.g., 1000
interactive	logical, if TRUE map will be plotted using function <code>mapview::mapview</code>
jitter	If you use jitter, the amount by which to jitter points in width, height, or both.
plot	logical
gazetter	logical if Gazetter should be used to add long lat for USA counties where coordinates are missing; default = TRUE

Value

Map (using [ggplot2](#) package) of points or tiles on a world map.

Author(s)

Franz-Sebastian Krahe

Examples

```
## Not run:
am.dist <- symbiota(taxon = "Amanita muscaria", db = "MyCoPortal")
head(recordsTable(am.dist))
plot_distmap(am.dist, mapdatabase = "state", interactive = TRUE)
plot_distmap(am.dist, mapdatabase = "state", interactive = FALSE)

## End(Not run)
```

plot_recordstreemap *Treemap of records data*

Description

Treemap of records data

Usage

```
plot_recordstreemap(x, groupvar = "country", log = TRUE)
```

Arguments

x	an object of class "records", see symbiota
groupvar	character of grouping variable, e.g., Country
log	logical whether data should be log-transformed
...	further arguments may be passed to treemap

Details

Makes use of R package 'treemap'

Value

Map (using treemap package)

Author(s)

Franz-Sebastian Krahl

Examples

```
## Not run:
am.dist <- symbiota(taxon = "Amanita muscaria", db = "MyCoPortal")
head(recordsTable(am.dist))
plot_recordstreemap(am.dist, log = FALSE)

## End(Not run)
```

portal	<i>Find URL for portal db</i>
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Description

Find URL for portal db

Usage

```
portal(db = "lichen")
```

Arguments

db character string specifying Symbiota database

Author(s)

Franz-Sebastian Krah

Examples

```
## Not run:  
portal(db = "lichen")  
  
## End(Not run)
```

portals	<i>Portals available through Symbiota</i>
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Description

Portals available through Symbiota

Usage

```
portals()
```

Details

Symbiota is an open source content management system for curating specimen- and observation-based biodiversity data

Author(s)

Franz-Sebastian Krah

Examples

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

records	<i>Create a records objects</i>
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Description

Create a records objects

Usage

```
records(nr.records, citation, query, records, db)
```

Arguments

nr.records	A numeric giving the number of records retrieved
citation	A character string with the recommended citation from the website
query	A list of the user arguments used
records	A data.frame with the query records results
db	A character string specifying the database

Author(s)

Franz-Sebastian KraH

Examples

```
## Not run:  
help("records-class")  
  
## End(Not run)
```

records-class	<i>"records" class An S4 Class to represent query result from the function symbiota records holds a records table together with the query meta data and recommended citation</i>
---------------	--

Description

"records" class An S4 Class to represent query result from the function [symbiota](#) records holds a records table together with the query meta data and recommended citation

Slots

nr.records A numeric giving the number of records retrieved
 citation A character string with the recommended citation from the website
 query A list of the user arguments used
 records A data.frame with the query records results
 db A character string specifying the database

Author(s)

Franz-Sebastian KraH

Examples

```
showClass("records")
```

recordsTable, records-method	<i>Extract records table from class records</i>
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Description

Extract records table from class records

Usage

```
## S4 method for signature 'records'  
recordsTable(object)
```

Arguments

object object of class records

Value

data.frame

Author(s)

Franz-Sebastian Krah

start_docker	<i>Start Docker</i>
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Description

Start Docker

Usage

```
start_docker(verbose = TRUE, wait = 2)
```

Arguments

verbose	logical
wait	Waiting time for system call to finish

DetailsDocker available for download at: <https://www.docker.com>**Examples**

```
## Not run:  
## Usually these functions are only used internally.  
## However, if there are errors in the function leading to problems running 'symbiota' again  
## it might be necessary to stop_docker.  
start_docker() # starts docker  
stop_docker() # stops docker  
  
## End(Not run)
```

stop_docker	<i>Stop Docker</i>
-------------	--------------------

Description

Stop Docker

Usage

```
stop_docker(sleep = 2)
```

Arguments

sleep waiting time for system call to finish

Details

This should run for Unix platforms (e.g., Mac) and Windows. Docker available for download at: <https://www.docker.com>

symbiota *Retrieve records from the Symbiota portals*

Description

Retrieve records from the Symbiota portals

Usage

```
symbiota(taxon = "Amanita muscaria", db = "mycoportal", country = "",
state = "", county = "", locality = "", elevation_from = "",
elevation_to = "", host = "", taxon_type = 1, north_lat = "",
south_lat = "", west_lon = "", east_lon = "", point_lat = "",
point_lon = "", radius = "", collector = "", collector_num = "",
coll_date1 = "", coll_date2 = "", syns = TRUE, verbose = FALSE,
screenshot = FALSE, port = 4445L, browserName = "chrome",
remoteServerAddr = "localhost", wait = 4, max_attempts = 5)
```

Arguments

taxon	character string specifying the taxon name (e.g., species name, family name or higher taxon)
db	portal name, for an overview see portals
country	character string specifying country, e.g., "USA"
state	character string specifying state, e.g., "Massachusetts"
county	character string specifying county, e.g., "Worcester"
locality	character string specifying locality, e.g., "Harvard Forest"
elevation_from	character string, meter, e.g., "1000"
elevation_to	character string, meter
host	character string specifying host species, e.g., "Betula alba"
taxon_type	integer, one of 1 to 5 representing "Family or Scientific Name", "Scientific Name only", "Family Only", "Higher Taxonomy", "Common Name"
north_lat	character string, coordinate e.g., "45"
south_lat	character string, coordinate
west_lon	character string, coordinate, e.g., "-72"

east_lon	character string, coordinate
point_lat	character string, coordinate
point_lon	character string, coordinate
radius	character string, km, e.g., "50"
collector	character string specifying collector name
collector_num	character string specifying collector number
coll_date1	character string specifying collection data from, e.g., "19 August 1926"
coll_date2	character string specifying collection data from, e.g., "19 August 2018"
syms	logical, if TRUE synonyms from MycoBank and IndexFungorum are searched
verbose	logical
screenshot	logical, whether screenshot of results should be displayed in Viewer
port	default is 4445L
browserName	character string specifying the browser to use, recommended: "chrome"
remoteServerAddr	default is "localhost"
wait	numeric specifying the seconds to wait for website to load, recommended 2 for good internet connections; higher otherwise. It would be good to first look up the number of pages for a species and to compare it with the function output to see whether loading times are sufficient.
max_attempts	maximum number of tries in case of internet instability or lost connection

Details

Interface to the web databases of the Symbiota portals. Symbiota is an open source content management system for curating specimen- and observation-based biodiversity data. Currently ca. 40 portals are available: Consortium of North American Lichen Herbaria, Arctic Lichen Flora, Consortium of North American Bryophyte Herbaria, Frullania Collaborative Research Network, Macroalgal Consortium Herbarium Portal, MyCoPortal, Smithsonian Tropical Research Institute Portal (STRI), Aquatic Invasives, Aquatic Invasives, Aquatic Invasives, Consortium of Midwest Herbaria, SEINet, Intermountain Region Herbaria Network (IRHN), SouthEast Regional Network of Expertise and Collections (SERNEC), North American Network of Small Herbaria, Northern Great Plains Herbaria, Consortium of Northeastern Herbaria (CNH), Madrean Archipelago Biodiversity Assessment (MABA), Madrean Archipelago Biodiversity Assessment (MABA) - Fauna, Herbario Virtual Austral Americano, CoTRAM – Cooperative Taxonomic Resource for Amer. Myrtaceae, InvertEBase Data Portal, Symbiota Collections of Arthropods Network (SCAN), Lepidoptera of North America Network (LepNet), Neotropical Entomology, Neotropical Flora, Monarch (California Academy of Sciences), The Lundell Plant Diversity Portal, Virtual Flora of Wisconsin, Red de Herbarios del Noroeste de México, University of Colorado Herbarium, The Open Herbarium, Consortium of Pacific Herbaria, Minnesota Biodiversity Atlas, Documenting Ethnobiology in Mexico and Central America, OpenZooMuseum, Mid-Atlantic Herbaria Consortium, Channel Islands Biodiversity Information System, Consortium of Small Vertebrate Collections (CSVColl), The University of New Hampshire Collection of Insects and Other Arthropods. For an overview and URLs see [portals](#). The function currently searches all collections, because the package is meant for large-scale access.

Value

x an object of class records with the following components:

nr.records	A numeric giving the number of records retrieved
citation	A character string with the recommended citation from the website
query	A list of the user arguments used
records	A data.frame with the query records results (accessible via 'at' symbol)
db	A character string specifying the database

Author(s)

Franz-Sebastian Krah

References

<http://symbiota.org/docs/>

Gries, C., Gilbert, E. E., and Franz, N. M. (2014). Symbiota—a virtual platform for creating voucher-based biodiversity information communities. *Biodiversity Data Journal*, (2).

Examples

```
## Not run:
## Download Amanita muscaria observations and plot visualize data
spec.dist <- symbiota(taxon = "Helvella", db = "mycoportal", wait = 3)
# for all available portals and examples see vignette
## increase wait if your internet is slow (in general fast internet is recommended)

# This is how the records table can be accessed:
recordsTable(spec.dist)

## However, for the other functions of the package, the output of 'symbiota'
## can be directly forwarded, for example:

plot_distmap(x = spec.dist, mapdatabase = "world", interactive = FALSE,
gazetter = TRUE)
plot_distmap(x = spec.dist, mapdatabase = "usa", interactive = FALSE)
plot_distmap(x = spec.dist, mapdatabase = "world", interactive = TRUE)
plot_datamap(x = spec.dist, mapdatabase = "state", index = "rec")
plot_recordstreemap(x = spec.dist, log = FALSE)

## End(Not run)
```

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