

Package ‘rcites’

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Type Package

Title R Interface to the Species+ Database

Version 1.1.0

Description A programmatic interface to the Species+ <<https://speciesplus.net/>> database via the Species+/CITES Checklist API <<https://api.speciesplus.net/>>.

URL <https://docs.ropensci.org/rcites/>,
<https://github.com/ropensci/rcites>

BugReports <https://github.com/ropensci/rcites/issues>

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Suggests knitr, testthat, tibble, rmarkdown, rworldmap

VignetteBuilder knitr

NeedsCompilation no

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| | |
|-----------|---|
| print.spp | <i>Print methods for objects of class spp_raw*.</i> |
|-----------|---|

Description

Print the outputs of a Species+ API call.

Usage

```
## S3 method for class 'spp_raw'
print(x, ...)

## S3 method for class 'spp_raw_multi'
print(x, ...)

## S3 method for class 'spp_cites_leg'
print(x, ...)

## S3 method for class 'spp_cites_leg_multi'
print(x, ...)

## S3 method for class 'spp_distr'
print(x, ...)

## S3 method for class 'spp_distr_multi'
print(x, ...)

## S3 method for class 'spp_eu_leg'
print(x, ...)

## S3 method for class 'spp_eu_leg_multi'
print(x, ...)

## S3 method for class 'spp_refs'
print(x, ...)
```

```
## S3 method for class 'spp_refs_multi'  
print(x, ...)  
  
## S3 method for class 'spp_taxon'  
print(x, ...)
```

Arguments

x an object of class spp_raw*.
... ignored.

Value

The JSON result.

| | |
|-----------|------------------------------|
| set_token | <i>Login helper function</i> |
|-----------|------------------------------|

Description

Set and forget the authentication token for the current session.

Usage

```
set_token(token = NULL)  
  
forget_token()
```

Arguments

token a character string (with quotes) containing your token. If NULL, then the token can be passed without quotes (not as character string) after a prompt.

Functions

- set_token: set the environment variable SPECIESPLUS_TOKEN.
- forget_token: forget the environment variable SPECIESPLUS_TOKEN.

References

<https://api.speciesplus.net/documentation>

Examples

```
## Not run:
# NB: the token below is not working
set_token('8QW6Qgh57sBG2k0gtt')
# interactively
set_token()

## End(Not run)
```

spp_cites_legislation *Get current CITES appendix listings and reservations*

Description

Retrieve current CITES appendix listings and reservations, CITES quotas, and CITES suspensions for a given taxon concept.

Usage

```
spp_cites_legislation(
  taxon_id,
  scope = "current",
  language = "en",
  raw = FALSE,
  token = NULL,
  verbose = TRUE,
  pause = 1,
  ...
)
```

Arguments

| | |
|----------|--|
| taxon_id | a vector of character strings containing species' taxon concept identifiers (see spp_taxonconcept()). |
| scope | vector of character strings indicating the time scope of legislation, values are taken among current, historic and all. Default is current. |
| language | vector of character strings indicating the language for the text of legislation notes, values are taken among en (English), fr (French) and es (Spanish). Default is en. |
| raw | a logical. Should raw data be returned? |
| token | a character string containing the authentication token, see https://api.speciesplus.net/documentation . Default is set to NULL and requires the environment variable SPECIESPLUS_TOKEN to be set directly in Renvi ron. Alternatively, set_token() can be used to set SPECIESPLUS_TOKEN for the current session. |
| verbose | a logical. Should extra information be reported on progress? |

pause a duration (in second) to suspend execution for (see `Sys.sleep()`). This was added cause the web API returns a 404 error too many requests in a short time interval.

... Further named parameters, see `httr::GET()`.

Value

If `raw` is set to `TRUE` then an object of class `spp_raw` (or `spp_raw_multi` if `length(taxon_id)>1`) is returned which is essentially a list of lists (see option `as = 'parsed'` in `httr::content()`). Otherwise, an object of class `spp_cites_leg` (or `spp_cites_leg_multi` if `length(taxon_id)>1`) is returned which is a list of three data frames:

1. `cites_listings`: lists CITES annex listings EU suspensions,
2. `cites_quotas`: lists CITES quotas,
3. `cites_suspensions`: lists CITES suspensions.

References

https://api.speciesplus.net/documentation/v1/cites_legislation/index.html

Examples

```
res1 <- spp_cites_legislation(taxon_id = 4521)
res2 <- spp_cites_legislation(taxon_id = c('4521', '3210', '10255'))
res3 <- spp_cites_legislation(taxon_id = 4521, scope = 'all',
verbose = FALSE, config=httr::verbose())
res4 <- spp_cites_legislation(taxon_id = 4521, language = 'fr')
```

spp_distributions *Get distributions data available for a given taxon concept*

Description

Retrieve distributions data available for a given taxon concept for which the the taxon identifier is known.

Usage

```
spp_distributions(
  taxon_id,
  language = "en",
  raw = FALSE,
  token = NULL,
  verbose = TRUE,
  pause = 1,
  ...
)
```

Arguments

| | |
|----------|--|
| taxon_id | a vector of character strings containing species' taxon concept identifiers (see spp_taxonconcept()). |
| language | vector of character strings indicating the language for the names of distributions, values are taken among en (English), fr (French) and es (Spanish). Default is en. |
| raw | a logical. Should raw data be returned? |
| token | a character string containing the authentication token, see https://api.speciesplus.net/documentation . Default is set to NULL and requires the environment variable SPECIESPLUS_TOKEN to be set directly in Renvirom. Alternatively, <code>set_token()</code> can be used to set SPECIESPLUS_TOKEN for the current session. |
| verbose | a logical. Should extra information be reported on progress? |
| pause | a duration (in second) to suspend execution for (see Sys.sleep()). This was added cause the web API returns a 404 error too many requests in a short time interval. |
| ... | Further named parameters, see httr::GET() . |

Value

If `raw` is set to `TRUE` then an object of class `spp_raw` (or `spp_raw_multi` if `length(taxon_id)>1`) is returned which is essentially a list of lists (see option `as = 'parsed'` in [httr::content\(\)](#)). Otherwise, an object of class `spp_distr` (or `spp_distr_multi` if `length(taxon_id)>1`) is returned which is a list of two data frames:

1. `distributions`: lists distributions for a given taxon concept,
2. `references`: lists the corresponding references. In case `taxon_id` includes several elements

References

<https://api.speciesplus.net/documentation/v1/distributions/index.html>

Examples

```
res1 <- spp_distributions(taxon_id = '4521')
res2 <- spp_distributions(taxon_id = c('4521', '3210', '10255'))
res3 <- spp_distributions(taxon_id = '4521', raw = TRUE)
res4 <- spp_distributions(taxon_id = '4521', language = 'fr',
  verbose = FALSE, config = httr::progress())
```

spp_eu_legislation *Get current EU annex listings, SRG opinions, and EU suspensions*

Description

Retrieve current EU annex listings, SRG opinions, and EU suspensions for a given taxon concept (identifier must be known).

Usage

```
spp_eu_legislation(
  taxon_id,
  scope = "current",
  language = "en",
  raw = FALSE,
  token = NULL,
  verbose = TRUE,
  pause = 1,
  ...
)
```

Arguments

| | |
|----------|--|
| taxon_id | a vector of character strings containing species' taxon concept identifiers (see spp_taxonconcept()). |
| scope | vector of character strings indicating the time scope of legislation, values are taken among current, historic and all. Default is set to current. |
| language | vector of character strings indicating the language for the text of legislation notes, values are taken among en (English), fr (French) and es (Spanish). Default is en. |
| raw | a logical. Should raw data be returned? |
| token | a character string containing the authentication token, see https://api.speciesplus.net/documentation . Default is set to NULL and requires the environment variable SPECIESPLUS_TOKEN to be set directly in Renvi ron. Alternatively, set_token() can be used to set SPECIESPLUS_TOKEN for the current session. |
| verbose | a logical. Should extra information be reported on progress? |
| pause | a duration (in second) to suspend execution for (see Sys.sleep()). This was added cause the web API returns a 404 error too many requests in a short time interval. |
| ... | Further named parameters, see httr::GET() . |

Value

If `raw` is set to `TRUE` then an object of class `spp_raw` (or `spp_raw_multi` if `length(taxon_id)>1`) is returned which is essentially a list of lists (see option `as = 'parsed'` in `httr::content()`). Otherwise, an object of class `spp_eu_leg` (or `spp_eu_leg_multi` if `length(taxon_id)>1`) is returned which is a list of two data frames:

1. `eu_listings`: lists EU annex listings EU suspensions,
2. `eu_decisions`: lists EU decisions

References

https://api.speciesplus.net/documentation/v1/eu_legislation/index.html

Examples

```
res1 <- spp_eu_legislation(taxon_id = '4521')
res2 <- spp_eu_legislation(taxon_id = c('4521', '3210', '10255'))
res3 <- spp_eu_legislation(taxon_id = '4521', scope = 'historic')
res4 <- spp_eu_legislation(taxon_id = '4521', scope = 'all', language='fr',
  verbose = FALSE, config=httr::verbose())
```

spp_references

Get references for a given taxon concept

Description

Retrieve available references for a given taxon concept.

Usage

```
spp_references(
  taxon_id,
  raw = FALSE,
  token = NULL,
  verbose = TRUE,
  pause = 1,
  ...
)
```

Arguments

`taxon_id` a vector of character strings containing species' taxon concept identifiers (see `spp_taxonconcept()`).

`raw` a logical. Should raw data be returned?

| | |
|---------|---|
| token | a character string containing the authentication token, see https://api.speciesplus.net/documentation . Default is set to NULL and requires the environment variable SPECIESPLUS_TOKEN to be set directly in Renvi ron. Alternatively, <code>set_token()</code> can be used to set SPECIESPLUS_TOKEN for the current session. |
| verbose | a logical. Should extra information be reported on progress? |
| pause | a duration (in second) to suspend execution for (see <code>Sys.sleep()</code>). This was added cause the web API returns a 404 error too many requests in a short time interval. |
| ... | Further named parameters, see <code>httr::GET()</code> . |

Value

If `raw` is set to TRUE then an object of class `spp_raw` (or `spp_raw_multi` if `length(taxon_id) > 1`) is returned which is essentially a list of lists (see option `as = 'parsed'` in `httr::content()`). Otherwise, an object of class `spp_refs` (or `spp_refs_multi` if `length(taxon_id) > 1`) is returned which is a list of one data frame:

- references that includes the identifier of the reference and the corresponding citation.

References

<https://api.speciesplus.net/documentation/v1/references/index.html>

Examples

```
res1 <- spp_references(taxon_id = '4521')
res2 <- spp_references(c('4521', '3210', '10255'))
res3 <- spp_references(taxon_id = '4521', raw = TRUE, verbose = FALSE,
  config = httr::progress())
```

| | |
|------------------|---|
| spp_taxonconcept | <i>Get taxon concepts for a search term</i> |
|------------------|---|

Description

Retrieve the taxon concept of a specific taxon (scientific name).

Usage

```
spp_taxonconcept(
  query_taxon,
  taxonomy = "CITES",
  with_descendants = FALSE,
  language = NULL,
  updated_since = NULL,
```

```

per_page = 500,
pages = NULL,
raw = FALSE,
token = NULL,
verbose = TRUE,
pause = 1,
...
)

```

Arguments

| | |
|------------------|--|
| query_taxon | a character string containing the query (e.g. species). Scientific taxa only (max 255 characters). |
| taxonomy | filter taxon concepts by taxonomy, accepts either 'CITES' or 'CMS' as its value. Default sets to 'CITES'. |
| with_descendants | a logical. Should the search by name be broadened to include higher taxa? |
| language | filter languages returned for common names. Value should be a vector of character strings including one or more country codes (two-letters country code ISO 3166-1 alpha-2). Default is set to NULL, showing all available languages. |
| updated_since | a timestamp. Only entries updated after (and including) this timestamp will be pulled. |
| per_page | an integer that indicates how many objects are returned per page for paginated responses. Default set to 500 which is the maximum. |
| pages | a vector of integer that contains page numbers. Default is set to NULL, i.e. all pages are accessed. |
| raw | a logical. Should raw data be returned? |
| token | a character string containing the authentication token, see https://api.speciesplus.net/documentation . Default is set to NULL and requires the environment variable SPECIESPLUS_TOKEN to be set directly in Renvi ron. Alternatively, set_token() can be used to set SPECIESPLUS_TOKEN for the current session. |
| verbose | a logical. Should extra information be reported on progress? |
| pause | a duration (in second) to suspend execution for (see Sys.sleep()). This was added cause the web API returns a 404 error too many requests in a short time interval. |
| ... | Further named parameters, see http::GET() . |

Value

If raw = TRUE, then a object of class spp_raw is returned, which is a list of lists. If raw = FALSE, then an object of class spp_taxon is returned, it is a collection of seven data frames:

1. all_id: general information for all entries, including non-active taxon concepts,
2. general: includes general information for active taxon concepts,
3. higher_taxa: includes taxonomy information,

4. `accepted_names`: list of accepted names (only for synonyms),
5. `common_names`: list of common names (only for accepted names),
6. `synonyms`: list of synonyms (only for accepted names),
7. `cites_listing`: list of current CITES listings with annotations (missing if `taxonomy == 'CMS'`).

References

https://api.speciesplus.net/documentation/v1/taxon_concepts/index.html

Examples

```
res1 <- spp_taxonconcept(query_taxon = 'Loxodonta africana')
res2 <- spp_taxonconcept(query_taxon = 'Amazilia versicolor', raw = TRUE)
res3 <- spp_taxonconcept(query_taxon = '', taxonomy = 'CMS', pages = c(1, 3),
  language = 'EN', verbose = FALSE, config = httr::progress())
res4 <- spp_taxonconcept(query_taxon = '', per_page = 20, pages = 44)
```

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