Package ‘rredlist’

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Type Package
Title 'IUCN' Red List Client
The 'IUCN' Red List is a global list of threatened and endangered species.
Functions cover all of the Red List 'API' routes. An 'API' key is required.

Version 0.5.0
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URL https://github.com/ropensci/rredlist

BugReports https://github.com/ropensci/rredlist/issues

Imports crul (>= 0.3.8), jsonlite (>= 1.1)
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**Description**

rredlist - IUCN Red List Client

**Taxonomic Names vs. IUCN IDs**

From the documentation (quoting): "It is advisable wherever possible to use the taxon name (species name) to make your API calls, rather than using IDs. IDs are not immovable are expected to be used mainly by organisations that work closely with the IUCN Red List."

**Authentication**

IUCN requires you to get your own API key, an alphanumeric string that you need to send in every request. See key A IUCN API token. See `rl_use_iucn` for help getting and storing it. Get it at [http://apiv3.iucnredlist.org/api/v3/token](http://apiv3.iucnredlist.org/api/v3/token) Keep this key private. You can pass the key in to each function via the `key` parameter, but it's better to store the key either as a environment variable (IUCN_REDLIST_KEY) or an R option (iucn_redlist_key) - we recommend using the former option.

**High vs. Low level package APIs**

- **High level API** High level functions do the HTTP request and parse data to a data.frame for ease of downstream use. The high level functions have no underscore on the end of the function name, e.g., `rl_search()`

- **Low level API** The parsing to data.frame in the high level API does take extra time. The low level API only does the HTTP request, and gives back JSON without doing any more parsing. The low level functions DO have an underscore on the end of the function name, e.g., `rl_search_()`
No Spatial

This package does not include support for the spatial API, described at http://apiv3.iucnredlist.org/spatial

Citing the Red List API

The citation is IUCN 2015. IUCN Red List of Threatened Species. Version 2015-4 <www.iucnredlist.org> You can get this programatically via \texttt{rl_citation()}

Rate limiting

From the IUCN folks: Too many frequent calls, or too many calls per day might get your access blocked temporarily. If you’re a heavy API user, the Red List Unit asked that you contact them, as there might be better options. They suggest a 2-second delay between your calls if you plan to make a lot of calls.

Citing the IUCN Red List API

See http://apiv3.iucnredlist.org/about

Author(s)

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\begin{verbatim}
rl_citation Get the citation Red List API version
\end{verbatim}

Description

Get the citation Red List API version

Usage

\begin{verbatim}
rl_citation()
\end{verbatim}

Arguments

\begin{verbatim}
...
\end{verbatim}

Curl options passed to \texttt{curl::HttpClient()}

Value

API citation as character string

Examples

\begin{verbatim}
## Not run:
rl_citation()

## End(Not run)
\end{verbatim}
rl_common_names

Get common names for a given taxonomic name

Description

Get common names for a given taxonomic name

Usage

rl_common_names(name = NULL, key = NULL, parse = TRUE, ...)

Arguments

name (character) Binomial taxonomic name
key A IUCN API token. See `rl_use_iucn`.
parse (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
... Curl options passed to `HttpClient`

Value

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case json as character string is returned.

References

API docs at `http://apiv3.iucnredlist.org/api/v3/docs`

Examples

```r
## Not run:
rl_common_names('Loxodonta africana')
rl_common_names_('Loxodonta africana')

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

Information about comprehensive groups

**Usage**

```r
rl_comp_groups(group = NULL, key = NULL, parse = TRUE, ...)
rl_comp_groups_(group = NULL, key = NULL, ...)
```

**Arguments**

- `group` (character) A comprehensive group name. Call `rl_comp_groups()` without passing this parameter to get the list of comprehensive groups.
- `key` A IUCN API token. See `rl_use_iucn`.
- `parse` (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE.
- `...` Curl options passed to `HttpClient`

**Value**

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case `json` as character string is returned.

**References**


**Examples**

```r
## Not run:
rl_comp_groups()
rl_comp_groups('mammals')
rl_comp_groups('groupers')

rl_comp_groups_()
rl_comp_groups_('groupers')

## End(Not run)
```
### rl_countries

*Get countries*

#### Description
Get countries

#### Usage

```r
countries <- rl_countries(key = NULL, parse = TRUE, ...)
countries_ <- rl_countries_(key = NULL, ...)
```

#### Arguments

- **key**: A IUCN API token. See `rl_use_iucn`.
- **parse**: (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **...**: Curl options passed to `HttpClient`

#### Value
A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case json as character string is returned.

#### References

#### Examples
```r
## Not run:
countries <- rl_countries()
countries_ <- rl_countries_(

## End(Not run)
```

### rl_growth_forms

*Get plant species growth forms by taxon name, IUCN id, and region*

#### Description
Get plant species growth forms by taxon name, IUCN id, and region
Usage

```r
dl_growth_forms(name = NULL, id = NULL, region = NULL, key = NULL, 
  parse = TRUE, ...)

dl_growth_forms_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
```

Arguments

- **name** (character) A taxonomic name
- **id** (character) An IUCN identifier
- **region** (character) A region name, see `rl_regions` for acceptable region identifiers
- **key** A IUCN API token. See `rl_use_iucn`.
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **...** Curl options passed to `HttpClient`

Value

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case `json` as character string is returned.

References


Examples

```r
## Not run:
dl_growth_forms('Quercus robur')
dl_growth_forms('Quercus robur', region = 'europe')
dl_growth_forms(id = 63532)
dl_growth_forms(id = 63532, region = 'europe')

dl_growth_forms('Mucuna bracteata')
dl_growth_forms('Abarema villifera')
dl_growth_forms('Adansonia perrieri')
dl_growth_forms('Adenostemma harlingii')

dl_growth_forms_('Quercus robur')
dl_growth_forms_(id = 63532, region = 'europe')

## End(Not run)
```
\texttt{rl\_habitats} \hspace{1cm} \textit{Get species habitats by taxon name, IUCN id, and region}

**Description**

Get species habitats by taxon name, IUCN id, and region

**Usage**

\begin{verbatim}
rl\_habitats(name = NULL, id = NULL, region = NULL, key = NULL, 
  parse = TRUE, ...)

rl\_habitats\_?(name = NULL, id = NULL, region = NULL, key = NULL, ...)

rl\_history\_?(name = NULL, id = NULL, region = NULL, key = NULL, ...)
\end{verbatim}

**Arguments**

- **name** (character) A taxonomic name
- **id** (character) An IUCN identifier
- **region** (character) A region name, see \texttt{rl\_regions} for acceptable region identifiers (use the entries in the identifier column)
- **key** A IUCN API token. See \texttt{rl\_use\_iucn}.
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **...** Curl options passed to \texttt{HttpClient}

**Value**

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**

API docs at \url{http://apiv3.iucnredlist.org/api/v3/docs}

**Examples**

```r
## Not run:
rl\_habitats('Fratercula arctica')
rl\_habitats('Fratercula arctica', region = 'europe')
rl\_habitats(id = 12392)
rl\_habitats(id = 22694927, region = 'europe')

rl\_habitats\_?(Fratercula arctica')
rl\_habitats\_?(id = 12392)

## End(Not run)
```
**rl_history**

*Get historical assessments by taxon name, IUCN id, and region*

**Description**

Get historical assessments by taxon name, IUCN id, and region

**Usage**

```r
rl_history(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)
```

**Arguments**

- `name` (character) A taxonomic name
- `id` (character) An IUCN identifier
- `region` (character) A region name, see `rl_regions` for acceptable region identifiers (use the entries in the identifier column)
- `key` A IUCN API token. See `rl_use_iucn`.
- `parse` (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- `...` Curl options passed to `HttpClient`

**Value**

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**

API docs at http://apiv3.iucnredlist.org/api/v3/docs

**Examples**

```r
## Not run:
rl_history('Loxodonta africana')
rl_history('Ursus maritimus', region = 'europe')
rl_history(id = 12392)
rl_history(id = 22823, region = 'europe')

rl_history_('Loxodonta africana')
rl_history_(id = 12392)

## End(Not run)
```
rl_measures

Get species conservation measures by taxon name, IUCN id, and region

Description

Get species conservation measures by taxon name, IUCN id, and region

Usage

rl_measures(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)

rl_measures_(name = NULL, id = NULL, region = NULL, key = NULL, ...)

Arguments

name (character) A taxonomic name
id (character) An IUCN identifier
region (character) A region name, see rl_regions for acceptable region identifiers (use the entries in the identifier column)
key A IUCN API token. See rl_use_iucn.
parse (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
... Curl options passed to HttpClient

Value

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

References

API docs at http://apiv3.iucnredlist.org/api/v3/docs

Examples

## Not run:
rl_measures('Fratercula arctica')
rl_measures('Fratercula arctica', region = 'europe')
rl_measures(id = 12392)
rl_measures(id = 22694927, region = 'europe')

rl_measures_( 'Fratercula arctica')
rl_measures_( id = 22694927, region = 'europe')

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

Get species narrative information by taxon name, IUCN id, and region

**Usage**

```r
rl_narrative(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)
```

```r
rl_narrative_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
```

**Arguments**

- **name** (character) A taxonomic name
- **id** (character) An IUCN identifier
- **region** (character) A region name, see `rl_regions` for acceptable region identifiers (use the entries in the identifier column)
- **key** A IUCN API token. See `rl_use_iucn`.
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **...** Curl options passed to `HttpClient`

**Value**

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**


**Examples**

```r
# Not run:
rl_narrative('Fratercula arctica')
rl_narrative('Fratercula arctica', region = 'europe')
rl_narrative(id = 12392)
rl_narrative(id = 22694927, region = 'europe')

rl_narrative_('Fratercula arctica')
rl_narrative_('Fratercula arctica', region = 'europe')
```

## End(Not run)
rl_occ_country

**Get country occurrence by species name or ID**

**Description**

Get country occurrence by species name or ID

**Usage**

```r
rl_occ_country(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)
```

**Arguments**

- `name` (character) A taxonomic name
- `id` (character) An IUCN identifier
- `region` (character) A region name, see `rl_regions` for acceptable region identifiers (use the entries in the identifier column)
- `key` A IUCN API token. See `rl_use_iucn`
- `parse` (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- `...` Curl options passed to `HttpClient`

**Value**

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**


**Examples**

```r
## Not run:
rl_occ_country('Loxodonta africana')
rl_occ_country('Fratercula arctica', region = 'europe')
rl_occ_country(id = 12392)
rl_occ_country(id = 22694927, region = 'europe')

rl_occ_country('Fratercula arctica', parse = FALSE)
rl_occ_country_('Fratercula arctica')
rl_occ_country_('Fratercula arctica', region = 'europe')

## End(Not run)
```
# rl_occ_country

Search by taxon name, IUCN id, and region

## Description

Search by taxon name, IUCN id, and region

## Usage

```r
dl_occ_country_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
dl_search(name = NULL, id = NULL, region = NULL, key = NULL,
          parse = TRUE, ...)
dl_search_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
```

## Arguments

- **name** (character) A taxonomic name
- **id** (character) An IUCN identifier
- **region** (character) A region name, see `rl_regions` for acceptable region identifier (use the entries in the identifier column)
- **key** A IUCN API token. See `rl_use_iucn`
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE

## Value

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case json as character string is returned.

## References


## Examples

```r
## Not run:
rl_search('Fratercula arctica')
rl_search('Fratercula arctica', region = 'europe')
rl_search(id = 12392)
rl_search(id = 22694927, region = 'europe')

rl_search('Fratercula arctica', parse = FALSE)
rl_search_('Fratercula arctica')
rl_search_('Fratercula arctica', region = 'europe')

## End(Not run)
```
rl_regions

Description

Get regions

Usage

rl_regions(key = NULL, parse = TRUE, ...)

rl_regions_(key = NULL, ...)

Arguments

key A IUCN API token. See rl_use_iucn.
parse (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
... Curl options passed to HttpClient

Value

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

References

API docs at http://apiv3.iucnredlist.org/api/v3/docs

Examples

## Not run:
rl_regions()
rl_regions(parse = FALSE)
rl_regions_()

## End(Not run)
Get species

Usage

```r
rl_sp(page = 0, key = NULL, parse = TRUE, all = FALSE, quiet = FALSE, ...)
```

```r
rl_sp_(page, key = NULL, all = FALSE, quiet = FALSE, ...)
```

Arguments

- **page** (integer/numeric) Page to get. Default: 0. You can get up to 10,000 records per page. Paging is required because it's too much burden on a server to just "get all the data" in one request.
- **key** A IUCN API token. See `rl_use_iucn`.
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **all** (logical) to get all results or not. Default: FALSE. This means we do the paging internally for you. Result is a list of results, so you have to bind them together yourself into a data.frame, see example.
- **quiet** (logical) give progress for download or not. Default: FALSE (that is, give progress). ignored if all = FALSE
- **...** Curl options passed to `HttpClient`

Examples

```r
## Not run:
rl_sp(page = 3)

# get all results
out <- rl_sp(all = TRUE)
length(out)
vapply(out, "[[", 1, "count")
all_df <- do.call(rbind, lapply(out, "[[", "result"))
head(all_df)
NROW(all_df)

## End(Not run)
```
**rl_sp_category**  
*Get species by category*

**Description**
Get species by category

**Usage**

```r
rl_sp_category(category, key = NULL, parse = TRUE, ...)
rl_sp_category_(category, key = NULL, parse = TRUE, ...)
```

**Arguments**

- **key** A IUCN API token. See `rl_use_iucn`.
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE

**Examples**

```r
## Not run:
rl_sp_category('VU')
rl_sp_category('LRlc')
rl_sp_category('EN')
rl_sp_category('EX')
rl_sp_category('EX', parse = FALSE)
## End(Not run)
```

**rl_sp_citation**  
*Get citations by taxon name, IUCN id, and region*

**Description**
Get citations by taxon name, IUCN id, and region

**Usage**

```r
rl_sp_citation(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)
rl_sp_citation_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
```
Arguments

- **name** (character) A taxonomic name
- **id** (character) An IUCN identifier
- **region** (character) A region name, see `rl_regions` for acceptable region identifiers (use the entries in the identifier column)
- **key** A IUCN API token. See `rl_use_iucn`
- **parse** (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- **...** Curl options passed to `HttpClient`

Value

A list, with the data in the `result` slot, unless using a function with a trailing underscore, in which case json as character string is returned.

References


Examples

```r
## Not run:
rl_sp_citation('Balaena mysticetus')
rl_sp_citation('Balaena mysticetus', region = 'europe')
rl_sp_citation(id = 12392)

rl_sp_citation(id = 2467, region = 'europe')
rl_sp_citation(id = 2467, region = 'europe', parse = FALSE)
rl_sp_citation_(id = 2467, region = 'europe')

## End(Not run)
```

---

**rl_sp_count** *Get total species count of taxa in the Red List*

Description

Get total species count of taxa in the Red List

Usage

```r
rl_sp_count(key = NULL, parse = TRUE, ...)

rl_sp_count_(key = NULL, ...)
```
Arguments

key A IUCN API token. See `rl_use_iucn`.
parse (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
... Curl options passed to HttpClient

Value

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

References


Examples

```r
## Not run:
rl_sp_count()
rl_sp_count()

## End(Not run)
```

---

**rl_sp_country**  Get species by country

Description

Get species by country

Usage

```r
rl_sp_country(country, key = NULL, parse = TRUE, ...)
rl_sp_country_(country, key = NULL, ...)
```

Arguments

```r
country (character) A two-letter country code. See isocode column in result of `rl_countries()` request for country codes.
key A IUCN API token. See `rl_use_iucn`.
parse (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
... Curl options passed to HttpClient
```

Value

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.
References

API docs at http://apiv3.iucnredlist.org/api/v3/docs

Examples

```r
## Not run:
rl_sp_country('AZ')
rl_sp_country('NZ')

# don't parse to data.frame, gives list
rl_sp_country('NZ', parse = FALSE)
# don't parse at all, get json back
rl_sp_country_('NZ')

# curl options
res <- rl_sp_country('NZ', verbose = TRUE)
```

## End(Not run)

### `rl_synonyms`

*Get species synonym information by taxonomic name*

**Description**

Get species synonym information by taxonomic name

**Usage**

```r
rl_synonyms(name = NULL, key = NULL, parse = TRUE, ...)
rl_synonyms_(name = NULL, key = NULL, ...)
```

**Arguments**

- `name` (character) Binomial taxonomic name
- `key` A IUCN API token. See `rl_use_iucn`.
- `parse` (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- `...` Curl options passed to `HttpClient`

**Value**

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**

API docs at http://apiv3.iucnredlist.org/api/v3/docs
Examples

```r
## Not run:
rl_synonyms('Loxodonta africana')
rl_synonyms('Loxodonta africana', parse = FALSE)
rl_synonyms_('Loxodonta africana')

## End(Not run)
```

---

**rl_threats**

*Get species threats by taxon name, IUCN id, and region*

**Description**

Get species threats by taxon name, IUCN id, and region

**Usage**

```r
rl_threats(name = NULL, id = NULL, region = NULL, key = NULL, parse = TRUE, ...)
```

```r
rl_threats_(name = NULL, id = NULL, region = NULL, key = NULL, ...)
```

**Arguments**

- `name` (character) A taxonomic name
- `id` (character) An IUCN identifier
- `region` (character) A region name, see `rl_regions` for acceptable region identifiers (use the entries in the identifier column)
- `key` A IUCN API token. See `rl_use_iucn`.
- `parse` (logical) Whether to parse to list (FALSE) or data.frame (TRUE). Default: TRUE
- `...` Curl options passed to `HttpClient`

**Value**

A list, with the data in the result slot, unless using a function with a trailing underscore, in which case json as character string is returned.

**References**

Examples

```r
## Not run:
rl_threats('Fratercula arctica')
rl_threats('Fratercula arctica', region = 'europe')
rl_threats(id = 12392)
rl_threats(id = 22694927, region = 'europe')
rl_threats(name = 'Abies numidica')
rl_threats_('Fratercula arctica')

rl_threats(id = 62290750)

## End(Not run)
```

---

### `rl_use_iucn`

**Helper to get and save IUCN API key**

**Description**

Browse IUCN Red List API key request URL and provides instruction on how to store the key.

**Usage**

```r
rl_use_iucn()
```

**Details**

Note that after filling the online form, you should receive an API key shortly but not immediately.

---

### `rl_version`

**Get the Red List API version**

**Description**

Get the Red List API version

**Usage**

```r
rl_version(...)```

**Arguments**

```r
...  

Curl options passed to `curl::HttpClient()````

**Value**

API version as character string
Examples

## Not run:
rl_version()

## End(Not run)
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