Package ‘rbiodatacr’

May 9, 2026

Type Package

Title R Client for the BIODATACR Biodiversity Data Platform of Costa Rica

Version 0.1.1

Description Provides functions to query occurrence records, species information, and datasets from BIODATACR <https://biodiversidad.go.cr>, the national biodiversity information platform of Costa Rica managed by the Technical Office of CONAGEBIO, Costa Rica. Built on the Atlas of Living Australia (ALA) API infrastructure.

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Encoding UTF-8

URL https://github.com/ManuelSpinola/rbiodatacr, https://manuelspinola.github.io/rbiodatacr/

BugReports https://github.com/ManuelSpinola/rbiodatacr/issues

Suggests CoordinateCleaner, ggplot2, knitr, rmarkdown, sf, testthat (>= 3.0.0)

Config/testthat/edition 3

Imports cli, dplyr, httr, jsonlite, purrr

RoxygenNote 7.3.3

VignetteBuilder knitr

Depends R (>= 4.1.0)

LazyData true

Language en-US

NeedsCompilation no

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Repository CRAN

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Contents

`bdcr_count` *Count occurrence records for a taxon*

Description

Count occurrence records for a taxon

Usage

```
bdcr_count(taxon)
```

Arguments

`taxon`	Character. Scientific name (e.g. ‘"Panthera onca"‘).

Value

Integer with the total number of available records, or ‘NA_integer_‘ if the service is unavailable.

Examples

```
## Not run:
bdcr_count("Panthera onca")

## End(Not run)
```

`bdcr_count_batch` *Count occurrence records for multiple taxa*

Description

Count occurrence records for multiple taxa

Usage

```
bdcr_count_batch(taxa, wait = 1)
```

Arguments

`taxa`	Character vector. Scientific names.
`wait`	Numeric. Seconds to pause between requests. Default 1.

Value

A ‘tibble‘ with columns ‘taxon‘ and ‘n_records‘.

Examples

```
## Not run:
spp <- c("Tapirus bairdii", "Panthera onca")
bdcr_count_batch(spp)

## End(Not run)
```

`bdcr_occurrences` *Download occurrence records from BIODATACR*

Description

Download occurrence records from BIODATACR

Usage

```
bdcr_occurrences(taxon, rows = 100, start = 0)
```

Arguments

`taxon`	Character. Scientific name of the taxon.
`rows`	Integer. Maximum number of records to download. Default 100.
`start`	Integer. Starting record for pagination. Default 0.

Value

A ‘tibble‘ with columns: ‘scientificName‘, ‘vernacularName‘, ‘decimalLatitude‘, ‘decimalLongitude‘, ‘year‘, ‘month‘, ‘basisOfRecord‘, ‘dataResourceName‘, ‘country‘, ‘family‘, ‘species‘, ‘collector‘, ‘license‘, ‘geospatialKosher‘, ‘taxonomicKosher‘. Returns an empty ‘tibble‘ if the service is unavailable or no records are found.

Examples

```
## Not run:
bdcr_occurrences("Panthera onca", rows = 50)

## End(Not run)
```

`bdcr_occurrences_batch` *Download occurrence records for multiple taxa*

Description

Download occurrence records for multiple taxa

Usage

```
bdcr_occurrences_batch(taxa, rows = 100, wait = 1)
```

Arguments

`taxa`	Character vector. Scientific names.
`rows`	Integer. Records per taxon. Default 100.
`wait`	Numeric. Seconds to pause between requests. Default 1.

Value

Named list of tibbles, one per taxon. If the service is unavailable for a given taxon, the corresponding element will be an empty ‘tibble‘.

Examples

```
## Not run:
spp <- c("Tapirus bairdii", "Panthera onca")
bdcr_occurrences_batch(spp, rows = 50)

## End(Not run)
```

`bdcr_quality_check` *Quality check for occurrence records*

Description

Adds a ‘quality_flag‘ column to an occurrence tibble. Requires that ‘geospatialKosher‘ and ‘taxonomicKosher‘ are logical — a condition guaranteed by ‘bdcr_occurrences()‘.

Usage

```
bdcr_quality_check(df, min_year = 1950)
```

Arguments

`df`	A ‘tibble‘ of occurrence records (output of ‘bdcr_occurrences()‘).
`min_year`	Integer. Minimum acceptable year. Default 1950.

Value

The same ‘tibble‘ with an additional ‘quality_flag‘ column. Possible values:

‘"ok"‘ No issues detected.

‘"no_coords"‘ Missing coordinates.

‘"geospatial_issue"‘ ‘geospatialKosher == FALSE‘.

‘"taxonomic_issue"‘ ‘taxonomicKosher == FALSE‘.

‘"old_record"‘ Year before ‘min_year‘.

Examples

```
## Not run:
df <- bdcr_occurrences("Panthera onca", rows = 50)
bdcr_quality_check(df)

## End(Not run)
```

`bdcr_species_search` *Search for taxonomic information of a species in BIODATACR*

Description

Queries the BIE (Biodiversity Information Explorer) index of BIODATACR to retrieve taxonomic information for a species.

Usage

```
bdcr_species_search(name, rows = 10)
```

Arguments

`name`	Character. Scientific name (may be a synonym or partial name).
`rows`	Integer. Maximum number of results. Default 10.

Value

A ‘tibble‘ with columns: ‘name‘, ‘guid‘, ‘commonName‘, ‘scientificName‘, ‘rank‘, ‘taxonomicStatus‘, ‘nameComplete‘. Returns an empty ‘tibble‘ if the service is unavailable or no results are found.

Examples

```
## Not run:
bdcr_species_search("Panthera onca")

## End(Not run)
```

`cr_outline` *Costa Rica national boundary*

Description

An ‘sf‘ object with the national boundary of Costa Rica from GADM.

Usage

```
cr_outline
```

Format

An ‘sf‘ object with 1 row and the following columns:

GID_0 Country code (CRI)

COUNTRY Country name

geometry MULTIPOLYGON geometry

Source

https://gadm.org/

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