

Package ‘rbiodatacr’

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Type Package

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

Version 0.1.2

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. 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

VignetteBuilder knitr

Depends R (>= 4.1.0)

LazyData true

Language en-US

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bdcr_count	<i>Count occurrence records for a taxon</i>
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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	<i>Count occurrence records for multiple taxa</i>
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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	<i>Download occurrence records from BIODATACR</i>
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Description

Download occurrence records from BIODATACR

Usage

```
bdcr_occurrences(taxon, rows = 100, start = 0, page_size = 300, wait = 1)
```

Arguments

taxon	Character. Scientific name of the taxon.
rows	Integer. Maximum number of records to download. Default 100. Pass 'Inf' (or the taxon's true total, e.g. from [bdcr_count()]) to download every available record, paginating as needed. If fewer records are downloaded than actually exist, an informative message reports the true total so the result is never mistaken for the complete dataset.
start	Integer. Starting record for pagination. Default 0.
page_size	Integer. Records requested per HTTP call. Default 300. Kept below 'rows' and used to chunk large downloads into several polite requests instead of one giant one.
wait	Numeric. Seconds to pause between paginated requests (only relevant when more than one page is needed). Default 1.

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)
bdcr_occurrences("Panthera onca")           # primeros 100 (default)
bdcr_occurrences("Panthera onca", rows = Inf) # todos los registros

## 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, page_size = 300, wait = 1)
```

Arguments

taxa	Character vector. Scientific names.
rows	Integer. Maximum records per taxon. Default 100, matching [bdcr_occurrences()]. Pass 'Inf' to download every available record for each taxon; a message will report the true total for any taxon where the download is capped below it.
page_size	Integer. Records requested per HTTP call within each taxon's pagination. Default 300.
wait	Numeric. Seconds to pause between requests (both between taxa and between pages within a taxon). 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)
bdcr_occurrences_batch(spp, rows = Inf) # descarga todos los registros

## End(Not run)
```

bdcr_quality_check	<i>Quality check for occurrence records</i>
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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’, ‘taxonomic-Status’, ‘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	<i>Costa Rica national boundary</i>
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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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* **datasets**

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