

Package ‘rbiodatacr’

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Type Package

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

Version 0.1.0

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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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").
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Value

Integer with the total number of available records.

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)
```

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'.

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.

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’.

Examples

```
## Not run:
bdc_r_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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