# Package ‘rbiodatacr’

May 6, 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.

**License** MIT + file LICENSE

**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

**Author** Manuel Spinola [aut, cre] (ORCID: <https://orcid.org/0000-0002-7839-1908>)

**Maintainer** Manuel Spinola <mspinola10@gmail.com>

**Repository** CRAN

**Date/Publication** 2026-05-05 22:30:16 UTC

# 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/

# Index