Package ‘rgbif’

May 8, 2019

Title Interface to the Global 'Biodiversity' Information Facility API

Description A programmatic interface to the Web Service methods provided by the Global Biodiversity Information Facility ('GBIF'; <https://www.gbif.org/developer/summary>). 'GBIF' is a database of species occurrence records from sources all over the globe. 'rgbif' includes functions for searching for taxonomic names, retrieving information on data providers, getting species occurrence records, getting counts of occurrence records, and using the 'GBIF' tile map service to make 'rasters' summarizing huge amounts of data.

Version 1.3.0

License MIT + file LICENSE

URL https://github.com/ropensci/rgbif,
      https://ropensci.github.io/rgbif,
      https://ropensci.github.io/occurrence-manual

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

LazyData true

LazyLoad true

VignetteBuilder knitr

Encoding UTF-8

Language en-US

Imports xml2, ggplot2, crul (>= 0.7.4), data.table, whisker, magrittr, jsonlite (>= 1.6), oai (>= 0.2.2), geoaxe, tibble, wicket (>= 0.4.0), lazyeval

Suggests testthat, knitr, sp, rgeos, png, raster, vcr

RoxygenNote 6.1.1

X-schema.org-applicationCategory Biodiversity

X-schema.org-keywords GBIF, specimens, API, web-services, occurrences, species, taxonomy

X-schema.org-isPartOf https://ropensci.org

NeedsCompilation no
R topics documented:

- rgbif-package
- check_wkt
- count_facet
- datasets
- dataset_metrics
- dataset_search
- dataset_suggest
- downloads
- elevation
- enumeration
- gbif_bbox2wkt
- gbif_citation
- gbif_issues
- gbif_names
- gbif_oai
- gbif_photos
- installations
- isocodes
- many-values
- map_fetch
- name_backbone
- name_issues
- name_lookup
- name_suggest
- name_usage
- networks
- nodes
- occ_count
- occ_data
- occ_download
- occ_download_cancel
- occ_download_datasets
- occ_download_dataset_activity
- occ_download_get
Description

rgbif: A programmatic interface to the Web Service methods provided by the Global Biodiversity Information Facility.

About

This package gives you access to data from GBIF http://www.gbif.org/ via their API.

A note about the old GBIF API

The old GBIF API was at http://data.gbif.org/tutorial/services, but is now defunct - that is, not available anymore. We used to have functions that worked with the old API, but those functions are now not available anymore because GBIF made the old API defunct.

Documentation for the GBIF API

- summary http://www.gbif.org/developer/summary - Summary of the GBIF API
- registry http://www.gbif.org/developer/registry - Metadata on datasets, and contributing organizations
- species names http://www.gbif.org/developer/species - Species names and metadata
- occurrences http://www.gbif.org/developer/occurrence - Occurrences
- maps http://www.gbif.org/developer/maps - Maps - these APIs are not implemented in rgbif, and are meant more for integration with web based maps.
Note

See many-values for discussion of how functions vary in how they accept values (single vs. many for the same HTTP request vs. many for different HTTP requests)

Author(s)

Scott Chamberlain <myrmecocystus@gmail.com>
Karthik Ram <karthik@ropensci.org>
Dan McGlinn <danmcglinn@gmail.com>
Vijay Barve <vijay.barve@gmail.com>

---

check_wkt

**Check input WKT**

Description

Check input WKT

Usage

check_wkt(wkt = NULL, skip_validate = FALSE)

Arguments

- wkt (character) one or more Well Known Text objects
- skip_validate (logical) whether to skip `wicket::wkt_validate` call or not. Default: FALSE

Examples

```r
## Not run:
check_wkt('POLYGON((30.1 10.1, 10 20, 20 60, 60 60, 30.1 10.1))')
check_wkt('POINT(30.1 10.1)')
check_wkt('LINESTRING(3 4,10 50,20 25)')

# check many passed in at once
check_wkt(c('POLYGON((30.1 10.1, 10 20, 20 60, 60 60, 30.1 10.1))',
            'POINT(30.1 10.1)'))

# bad WKT
# wkt <- 'POLYGON((30.1 10.1, 10 20, 20 60, 60 60, 30.1 a))'
# check_wkt(wkt)

# many wkt's, semi-colon separated, for many repeated "geometry" args
wkt <- "POLYGON((-102.2 46.0,-93.9 46.0,-93.9 43.7,-102.2 43.7,-102.2 46.0))
;POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))"
check_wkt(gsub(`\n`, '\'', wkt))

## End(Not run)
```
count_facet

Faceted count occurrence search.

Description
Faceted count occurrence search.

Usage
```
count_facet(keys = NULL, by = "country", countries = 10, removezeros = FALSE)
```

Arguments
- `keys` (numeric) GBIF keys, a vector.
- `by` (character) One of georeferenced, basisOfRecord, country, or publishingCountry.
- `countries` (numeric) Number of countries to facet on, or a vector of country names
- `removezeros` (logical) Default is FALSE

Examples
```
## Not run:
# Select number of countries to facet on
count_facet(by='country', countries=3, removezeros = TRUE)
# Or, pass in country names
count_facet(by='country', countries='AR', removezeros = TRUE)

spplist <- c('Geothlypis trichas','Tiaris olivacea','Pterodroma axillaris',
              'Calidris ferruginea','Pterodroma macroptera',
              'Gallirallus australis',
              'Falco cenchroides','Telespiza cantans','Oreomystis bairdi',
              'Cistothorus palustris')
keys <- sapply(spplist, function(x) name_backbone(x, rank="species")$usageKey)
count_facet(keys, by='country', countries=3, removezeros = TRUE)
count_facet(keys, by='country', countries=3, removezeros = FALSE)
count_facet(by='country', countries=20, removezeros = TRUE)

# Pass in country names instead
countries <- isocodes$code[1:10]
count_facet(by='country', countries=countries, removezeros = TRUE)

# get occurrences by georeferenced state
## across all records
count_facet(by='georeferenced')

## by keys
count_facet(keys, by='georeferenced')
```
# by basisOfRecord
count_facet(by="basisOfRecord")

## End(Not run)

## datasets

### Search for datasets and dataset metadata.

#### Description

Search for datasets and dataset metadata.

#### Usage

```r
datasets(data = "all", type = NULL, uuid = NULL, query = NULL,
         id = NULL, limit = 100, start = NULL, curlopts = list())
```

#### Arguments

- **data**: The type of data to get. One or more of: 'organization', 'contact', 'endpoint', 'identifier', 'tag', 'machineetag', 'comment', 'constituents', 'document', 'metadata', 'deleted', 'duplicate', 'subDataset', 'withNoEndpoint', or the special 'all'. Default: all
- **type**: Type of dataset. Options: include occurrence, checklist, metadata, or sampling_event.
- **uuid**: UUID of the data node provider. This must be specified if data is anything other than all
- **query**: Query term(s). Only used when data=all
- **id**: A metadata document id.
- **limit**: Number of records to return. Default: 100. Maximum: 1000.
- **start**: Record number to start at. Default: 0. Use in combination with limit to page through results.
- **curlopts**: list of named curl options passed on to HttpClient. see curl_options for curl options

#### Value

A list.

#### References

[http://www.gbif.org/developer/registry#datasets](http://www.gbif.org/developer/registry#datasets)
**dataset_metrics**

*Get details on a GBIF dataset.*

---

### Examples

```r
## Not run:
dataset_metrics(uuid = "a6998220-7e3a-485d-9cd6-73076bd85657")
dataetset_metrics(data = 'contact', uuid = "a6998220-7e3a-485d-9cd6-73076bd85657")
dataetset_metrics(data = 'metadata', uuid = "a6998220-7e3a-485d-9cd6-73076bd85657", id = 598)
dataetset_metrics(data = c('deleted','duplicate'))
dataetset_metrics(data = c('deleted','duplicate'), limit=1)

# curl options
dataetset_metrics(data = c('deleted','duplicate'), curlopts = list(verbost=TRUE))

## End(Not run)
```

---

### Description

Get details on a GBIF dataset.

### Usage

```r
dataset_metrics(uuid, curlopts = list())
```

### Arguments

- **uuid** (character) One or more dataset UUIDs. See examples.
- **curlopts** list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

### Note

Dataset metrics are only available for checklist type datasets.

### References

[http://www.gbif.org/developer/registry#datasetMetrics](http://www.gbif.org/developer/registry#datasetMetrics)
Examples

```r
dataframe_metrics(uuid='863e6d6b-f602-4495-ac30-881482b6f799')
dataframe_metrics(uuid='66dd0960-2d7d-46ee-a491-87b9adcf7b1')
dataframe_metrics(uuid='863e6d6b-f602-4495-ac30-881482b6f799',
  '66dd0960-2d7d-46ee-a491-87b9adcf7b1')
dataframe_metrics(uuid='66dd0960-2d7d-46ee-a491-87b9adcf7b1',
curlopts = list(verbosetherue))
```

## End(Not run)

### dataset_search

Search datasets in GBIF.

**Description**

This function does not search occurrence data, only metadata on the datasets that contain occurrence data.

**Usage**

```r
dataset_search(query = NULL, country = NULL, type = NULL,
  keyword = NULL, publishingOrg = NULL, hostingOrg = NULL,
  publishingCountry = NULL, decade = NULL, facet = NULL,
  facetMincount = NULL, facetMultiselect = NULL, limit = 100,
  start = NULL, pretty = FALSE, return = "all", curlopts = list())
```

**Arguments**

- **query**
  
  Query term(s) for full text search. The value for this parameter can be a simple word or a phrase. Wildcards can be added to the simple word parameters only, e.g. `q=*puma*`

- **country**
  
  NOT YET IMPLEMENTED. Filters by country as given in `isocodes$gbif_name`, e.g. `country=CANADA`

- **type**
  
  Type of dataset, options include occurrence, metadata, checklist, sampling_event (http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/DatasetType.html)

- **keyword**
  
  Keyword to search by. Datasets can be tagged by keywords, which you can search on. The search is done on the merged collection of tags, the dataset keywordCollections and temporalCoverages.

- **publishingOrg**
  
  Publishing organization. A uuid string. See `organizations`

- **hostingOrg**
  
  Hosting organization. A uuid string. See `organizations`

- **publishingCountry**
  
  Publishing country. See options at `isocodes$gbif_name`
Decade, e.g., 1980. Filters datasets by their temporal coverage broken down to decades. Decades are given as a full year, e.g. 1880, 1960, 2000, etc, and will return datasets wholly contained in the decade as well as those that cover the entire decade or more. Facet by decade to get the breakdown, e.g. /search?facet=DECADE&facet_only=true (see example below)

facet
A list of facet names used to retrieve the 100 most frequent values for a field. Allowed facets are: datasetKey, highertaxonKey, rank, status, extinct, habitat, and nameType. Additionally threat and nomenclaturalStatus are legal values but not yet implemented, so data will not yet be returned for them.

facetMincount
Used in combination with the facet parameter. Set facetMincount=#{} to exclude facets with a count less than #, e.g. http://bit.ly/1bMdByP only shows the type value ‘ACCEPTED’ because the other statuses have counts less than 7,000,000

facetMultiselect
Used in combination with the facet parameter. Set facetMultiselect=true to still return counts for values that are not currently filtered, e.g. http://bit.ly/19YLXPO still shows all status values even though status is being filtered by status=ACCEPTED

limit
Number of records to return. Default: 100. Maximum: 1000.

start
Record number to start at. Default: 0. Use in combination with limit to page through results.

pretty
Print informative metadata using cat. Not easy to manipulate output though.

return
What to return. One of meta, descriptions, data, facets, or all (Default).

curlopts
list of named curl options passed on to HttpClient. see curl_options for curl options

Value
A data.frame, list, or message printed to console (using pretty=TRUE).

Repeat parameter inputs
Some parameters can take many inputs, and treated as ‘OR’ (e.g., a or b or c). The following take many inputs:

- type
- keyword
- publishingOrg
- hostingOrg
- publishingCountry
- decade

References
http://www.gbif.org/developer/registry#datasetSearch
Examples

```r
# Not run:
dataset_search(type = "OCCURRENCE", limit = 10)

dataset_search(type = "OCCURRENCE", limit = 10)

# Fulltext search for all datasets having the word "amsterdam" somewhere in
# its metadata (title, description, etc).
dataset_search(query = "amsterdam", limit = 10)

# Limited search
dataset_search(type = "OCCURRENCE", limit = 2)
dataset_search(type = "OCCURRENCE", limit = 2, start = 10)

# Return just descriptions
dataset_search(type = "OCCURRENCE", return = "descriptions", limit = 10)

# Return metadata in a more human readable way (hard to manipulate though)
dataset_search(type = "OCCURRENCE", pretty = TRUE, limit = 10)

# Search by country code. Lookup isocodes first, and use US for United States
isocodes[agrep("UNITED", isocodes$gbif_name),]
dataset_search(country = "US", limit = 10)

# Search by decade
dataset_search(decade = 1980, limit = 10)

# Faceting
## just facets
dataset_search(facet = "decade", facetMincount = "10", limit = 0)

## data and facets
dataset_search(facet = "decade", facetMincount = "10", limit = 2)

# Some parameters accept many inputs, treated as OR
dataset_search(type = c("metadata", "checklist"))
dataset_search(keyword = c("fern", "algae"))
dataset_search(publishingOrg = c("e2e717bf-551a-4917-bdc9-4fa0f342c530",
"90fd6680-349f-11d8-aa2d-b8a03c50a862"))
dataset_search(hostingOrg = c("c5f7ef70-e233-11d9-a4d6-b8a03c50a862",
"c5e4331-7f2f-4a8d-aa56-81ece7814fc8"))
dataset_search(publishingCountry = c("DE", "NZ"))
dataset_search(decade = c(1910, 1930))

# curl options
dataset_search(facet = "decade", facetMincount = "10", limit = 2,
curlopts = list(verbose = TRUE))

# End(Not run)
```

---

**dataset_suggest**

*Suggest datasets in GBIF.*
**dataset_suggest**

Description

Suggest datasets in GBIF.

Usage

```java
dataset_suggest(query = NULL, country = NULL, type = NULL,
    subtype = NULL, keyword = NULL, publishingOrg = NULL,
    hostingOrg = NULL, publishingCountry = NULL, decade = NULL,
    continent = NULL, limit = 100, start = NULL, pretty = FALSE,
    description = FALSE, curlopts = list())
```

Arguments

- **query**: Query term(s) for full text search. The value for this parameter can be a simple word or a phrase. Wildcards can be added to the simple word parameters only, e.g. `q=*puma*`
- **country**: NOT YET IMPLEMENTED. Filters by country as given in isocodes$gbif_name, e.g. `country=CANADA`
- **type**: Type of dataset, options include occurrence, metadata, checklist, sampling_event (http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/DatasetType.html)
- **subtype**: NOT YET IMPLEMENTED. Will allow filtering of datasets by their dataset subtypes, DC or EML.
- **keyword**: Keyword to search by. Datasets can be tagged by keywords, which you can search on. The search is done on the merged collection of tags, the dataset keywordCollections and temporalCoverages.
- **publishingOrg**: Publishing organization. A uuid string. See organizations
- **hostingOrg**: Hosting organization. A uuid string. See organizations
- **publishingCountry**: Publishing country. See options at isocodes$gbif_name
- **decade**: Decade, e.g., 1980. Filters datasets by their temporal coverage broken down to decades. Decades are given as a full year, e.g. 1880, 1960, 2000, etc, and will return datasets wholly contained in the decade as well as those that cover the entire decade or more. Facet by decade to get the break down, e.g. `/search?facet=DECADE&facet_only=true` (see example below)
- **continent**: Not yet implemented, but will eventually allow filtering datasets by their continent(s) as given in our Continent enum.
- **limit**: Number of records to return. Default: 100. Maximum: 1000.
- **start**: Record number to start at. Default: 0. Use in combination with limit to page through results.
- **pretty**: Print informative metadata using `cat`. Not easy to manipulate output though.
- **description**: Return descriptions only (TRUE) or all data (FALSE, default)
- **curlopts**: list of named curl options passed on to HttpClient. see curl_options for curl options
dataset_suggest

Value

A data.frame, list, or message printed to console (using pretty=TRUE).

Repeat parameter inputs

Some parameters can take many inputs, and treated as ‘OR’ (e.g., a or b or c). The following take many inputs:

- type
- keyword
- publishingOrg
- hostingOrg
- publishingCountry
- decade

References

http://www.gbif.org/developer/registry#datasetSearch

Examples

```r
# Not run:
# Suggest datasets of type "OCCURRENCE".
dataset_suggest(query="Amazon", type="OCCURRENCE")

dataset_suggest(keyword="france")

dataset_suggest(query="amsterdam")

dataset_suggest(type="OCCURRENCE", limit=2)
dataset_suggest(type="OCCURRENCE", limit=2, start=10)

dataset_suggest(type="OCCURRENCE", limit = 5, description=TRUE)

dataset_suggest(country="US", limit = 5, pretty=TRUE)

dataset_suggest(country=agrep("UNITED", isocodes$gbif_name),]
dataset_suggest(decade=1980, limit = 30)
```

# Some parameters accept many inputs, treated as OR
Description
GBIF provides two ways to get occurrence data: through the /occurrence/search route (see `occ_search()`), or via the /occurrence/download route (many functions, see below). `occ_search()` is more appropriate for smaller data, while `occ_download*()` functions are more appropriate for larger data requests.

Settings
You’ll use `occ_download()` to kick off a download. You’ll need to give that function settings from your GBIF profile: your user name, your password, and your email. These three settings are required to use the function. You can specify them in one of three ways:

- Pass them to `occ_download` as parameters
- Use R options: As options either in the current R session using the `options()` function, or by setting them in your `.Rprofile` file, after which point they’ll be read in automatically
- Use environment variables: As env vars either in the current R session using the `Sys.setenv()` function, or by setting them in your `.Renviron`/`.bash_profile` or similar files, after which point they’ll be read in automatically

BEWARE
You can not perform that many downloads, so plan wisely. See Rate limiting below.

Rate limiting
If you try to launch too many downloads, you will receive an 420 "Enhance Your Calm" response. If there is less then 100 in total across all GBIF users, then you can have 3 running at a time. If there are more than that, then each user is limited to 1 only. These numbers are subject to change.
Functions

- `occ_download()` - Start a download
- `occ_download_prep()` - Prepare a download request
- `occ_download_queue()` - Start many downloads in a queue
- `occ_download_meta()` - Get metadata progress on a single download
- `occ_download_list()` - List your downloads
- `occ_download_cancel()` - Cancel a download
- `occ_download_cancel_staged()` - Cancels any jobs with status RUNNING or PREPARING
- `occ_download_get()` - Retrieve a download
- `occ_download_import()` - Import a download from local file system
- `occ_download_datasets()` - List datasets for a download
- `occ_download_dataset_activity()` - Lists the downloads activity of a dataset

Query length

 GBIF has a limit of 12,000 characters for a download query. This means that you can have a pretty long query, but at some point it may lead to an error on GBIF’s side and you’ll have to split your query into a few.

elevation

Get elevation for lat/long points from a data.frame or list of points.

description

Uses the GeoNames web service

Usage

elevation(input = NULL, latitude = NULL, longitude = NULL,
latlong = NULL, elevation_model = "srtm3",
username = Sys.getenv("GEONAMES_USER"), key, curlopts, ...)

Arguments

input A data.frame of lat/long data. There must be columns decimalLatitude and decimalLongitude.
latitude A vector of latitude’s. Must be the same length as the longitude vector.
longitude A vector of longitude’s. Must be the same length as the latitude vector.
latlong A vector of lat/long pairs. See examples.
elevation_model (character) one of srtm3 (default), srtm1, astergdem, or gtopo30. See "Elevation models" below for more
**username**  
(character) Required. An GeoNames user name. See Details.

**key, curl opts**  
defunct. see docs

...  
curl options passed on to `crl::verb-GET` see `crl::curl_options()` for curl options

**Value**

A new column named `elevation_geonames` in the supplied data.frame or a vector with elevation of each location in meters. Note that data from GBIF can already have a column named `elevation`, thus the column we add is named differently.

**GeoNames user name**

To get a GeoNames user name, register for an account at http://www.geonames.org/login - then you can enable your account for the GeoNames webservice on your account page. Once you are enabled to use the webservice, you can pass in your username to the `username` parameter. Better yet, store your username in your `.Renviron` file, or similar (e.g., .zshrc or .bash_profile files) and read it in via `Sys.getenv()` as in the examples below. By default we do `Sys.getenv("GEONAMES_USER")` for the `username` parameter.

**Elevation models**

• srtm3:
  – sample area: ca 90m x 90m
  – result: a single number giving the elevation in meters according to srtm3, ocean areas have been masked as "no data" and have been assigned a value of -32768

• srtm1:
  – sample area: ca 30m x 30m
  – result: a single number giving the elevation in meters according to srtm1, ocean areas have been masked as "no data" and have been assigned a value of -32768

• astergdem (Aster Global Digital Elevation Model V2 2011):
  – sample area: ca 30m x 30m, between 83N and 65S latitude
  – result: a single number giving the elevation in meters according to aster gdem, ocean areas have been masked as "no data" and have been assigned a value of -32768

• gtopo30:
  – sample area: ca 1km x 1km
  – result: a single number giving the elevation in meters according to gtopo30, ocean areas have been masked as "no data" and have been assigned a value of -9999

**References**

GeoNames http://www.geonames.org/export/web-services.html
Examples

```r
## Not run:
user <- Sys.getenv("GEONAMES_USER")

occ_key <- name_suggest('Puma concolor')$key[1]
dat <- occ_search(taxonKey = occ_key, return = 'data', limit = 300,
  hasCoordinate = TRUE)
head(elevation(dat, username = user))

# Pass in a vector of lat's and a vector of long's
elevation(latitude = dat$decimalLatitude[1:10],
  longitude = dat$decimalLongitude[1:10],
  username = user, verbose = TRUE)

# Pass in lat/long pairs in a single vector
pairs <- list(c(31.8496, -110.576060), c(29.15503, -103.59828))
elevation(latlong=pairs, username = user)

# Pass on curl options
pairs <- list(c(31.8496, -110.576060), c(29.15503, -103.59828))
elevation(latlong=pairs, username = user, verbose = TRUE)

# different elevation models
lats <- dat$decimalLatitude[1:5]
lons <- dat$decimalLongitude[1:5]
elevation(latitude = lats, longitude = lons, elevation_model = "srtm3", verbose = TRUE)
elevation(latitude = lats, longitude = lons, elevation_model = "srtm1", verbose = TRUE)
elevation(latitude = lats, longitude = lons, elevation_model = "astergdem", verbose = TRUE)
elevation(latitude = lats, longitude = lons, elevation_model = "gtopo30", verbose = TRUE)

## End(Not run)
```

---

table

<table>
<thead>
<tr>
<th>enumeration</th>
<th>Enumerations.</th>
</tr>
</thead>
</table>

Description

Many parts of the GBIF API make use of enumerations, i.e. controlled vocabularies for specific topics - and are available via these functions

Usage

```r
enumeration(x = NULL, curlopts = list())

enumeration_country(curlopts = list())
```
**gbif_bbox2wkt**

**Arguments**

- `x`  
  A given enumeration.

- `curlopts`  
  List of named curl options passed on to `HttpClient`. See `curl_options` for curl options.

**Value**

`enumeration` returns a character vector, while `enumeration_country` returns a data.frame.

**Examples**

```r
# Not run:
# basic enumeration
enumeration()
enumeration("NameType")
enumeration("MetadataType")
enumeration("TypeStatus")

# country enumeration
enumeration_country()

# curl options
enumeration(curlopts = list(verbosE=TRUE))
```

---

**gbif_bbox2wkt**  
*Convert a bounding box to a Well Known Text polygon, and a WKT to a bounding box*

**Description**

Convert a bounding box to a Well Known Text polygon, and a WKT to a bounding box

**Usage**

```r
gbif_bbox2wkt(minx = NA, miny = NA, maxx = NA, maxy = NA, bbox = NULL)
gbif_wkt2bbox(wkt = NULL)
```

**Arguments**

- `minx`  
  (numeric) Minimum x value, or the most western longitude

- `miny`  
  (numeric) Minimum y value, or the most southern latitude

- `maxx`  
  (numeric) Maximum x value, or the most eastern longitude

- `maxy`  
  (numeric) Maximum y value, or the most northern latitude
bbox (numeric) A vector of length 4, with the elements: minx, miny, maxx, maxy
wkt (character) A Well Known Text object.

Value

gbif_bbox2wkt returns an object of class character, a Well Known Text string of the form 'POLYGON((minx miny, maxx miny, maxx maxy, minx maxy, minx miny))'.
gbif_wkt2bbox returns a numeric vector of length 4, like c(minx, miny, maxx, maxy)

Examples

```r
## Not run:
## Convert a bounding box to a WKT
## Pass in a vector of length 4 with all values
gbif_bbox2wkt(bbox=c(-125.0,38.4,-121.8,40.9))

## Or pass in each value separately
gbif_bbox2wkt(minx=-125.0, miny=38.4, maxx=-121.8, maxy=40.9)

# Convert a WKT object to a bounding box
wkt <- "POLYGON((-125 38.4,-125 40.9,-121.8 40.9,-121.8 38.4,-125 38.4))"
gbif_wkt2bbox(wkt)

## End(Not run)
```

---

gbif_citation

**Description**

Get citation for datasets used

**Usage**

gbif_citation(x)

**Arguments**

x (character) Result of call to occ_search(), occ_download_get(), occ_download_meta(), a dataset key, or occurrence key (character or numeric)

**Details**

Returns a set of citations, one for each dataset. We pull out unique dataset keys and get citations, so the length of citations may not be equal to the number of records you pass in.

Currently, this function gives back citations at the dataset level, not at the individual occurrence level. If occurrence keys are passed in, then we track down the dataset the key is from, and get the citation for the dataset.
Value

list with S3 class assigned, used by a print method to pretty print citation information. Though you can unclass the output or just index to the named items as needed.

Examples

```r
## Not run:
res1 <- occ_search(taxonKey=9206251, limit=2)
(xx <- gbif_citation(res1))

res2 <- occ_search(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a',
  return='data', limit=20)
(xx <- gbif_citation(res2))

# if no datasetKey field included, we attempt to identify the dataset
## key field included - still works
res3 <- occ_search(taxonKey=9206251, fields=c('name','basisOfRecord','key'),
  limit=20)
(xx <- gbif_citation(res3))

## key field not included - errors
## res3 <- occ_search(taxonKey=9206251, fields=c('name','basisOfRecord','key')
## # protocol', limit=20)
# (xx <- gbif_citation(res3))

## character class inputs
## pass in a dataset key
gbif_citation(x='0ec3229f-2b53-484e-817a-de8ceb1fce2b')

## pass in an occurrence key
gbif_citation(x='1425976049')

## pass in an occurrence key as a numeric (won't work for a dataset key)
gbif_citation(x=1425976049)

## Downloads
## occ_download_get()
## dl <- occ_download("country = BG", "year <= 2011")
## key <- "0000122-171020152545675"
## occ_download_meta(key)
## dl <- occ_download_get(key, overwrite = TRUE)
## gbif_citation(dl)

## occ_download_meta()
## key <- "0000122-171020152545675"
## res <- occ_download_meta(key)
## gbif_citation(res)

## End(Not run)
```
gbif_issues

Table of GBIF issues, with codes used in data output, full issue name, and descriptions.

Description

Table has the following fields:

Usage

gbff_issues()

Details

- issue. Full name of the issue.
- description. Description of the issue.

Source


See Also

name_issues()
Examples

```r
## Not run:
# browse=FALSE returns path to file
gif_names(name_lookup(query='snake', hl=TRUE), browse=FALSE)

(out <- name_lookup(query='canada', hl=TRUE, limit=5))
gif_names(out)
gif_names(name_lookup(query='snake', hl=TRUE))
gif_names(name_lookup(query='bird', hl=TRUE))

# or not highlight
gif_names(name_lookup(query='bird', limit=200))
## End(Not run)
```

---

**gbif_oai**  
*GBIF registry data via OAI-PMH*

**Description**

GBIF registry data via OAI-PMH

**Usage**

```r
gif_oai_identify(...)

gif_oai_list_identifiers(prefix = "oai_dc", from = NULL,
                        until = NULL, set = NULL, token = NULL, as = "df", ...)

gif_oai_list_records(prefix = "oai_dc", from = NULL, until = NULL,
                    set = NULL, token = NULL, as = "df", ...)

gif_oai_list_metadataformats(id = NULL, ...)

gif_oai_list_sets(token = NULL, as = "df", ...)

gif_oai_get_records(ids, prefix = "oai_dc", as = "parsed", ...)
```

**Arguments**

- **prefix**  
  (character) A string to specify the metadata format in OAI-PMH requests issued to the repository. The default ("oai_dc") corresponds to the mandatory OAI unqualified Dublin Core metadata schema.

- **from**  
  (character) string giving datetstamp to be used as lower bound for datetstamp-based selective harvesting (i.e., only harvest records with datetstamps in the given range). Dates and times must be encoded using ISO 8601. The trailing Z must be used when including time. OAI-PMH implies UTC for data/time specifications.
until (character) Datestamp to be used as an upper bound, for datestamp-based selective harvesting (i.e., only harvest records with datestamps in the given range).

set (character) A set to be used for selective harvesting (i.e., only harvest records in the given set).

token (character) a token previously provided by the server to resume a request where it last left off. 50 is max number of records returned. We will loop for you internally to get all the records you asked for.

as (character) What to return. One of "df" (for data.frame; default), "list" (get a list), or "raw" (raw text). For gbif_oai_get_records, one of "parsed" or "raw"

id, ids (character) The OAI-PMH identifier for the record. Optional.

Details
These functions only work with GBIF registry data, and do so via the OAI-PMH protocol (https://www.openarchives.org/OAI/openarchivesprotocol.html)

Value
raw text, list or data.frame, depending on requested output via as parameter

Examples

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

today <- format(Sys.Date(), "%Y-%m-%d")
gbif_oai_list_identifiers(from = today)
gbif_oai_list_identifiers(set = "country:NL")

gbif_oai_list_records(from = today)
gbif_oai_list_records(set = "country:NL")

gbif_oai_list_metadataformats()
gbif_oai_list_metadataformats(id = "9c4e36c1-d3f9-49ce-8ec1-8c434fa9e6eb")

gbif_oai_list_sets()
gbif_oai_list_sets(as = "list")

gbif_oai_get_records("9c4e36c1-d3f9-49ce-8ec1-8c434fa9e6eb")
ids <- c("9c4e36c1-d3f9-49ce-8ec1-8c434fa9e6eb",
         "e0f1bb8a-2d81-4b2a-9194-d92848d3b82e")
gbif_oai_get_records(ids)

## End(Not run)
```
**gbif_photos**  
*View photos from GBIF.*

---

**Description**

View photos from GBIF.

**Usage**

```r
gbif_photos(input, output = NULL, which = "table", browse = TRUE)
```

**Arguments**

- `input`: Input output from `occ_search`
- `output`: Output folder path. If not given uses temporary folder.
- `which`: One of map or table (default).
- `browse`: (logical) Browse output (default: TRUE)

**Details**

The max number of photos you can see when which="map" is ~160, so cycle through if you have more than that.

**BEWARE**

The maps in the table view may not show up correctly if you are using RStudio

**Examples**

```r
## Not run:
res <- occ_search(mediatype = 'StillImage', return = "media")
gbif_photos(res)
gbif_photos(res, which='map')

res <- occ_search(scientificName = "Aves", mediatype = 'StillImage',
                   return = "media", limit=150)
gbif_photos(res)
gbif_photos(res, output = '~/barfoo')

## End(Not run)
```
installations

Installations metadata.

Description

Installations metadata.

Usage

installations(data = "all", uuid = NULL, query = NULL,
identifier = NULL, identifierType = NULL, limit = 100,
start = NULL, curlopts = list())

Arguments

data               The type of data to get. One or more of: 'contact', 'endpoint', 'dataset', 'comment', 'deleted', 'nonPublishing', or the special 'all'. Default: 'all'
uuid               UUID of the data node provider. This must be specified if data is anything other than 'all'.
query              Query nodes. Only used when data='all'. Ignored otherwise.
identifier         The value for this parameter can be a simple string or integer, e.g. identifier=120. This parameter doesn’t seem to work right now.
identifierType     Used in combination with the identifier parameter to filter identifiers by identifier type. See details. This parameter doesn’t seem to work right now.
limit              Number of records to return. Default: 100. Maximum: 1000.
start              Record number to start at. Default: 0. Use in combination with limit to page through results.
curlopts           list of named curl options passed on to HttpClient. see curl_options for curl options

Details

identifierType options:

- DOI No description.
- FTP No description.
- GBIF_NODE Identifies the node (e.g: DK for Denmark, sp2000 for Species 2000).
- GBIF_PARTICIPANT Participant identifier from the GBIF IMS Filemaker system.
- GBIF_PORTAL Indicates the identifier originated from an auto_increment column in the portal.data_provider or portal.data_resource table respectively.
- HANDLER No description.
- LSID Reference controlled by a separate system, used for example by DOI.
- SOURCE_ID No description.
isocodes

- UNKNOWN No description.
- URI No description.
- URL No description.
- UUID No description.

References

http://www.gbif.org/developer/registry#installations

Examples

## Not run:
installations(limit=5)
installations(query="france", limit = 25)
installations(uuid="b77901f9-d9b0-47fa-94e0-dd96450aa2b4")
installations(data='contact', uuid="2e029a0c-87af-42e6-87d7-f38a50b78201")
installations(data='endpoint', uuid="b77901f9-d9b0-47fa-94e0-dd96450aa2b4")
installations(data='dataset', uuid="b77901f9-d9b0-47fa-94e0-dd96450aa2b4")
installations(data='deleted', limit = 25)
installations(data='deleted', limit=2)
installations(data=c('deleted','nonPublishing'), limit=2)
installations(identifierType='DOI', limit=2)

# Pass on curl options
installations(data='deleted', curlopts = list(verbse=TRUE))

## End(Not run)

<table>
<thead>
<tr>
<th>isocodes</th>
<th>Table of country two character ISO codes, and GBIF names</th>
</tr>
</thead>
</table>

Description

- code. Two character ISO country code.
- name. Name of country.
- gbif_name. Name of country used by GBIF - this is the name you want to use when searching by country in this package.
**map_fetch**

*Fetch aggregated density maps of GBIF occurrences*

**Description**

This function is a wrapper for the GBIF mapping api version 2.0. The mapping API is a web map tile service making it straightforward to visualize GBIF content on interactive maps, and overlay content from other sources. It returns tile maps or vector maps with number of GBIF records per area unit that can be used in a variety of ways, for example in interactive leaflet web maps. Map details are specified by a number of query parameters, some of them optional. Full documentation of the GBIF mapping api can be found at https://www.gbif.org/developer/maps

---

**many-values**

*Many value inputs to some parameters*

**Description**

Many value inputs to some parameters

**Details**

There are some differences in how functions across `rgbif` behave with respect to many values given to a single parameter (let’s call it `foo`).

The following functions originally only iterated over many values passed to `foo` as a vector (e.g., `foo = c(1, 2)`) with completely separate HTTP requests. But now these functions also support passing in many values to the same HTTP request (e.g., `foo = "1; 2"`). This is a bit awkward, but means that we don’t break existing code.

- `occ_search()`
- `occ_data()`

The following functions, unlike those above, only support passing in many values to the same HTTP request, which is done like `foo = c("1", "2")`.

- `dataset_search()`
- `dataset_suggest()`
- `name_lookup()`
- `name_suggest()`
- `name_usage()`

Last, some parameters in the functions above don’t accept more than one, and some functions don’t have any parameters that accept more than one value (i.e., none of those listed above).

Each function that has at least some parameters that accept many values also has documentation on this issue.
map_fetch

Usage

map_fetch(source = "density", x = 0, y = 0, z = 0,
            format = "@1x.png", srs = "EPSG:4326", bin = NULL,
            hexPerTile = NULL, squareSize = NULL, style = "classic.point",
            taxonKey = NULL, datasetKey = NULL, country = NULL,
            publishingOrg = NULL, publishingCountry = NULL, year = NULL,
            basisOfRecord = NULL, ...)

Arguments

source (character) Either density for fast, precalculated tiles, or adhoc for any search.
         Default: density
x (integer) the zoom. Default: 0
y (integer) the column. Default: 0
z (integer) the row. Default: 0
format (character) The data format, one of:
       • .mvt for a vector tile
       • @Hx.png for a 256px raster tile
       • @1x.png for a 512px raster tile (the default)
       • @2x.png for a 1024px raster tile
       • @3x.png for a 2048px raster tile
       • @4x.png for a 4096px raster tile
srs (character) Spatial reference system. One of:
       • EPSG:3857 (Web Mercator)
       • EPSG:4326 (WGS84 plate care?)
       • EPSG:3575 (Arctic LAEA on 10 degrees E)
       • EPSG:3031 (Antarctic stereographic)
bin (character) square or hex to aggregate occurrence counts into squares or hexagons.
       Points by default. optional
hexPerTile (integer) sets the size of the hexagons (the number horizontally across a tile).
            optional
squareSize (integer) sets the size of the squares. Choose a factor of 4096 so they tessellate
correctly: probably from 8, 16, 32, 64, 128, 256, 512. optional
style (character) for raster tiles, choose from the available styles. Defaults to clas-
cic.point. optional. THESE DON’T WORK YET.
taxonKey (integer/numeric/character) search by taxon key, can only supply 1. optional
datasetKey (character) search by taxon key, can only supply 1. optional
country (character) search by taxon key, can only supply 1. optional
publishingOrg (character) search by taxon key, can only supply 1. optional
publishingCountry (character) search by taxon key, can only supply 1. optional
map_fetch

year (integer) integer that limits the search to a certain year or, if passing a vector of integers, multiple years, for example 1984 or c(2016, 2017, 2018) or 2010:2015 (years 2010 to 2015). optional

basisOfRecord (character) one or more basis of record states to include records with that basis of record. The full list is: c("OBSERVATION", "HUMAN_OBSERVATION", "MACHINE_OBSERVATION", "MATERIAL_SAMPLE", "PRESERVED_SPECIMEN", "FOSSIL_SPECIMEN", "LIVING_SPECIMEN", "LITERATURE", "UNKNOWN"). optional

curl options passed on to curl::HttpClient

Details

This function uses the arguments passed on to generate a query to the GBIF web map API. The API returns a web tile object as png that is read and converted into an R raster object. The break values or nbreaks generate a custom colour palette for the web tile, with each bin corresponding to one grey value. After retrieval, the raster is reclassified to the actual break values. This is a somewhat hacky but nonetheless functional solution in the absence of a GBIF raster API implementation.

We add extent and set the projection for the output. You can reproject after retrieving the output.

Value

an object of class RasterLayer if png format used, or raw bytes when mvt format chosen

Note

Styles don’t work yet, sorry, we’ll try to fix it asap.

Author(s)

Laurens Geffert <laurensgeffert@gmail.com>

References

https://www.gbif.org/developer/maps

Examples

```r
## Not run:
if (requireNamespace("png", quietly = TRUE) && requireNamespace("raster", quietly = TRUE)) {
  x <- map_fetch(taxonkey = 2480498, year = 2007:2011)
  x
  # gives a RasterLayer object
  class(x)
  # visualize
  library(raster)
  plot(x)

  # different srs
  ## 3857
```
name_backbone

Lookup names in the GBIF backbone taxonomy.

Description

Lookup names in the GBIF backbone taxonomy.

Usage

name_backbone(name, rank = NULL, kingdom = NULL, phylum = NULL,
class = NULL, order = NULL, family = NULL, genus = NULL,
strict = FALSE, verbose = FALSE, start = NULL, limit = 100,
curlopts = list())

Arguments

name (character) Full scientific name potentially with authorship (required)
rank (character) The rank given as our rank enum. (optional)
kingdom (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

phylum (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

class (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

order (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

family (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

genus (character) If provided default matching will also try to match against this if no direct match is found for the name alone. (optional)

strict (logical) If TRUE (fuzzy) matches only the given name, but never a taxon in the upper classification (optional)

verbose (logical) If TRUE show alternative matches considered which had been rejected.

start Record number to start at. Default: 0. Use in combination with limit to page through results.

limit Number of records to return. Default: 100. Maximum: 1000.

curlopts list of named curl options passed on to HttpClient. see curl_options for curl options

Details

If you don’t get a match GBIF gives back a list of length 3 with slots synonym, confidence, and matchType='NONE'.

Value

A list for a single taxon with many slots (with verbose=FALSE)

• default), or a list of length two, first element for the suggested taxon match, and a data.frame with alternative name suggestions resulting from fuzzy matching (with verbose=TRUE).

References

http://www.gbif.org/developer/species#searching

Examples

## Not run:
name_backbone(name='Helianthus annuus', kingdom='plants')
name_backbone(name='Helianthus', rank='genus', kingdom='plants')
name_backbone(name='Poa', rank='genus', family='Poaceae')

# Verbose - gives back alternatives
name_backbone(name='Helianthus annuus', kingdom='plants', verbose=TRUE)
name_issues

# Strictness
name_backbone(name='Poa', kingdom='plants', verbose=TRUE, strict=FALSE)
name_backbone(name='Helianthus annuus', kingdom='plants', verbose=TRUE,
strict=TRUE)

# Non-existent name - returns list of length 3 stating no match
name_backbone(name='Aso')
name_backbone(name='Oenante')

# Pass on curl options
name_backbone(name='Oenante', curlopts = list(verbos=TRUE))

## End(Not run)

---

name_issues

Table of GBIF name usage issues, with codes used in data output, full
issue name, and descriptions.

Description

Table has the following fields:

Usage

name_issues()

Details

- issue. Full name of the issue.
- description. Description of the issue.

Source

https://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/NameUsageIssue.html

See Also

gbif_issues()
name_lookup

Lookup names in all taxonomies in GBIF.

Description

This service uses fuzzy lookup so that you can put in partial names and you should get back those things that match. See examples below.

Faceting: If facet=FALSE or left to the default (NULL), no faceting is done. And therefore, all parameters with facet in their name are ignored (facetOnly, facetMincount, facetMultiselect).

Usage

```r
name_lookup(query = NULL, rank = NULL, higherTaxonKey = NULL,
status = NULL, isExtinct = NULL, habitat = NULL, nameType = NULL,
datasetKey = NULL, origin = NULL, nomenclaturalStatus = NULL,
limit = 100, start = 0, facet = NULL, facetMincount = NULL,
facetMultiselect = NULL, type = NULL, hl = NULL, verbose = FALSE,
return = "all", curlopts = list())
```

Arguments

- **query**: Query term(s) for full text search.
- **rank**: `CLASS, CULTIVAR, CULTIVAR_GROUP, DOMAIN, FAMILY, FORM, GENUS, INFORMAL, INFRAGENERIC_NAME, INFRAORDER, INFRASPECIFIC_NAME, INFRASUBSPECIFIC_NAME, KINGDOM, ORDER, PHYLUM, SECTION, SERIES, SPECIES, STRAIN, SUBCLASS, SUBFAMILY, SUBFORM, SUBGENUS, SUBKINGDOM, SUBORDER, SUBPHYLUM, SUBSECTION, SUBSERIES, SUBSPECIES, SUBTRIBE, SUBVARIETY, SUPERCLASS, SUPERFAMILY, SUPERORDER, SUPERPHYLUM, SUPRAGENERIC_NAME, TRIBE, UNRANKED, VARIETY`
- **higherTaxonKey**: Filters by any of the higher Linnean rank keys. Note this is within the respective checklist and not searching nub keys across all checklists. This parameter accepts many inputs in a vector (passed in the same request).
- **status**: Filters by the taxonomic status as one of:
  - **ACCEPTED**
  - **DETERMINATION_SYNONYM** Used for unknown child taxa referred to via spec, ssp, ...
  - **DOUBTFUL** Treated as accepted, but doubtful whether this is correct.
  - **HETEROOTYPIC_SYNONYM** More specific subclass of SYNONYM.
  - **HOMOTYPIC_SYNONYM** More specific subclass of SYNONYM.
  - **INTERMEDIATE_RANK_SYNONYM** Used in nub only.
  - **MISAPPLIED** More specific subclass of SYNONYM.
  - **PROPARTE_SYNONYM** More specific subclass of SYNONYM.
  - **SYNONYM** A general synonym, the exact type is unknown.
isExtinct  (logical) Filters by extinction status (e.g. isExtinct=TRUE)
habitat  (character) Filters by habitat. One of: marine, freshwater, or terrestrial
nameType  Filters by the name type as one of:
  • BLACKLISTED surely not a scientific name.
  • CANDIDATUS Candidatus is a component of the taxonomic name for a bacterium that cannot be maintained in a Bacteriology Culture Collection.
  • CULTIVAR a cultivated plant name.
  • DOUBTFUL doubtful whether this is a scientific name at all.
  • HYBRID a hybrid formula (not a hybrid name).
  • INFORMAL a scientific name with some informal addition like "cf." or indetermined like Abies spec.
  • SCINAME a scientific name which is not well formed.
  • VIRUS a virus name.
  • WELLFORMED a well formed scientific name according to present nomenclatural rules.
datasetKey  Filters by the dataset's key (a uuid)
origin  (character) Filters by origin. One of:
  • SOURCE
  • DENORMED_CLASSIFICATION
  • VERBATIM_ACCEPTED
  • EX_AUTHOR_SYNONYM
  • AUTONYM
  • BASIONYM_PLACEHOLDER
  • MISSING_ACCEPTED
  • IMPLICIT_NAME
  • PROPARTE
  • VERBATIM_BASIONYM
nomenclaturalStatus  Not yet implemented, but will eventually allow for filtering by a nomenclatural status enum
limit  Number of records to return. Hard maximum limit set by GBIF API: 99999.
start  Record number to start at. Default: 0.
facet  A vector/list of facet names used to retrieve the 100 most frequent values for a field. Allowed facets are: datasetKey, higherTaxonKey, rank, status, isExtinct, habitat, and nameType. Additionally threat and nomenclaturalStatus are legal values but not yet implemented, so data will not yet be returned for them.
facetMincount  Used in combination with the facet parameter. Set facetMincount=# to exclude facets with a count less than #, e.g. http://bit.ly/1bMdByP only shows the type value 'ACCEPTED' because the other statuses have counts less than 7,000,000
facetMultiselect  (logical) Used in combination with the facet parameter. Set facetMultiselect=TRUE to still return counts for values that are not currently filtered, e.g. http://bit.ly/19YLXPO still shows all status values even though status is being filtered by status=ACCEPTED
**type**  
Type of name. One of occurrence, checklist, or metadata.

**hl**  
(logical) Set hl=TRUE to highlight terms matching the query when in fulltext search fields. The highlight will be an emphasis tag of class gbifH1 e.g. query='plant', hl=TRUE. Fulltext search fields include: title, keyword, country, publishing country, publishing organization title, hosting organization title, and description. One additional full text field is searched which includes information from metadata documents, but the text of this field is not returned in the response.

**verbose**  
(logical) If TRUE, all data is returned as a list for each element. If FALSE (default) a subset of the data that is thought to be most essential is organized into a data.frame.

**return**  
One of data, meta, facets, hierarchy, names or all. If data, a data.frame with the data. facets returns the facets, if facets=TRUE, or empty list if facets=FALSE. meta returns the metadata for the entire call. names returns the vernacular (common) names for each taxon. all gives all data back in a list. Each element is NULL if there is no contents in that element. hierarchies and names slots are named by the GBIF key, which matches the first column of the data.frame in the data slot. So if you wanted to combine those somehow, you could easily do so using the key.

**curlopts**  
list of named curl options passed on to HttpClient. see curl_options for curl options

**Value**

A list of length five:

- **metadata**
- **data**: either a data.frame (verbose=FALSE, default) or a list (verbose=TRUE).
- **facets**
- **hierarchies**
- **names**

**Repeat parameter inputs**

Some parameters can take many inputs, and treated as 'OR' (e.g., a or b or c). The following take many inputs:

- **rank**
- **higherTaxonKey**
- **status**
- **habitat**
- **nameType**
- **datasetKey**
- **origin**

see also many-values
References

http://www.gbif.org/developer/species#searching

Examples

```r
## Not run:
# Look up names like mammalia
name_lookup(query='mammalia', limit = 20)

# Start with an offset
name_lookup(query='mammalia', limit=1)
name_lookup(query='mammalia', limit=1, start=2)

# large requests (paging is internally implemented).
# hard maximum limit set by GBIF API: 99999
# name_lookup(query = "Carnivora", limit = 10000)

# Get all data and parse it, removing descriptions which can be quite long
out <- name_lookup('Helianthus annuus', rank="species", verbose=TRUE)
lapply(out$data, function(x) {
  x[['names(x) %inX c("descriptions","descriptionsSerialized")']}
})

# Search for a genus, returning just data
name_lookup(query='Cnaemidophorus', rank="genus", return="data")

# Just metadata
name_lookup(query='Cnaemidophorus', rank="genus", return="meta")

# Just hierarchies
name_lookup(query='Cnaemidophorus', rank="genus", return="hierarchy")

# Just vernacular (common) names
name_lookup(query='Cnaemidophorus', rank="genus", return="names")

# Limit records to certain number
name_lookup('Helianthus annuus', rank="species", limit=2)

# Query by habitat
name_lookup(habitat = "terrestrial", limit=2)
name_lookup(habitat = "marine", limit=2)
name_lookup(habitat = "freshwater", limit=2)

# Using faceting
name_lookup(facet='status', limit=0, facetMincount='70000')
name_lookup(facet=c('status','higherTaxonKey'), limit=0,
  facetMincount='700000')
name_lookup(facet='nameType', limit=0)
name_lookup(facet='habitat', limit=0)
name_lookup(facet='datasetKey', limit=0)
name_lookup(facet='rank', limit=0)
```
name_lookup(facet='isExtinct', limit=0)

name_lookup(isExtinct=TRUE, limit=0)

# text highlighting
## turn on highlighting
res <- name_lookup(query='canada', hl=TRUE, limit=5)
res$data
name_lookup(query='canada', hl=TRUE, limit=45, return='data')
## you can pass the output to gbif_names() function
res <- name_lookup(query='canada', hl=TRUE, limit=5)
gbif_names(res)

# Lookup by datasetKey (set up sufficient high limit, API maximum: 99999)
# name_lookup(datasetKey='3f8a1297-3259-4700-91fc-acc4170b27ce',
# limit = 50000)

# Some parameters accept many inputs, treated as OR
name_lookup(rank = c("family", "genus"))
name_lookup(higherTaxonKey = c("119", "120", "121", "284"))
name_lookup(status = c("misapplied", "synonym"))$data
name_lookup(habitat = c("marine", "terrestrial"))
name_lookup(nameType = c("cultivar", "doubtful"))
name_lookup(datasetKey = c("73605f3a-af85-4ade-bbc5-522bf90d847",
"d7c60346-44b6-400d-ba27-8d3f6beff8a5"))
name_lookup(datasetKey = "289244ee-e1c1-49aa-b2d7-d379391ce265",
origin = c("SOURCE", "DENORMED_CLASSIFICATION"))

# Pass on curl options
name_lookup(query='Cnaemidophorus', rank="genus",
curlopts = list(quiet = TRUE))

## End(Not run)

---

**name_suggest**

A quick and simple autocomplete service that returns up to 20 name usages by doing prefix matching against the scientific name. Results are ordered by relevance.

**Description**

A quick and simple autocomplete service that returns up to 20 name usages by doing prefix matching against the scientific name. Results are ordered by relevance.

**Usage**

```r
name_suggest(q = NULL, datasetKey = NULL, rank = NULL,
             fields = NULL, start = NULL, limit = 100, curlopts = list())
```
name_suggest

Arguments

- **q** (character, required) Simple search parameter. The value for this parameter can be a simple word or a phrase. Wildcards can be added to the simple word parameters only, e.g. `q=puma`
- **datasetKey** (character) Filters by the checklist dataset key (a uuid, see examples)
- **rank** (character) A taxonomic rank. One of class, cultivar, cultivar_group, domain, family, form, genus, informal, infrageneric_name, infraorder, infraspecific_name, infrasubspecific_name, kingdom, order, phylum, section, series, species, strain, subclass, subfamily, subform, subgenus, subkingdom, suborder, subphylum, subsection, subseries, subspecies, subtribe, subvariety, superclass, superfamily, superorder, superfAMILY, suprageneric_name, tribe, unranked, or variety.
- **fields** (character) Fields to return in output data.frame (simply prunes columns off)
- **start** Record number to start at. Default: 0. Use in combination with `limit` to page through results.
- **limit** Number of records to return. Default: 100. Maximum: 1000.
- **curlopts** list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

Value

A data.frame with fields selected by fields arg.

Repeat parameter inputs

Some parameters can take many inputs, and treated as 'OR' (e.g., a or b or c). The following take many inputs:

- **rank**
- **datasetKey**

see also many-values

References

http://www.gbif.org/developer/species#searching

Examples

```r
# Not run:
name_suggest(q='Puma concolor')
name_suggest(q='Puma')
name_suggest(q='Puma', rank="genus")
name_suggest(q='Puma', rank="subspecies")
name_suggest(q='Puma', rank="species")
name_suggest(q='Puma', rank="infraspecific_name")
name_suggest(q='Puma', limit=2)
name_suggest(q='Puma', fields=c('key','canonicalName'))
```
name_suggest(q='Puma', fields=c('key','canonicalName',
'higherClassificationMap'))

# Some parameters accept many inputs, treated as OR
name_suggest(rank = c("family", "genus"))
name_suggest(datasetKey = c("73605f3a-af85-4ade-bbc5-522bfb90d847",
"d7c60346-44b6-400d-ba27-8d3fbeff8a5"))

# Pass on curl options
name_suggest(q='Puma', limit=200, curlopts = list(verbos=TRUE))

## End(Not run)

table(name_usage)

<table>
<thead>
<tr>
<th>Usage</th>
<th>Lookup details for specific names in all taxonomies in GBIF.</th>
</tr>
</thead>
</table>

**Description**

Lookup details for specific names in all taxonomies in GBIF.

**Usage**

```r
name_usage(key = NULL, name = NULL, data = "all", language = NULL,
datasetKey = NULL, uuid = NULL, rank = NULL, shortname = NULL,
start = 0, limit = 100, return = "all", curlopts = list())
```

**Arguments**

- **key** (numeric or character) A GBIF key for a taxon
- **name** (character) Filters by a case insensitive, canonical namestring, e.g. 'Puma concolor'
- **data** (character) Specify an option to select what data is returned. See Description below.
- **language** (character) Language, default is english
- **datasetKey** (character) Filters by the dataset’s key (a uuid). Must be length=1
- **uuid** (character) A dataset key
- **rank** (character) Taxonomic rank. Filters by taxonomic rank as one of: CLASS, CULTIVAR, CULTIVAR_GROUP, DOMAIN, FAMILY, FORM, GENUS, INFORMAL, INFRAGENERIC_NAME, INFRAORDER, INFRASPECIFIC_NAME, INFRASUBSPECIFIC_NAME, KINGDOM, ORDER, PHYLUM, SECTION, SERIES, SPECIES, STRAIN, SUBCLASS, SUBFAMILY, SUBFORM, SUBGENUS, SUBKINGDOM, SUBORDER, SUBPHYLUM, SUBSECTION, SUBSERIES, SUBSPECIES, SUBTRIBE, SUBVARIETY, SUPERCLASS, SUPERFAMILY, SUPERORDER, SUPERPHYLUM, SUPRAGENERIC_NAME, TRIBE, UNRANKED, VARIETY
- **shortname** (character) A short name for a dataset - it may not do anything
name_usage

start  Record number to start at. Default: 0.
limit  Number of records to return. Default: 100.
return  One of data, meta, or all. If data, a data.frame with the data. meta returns the metadata for the entire call. all gives all data back in a list.
curlopts  list of named curl options passed on to HttpClient. see curl_options for curl options

Details

This service uses fuzzy lookup so that you can put in partial names and you should get back those things that match. See examples below.

This function is different from name_lookup() in that that function searches for names. This function encompasses a bunch of API endpoints, most of which require that you already have a taxon key, but there is one endpoint that allows name searches (see examples below).

Note that data="verbatim" hasn't been working.

Options for the data parameter are: 'all', 'verbatim', 'name', 'parents', 'children', 'related', 'synonyms', 'descriptions','distributions', 'media', 'references', 'speciesProfiles', 'vernacularNames', 'typeSpecimens', 'root'

This function used to be vectorized with respect to the data parameter, where you could pass in multiple values and the function internally loops over each option making separate requests. This has been removed. You can still loop over many options for the data parameter, just use an lapply family function, or a for loop, etc.

See name_issues() for information on name usage issues related to the issues column in output from this function

Value

If return="all", a list of length two, with metadata and data, each as data.frame's. If return="meta" only the metadata data.frame, and if return="data" only the data data.frame

Repeat parameter inputs

These parameters used to accept many inputs, but no longer do:

• rank
• name
• langugae
• datasetKey

see also many-values

References

https://www.gbif.org/developer/species#nameUsages
Examples

```r
## Not run:
# A single name usage
name_usage(key=1)

# Name usage for a taxonomic name
name_usage(names='Puma', rank="GENUS")

# Name usage for all taxa in a dataset
# (set sufficient high limit, but less than 100000)
# name_usage(datasetKey = "9ff7d317-609b-4c08-bd86-3bc404b77c42", limit = 10000)
# All name usages
name_usage()

# References for a name usage
name_usage(key=2435099, data='references')

# Species profiles, descriptions
name_usage(key=3119195, data='speciesProfiles')
name_usage(key=3119195, data='descriptions')
name_usage(key=2435099, data='children')

# Vernacular names for a name usage
name_usage(key=3119195, data='vernacularNames')

# Limit number of results returned
name_usage(key=3119195, data='vernacularNames', limit=3)

# Search for names by dataset with datasetKey parameter
name_usage(datasetKey="d7d3dbf4-2cf0-4f39-9b2a-bb099caae36c")

# Search for a particular language
name_usage(key=3119195, language="FRENCH", data='vernacularNames')

# Get root usage with a uuid
name_usage(data = "root", uuid = "73605f3a-af85-4ade-bbc5-522bfb90d847")

# Search by language
name_usage(language = 'spanish')

# Pass on curl options
name_usage(name='Puma concolor', limit=300, curlopts = list(verbosetrue))
## End(Not run)
```

networks

Networks metadata.

Description

Networks metadata.
Usage

```
networks(data = "all", uuid = NULL, query = NULL,
          identifier = NULL, identifierType = NULL, limit = 100,
          start = NULL, curlopts = list())
```

Arguments

data  The type of data to get. One or more of: 'contact', 'endpoint', 'identifier', 'tag',
       'machineTag', 'comment', 'constituents', or the special 'all'. Default: 'all'

uuid  UUID of the data network provider. This must be specified if data is anything
       other than 'all'. Only 1 can be passed in

query Query nodes. Only used when data='all'. Ignored otherwise.

identifier The value for this parameter can be a simple string or integer, e.g. identifier=120.
            This parameter doesn’t seem to work right now.

identifierType Used in combination with the identifier parameter to filter identifiers by identifi-
                 er type. See details. This parameter doesn’t seem to work right now.

limit  Number of records to return. Default: 100. Maximum: 1000.

start  Record number to start at. Default: 0. Use in combination with limit to page
        through results.

curlopts list of named curl options passed on to HttpClient. see curl_options for curl
         options.

Details

identifierType options:

- DOI No description.
- FTP No description.
- GBIF_NODE Identifies the node (e.g: DK for Denmark, sp2000 for Species 2000).
- GBIF_PARTICIPANT Participant identifier from the GBIF IMS Filemaker system.
- GBIF_PORTAL Indicates the identifier originated from an auto_increment column in the por-
  ral.data_provider or portal.data_resource table respectively.
- HANDLER No description.
- LSID Reference controlled by a separate system, used for example by DOI.
- SOURCE_ID No description.
- UNKNOWN No description.
- URI No description.
- URL No description.
- UUID No description.

References

http://www.gbif.org/developer/registry#networks
Examples

```r
## Not run:
networks()
networks(uuid = '2b7c7b4f-4d4f-40d3-94de-c28b6fa054a6')

# curl options
networks(curlopts = list(verbosetrue))

## End(Not run)
```

---

**nodes**

<table>
<thead>
<tr>
<th>Nodes metadata.</th>
</tr>
</thead>
</table>

**Description**

Nodes metadata.

**Usage**

```r
nodes(data = "all", uuid = NULL, query = NULL, identifier = NULL, identifierType = NULL, limit = 100, start = NULL, isocode = NULL, curlopts = list())
```

**Arguments**

- **data**
  The type of data to get. One or more of: 'organization', 'endpoint', 'identifier', 'tag', 'machineTag', 'comment', 'pendingEndorsement', 'country', 'dataset', 'installation', or the special 'all'. Default: 'all'
- **uuid**
  UUID of the data node provider. This must be specified if data is anything other than 'all'.
- **query**
  Query nodes. Only used when data='all'
- **identifier**
  The value for this parameter can be a simple string or integer, e.g. identifier=120. This parameter doesn’t seem to work right now.
- **identifierType**
  Used in combination with the identifier parameter to filter identifiers by identifier type. See details. This parameter doesn’t seem to work right now.
- **limit**
  Number of records to return. Default: 100. Maximum: 1000.
- **start**
  Record number to start at. Default: 0. Use in combination with limit to page through results.
- **isocode**
  A 2 letter country code. Only used if data='country'.
- **curlopts**
  list of named curl options passed on to HttpClient. see curl_options for curl options
Details

identifierType options:

- DOI No description.
- FTP No description.
- GBIF_NODE Identifies the node (e.g: DK for Denmark, sp2000 for Species 2000).
- GBIF_PARTICIPANT Participant identifier from the GBIF IMS Filemaker system.
- GBIF_PORTAL Indicates the identifier originated from an auto_increment column in the portal.data_provider or portal.data_resource table respectively.
- HANDLER No description.
- LSID Reference controlled by a separate system, used for example by DOI.
- SOURCE_ID No description.
- UNKNOWN No description.
- URL No description.
- UUID No description.

References

http://www.gbif.org/developer/registry#nodes

Examples

```bash
## Not run:
nodes(limit=5)
nodes(data='identifier', uuid="03e816b3-8f58-49ae-bc12-4e18b358d6d9")
nodes(data=c('identifier', 'organization', 'comment'),
    uuidid="03e816b3-8f58-49ae-bc12-4e18b358d6d9")

uuids = c("8cb55387-7802-40e8-86d6-d357a583c596",
"02c40d2a-1cba-4633-90b7-e36e5e97aba8",
"7a17efec-0a6a-424c-b743-f7715852c3c1f",
"b797ce0f-47e6-4231-b048-6b62ca3b0f55",
"1193638d-32d1-43f0-a855-8727c94299d8",
"d3499f89-5bc0-4454-8cdb-60bead228a6d",
"cdc9736d-5ff7-4ece-9959-3c744360cdb3",
"a8b16421-8d0b-4ef3-8f22-09801a89255",
"8df8d012-8e64-4c8a-886e-521a3bdf6a23",
"b35cf8f1-748d-467a-adca-4f9170f2d0a4e",
"03e816b3-8f58-49ae-bc12-4e18b358d6d9",
"073d1223-70b1-4433-bb21-dd70afe3053b",
"07df2f9-5116-4922-9a8a-3e0912276a72",
"886f5148-c0a8-469b-84cc-cc5342f9242",
"9909d601-bda2-42df-9e63-a6d51847ebce",
"0e181bf-9c78-4676-bd03-5475e661bb8",
"109a1a1-c252-4a85-96e2-f5f4d5d088f4",
```

occ_count

Get number of occurrence records.

Description

Get number of occurrence records.

Usage

occ_count(taxonKey = NULL, georeferenced = NULL,
          basisOfRecord = NULL, datasetKey = NULL, date = NULL,
          typeStatus = NULL, country = NULL, year = NULL, from = 2000,
          to = 2012, type = "count", publishingCountry = "US",
          curlopts = list())

Arguments

taxonKey Species key
georeferenced Return only occurrence records with lat/long data (TRUE) or those that don’t have that data (FALSE, default). Note that you can also get record count with occ_search() by setting limit=0
basisOfRecord Basis of record
datasetKey Dataset key
date Collection date
typeStatus A type status. See typestatus() dataset for options
country Country data was collected in, two letter abbreviation. See http://countrycode.org/ for abbreviations.
year Year data were collected in
from Year to start at
to Year to end at
type One of count (default), schema, basis_of_record, countries, or year.
**occ_count**

**publishingCountry**
Publishing country, two letter ISO country code

**protocol**
Protocol. E.g., 'DWC_ARCHIVE'

**curlopts**
list of named curl options passed on to HttpClient. see curl_options for curl options

**Details**
There is a slight difference in the way records are counted here vs. results from occ_search(). For equivalent outcomes, in the occ_search() function use hasCoordinate=TRUE, and hasGeospatialIssue=FALSE to have the same outcome for this function using georeferenced=TRUE.

**Value**
A single numeric value, or a list of numerics.

**Supported dimensions**
That is, there are only a certain set of supported query parameter combinations that GBIF allows on this API route. They can be found with the call occ_count(type='schema'). They are also presented below:

- basisOfRecord
- basisOfRecord, country
- basisOfRecord, country, isGeoreferenced
- basisOfRecord, country, isGeoreferenced, taxonKey
- basisOfRecord, country, taxonKey
- basisOfRecord, datasetKey
- basisOfRecord, datasetKey, isGeoreferenced
- basisOfRecord, datasetKey, isGeoreferenced, taxonKey
- basisOfRecord, datasetKey, taxonKey
- basisOfRecord, isGeoreferenced
- basisOfRecord, isGeoreferenced, publishingCountry
- basisOfRecord, isGeoreferenced, publishingCountry, taxonKey
- basisOfRecord, publishingCountry
- basisOfRecord, publishingCountry, taxonKey
- basisOfRecord, taxonKey
- country
- country, datasetKey, isGeoreferenced
- country, isGeoreferenced
- country, isGeoreferenced, publishingCountry
- country, isGeoreferenced, taxonKey
- country, publishingCountry
• country, taxonKey
• country, typeStatus
• datasetKey
• datasetKey, isGeoreferenced
• datasetKey, isGeoreferenced, taxonKey
• datasetKey, issue
• datasetKey, taxonKey
• datasetKey, typeStatus
• isGeoreferenced
• isGeoreferenced, publishingCountry
• isGeoreferenced, publishingCountry, taxonKey
• isGeoreferenced, taxonKey
• issue
• publishingCountry
• publishingCountry, taxonKey
• publishingCountry, typeStatus
• taxonKey
• taxonKey, typeStatus
• typeStatus
• protocol
• year

References

http://www.gbif.org/developer/occurrence#metrics

Examples

```r
## Not run:
occ_count(basisOfRecord='OBSERVATION')
occ_count(georeferenced=TRUE)
occ_count(country='DE')
occ_count(country='CA', georeferenced=TRUE, basisOfRecord='OBSERVATION')
occ_count(datasetKey='9e7e1a06-0bf8-4087-bb61-dfe4f29e0f17')
occ_count(year=2012)
occ_count(taxonKey=2435099)
occ_count(taxonKey=2435099, georeferenced=TRUE)
occ_count(protocol='DWC_ARCHIVE')

# Just schema
occ_count(type='schema')

# Counts by basisOfRecord types
occ_count(type='basisOfRecord')
```
occ_data

# Counts by basisOfRecord types
occ_count(typeStatus='ALLOTYPE')
occ_count(typeStatus='HOLOTYPE')

# Counts by countries. publishingCountry must be supplied (default to US)
occ_count(type='countries')

# Counts by year. from and to years have to be supplied, default to 2000
# and 2012
occ_count(type='year', from=2000, to=2012)

# Counts by publishingCountry, must supply a country (default to US)
occ_count(type='publishingCountry')
occ_count(type='publishingCountry', country='BZ')

# Pass on curl options
occ_count(type='year', from=2000, to=2012, curlopts = list(verbose = TRUE))

## End(Not run)

---

**occ_data**

Search for GBIF occurrences - simplified for speed

**Description**

Search for GBIF occurrences - simplified for speed

**Usage**

```r
occ_data(taxonKey = NULL, scientificName = NULL, country = NULL,
          publishingCountry = NULL, hasCoordinate = NULL, typeStatus = NULL,
          recordNumber = NULL, lastInterpreted = NULL, continent = NULL,
          geometry = NULL, geom_big = "asis", geom_size = 40, geom_n = 10,
          recordedBy = NULL, basisOfRecord = NULL, datasetKey = NULL,
          eventoDate = NULL, catalogNumber = NULL, year = NULL,
          month = NULL, decimalLatitude = NULL, decimalLongitude = NULL,
          elevation = NULL, depth = NULL, institutionCode = NULL,
          collectionCode = NULL, hasGeospatialIssue = NULL, issue = NULL,
          search = NULL, mediaType = NULL, subgenusKey = NULL,
          repatriated = NULL, phylumKey = NULL, kingdomKey = NULL,
          classKey = NULL, orderKey = NULL, familyKey = NULL,
          genusKey = NULL, establishmentMeans = NULL, protocol = NULL,
          license = NULL, organismId = NULL, publishingOrg = NULL,
          stateProvince = NULL, waterBody = NULL, locality = NULL,
          limit = 500, start = 0, spellCheck = NULL, skip_validate = TRUE,
          curlopts = list())
```
Arguments

- **taxonKey**: (numeric) A taxon key from the GBIF backbone. All included and synonym taxa are included in the search, so a search for aves with taxonKey=212 (i.e. /occurrence/search?taxonKey=212) will match all birds, no matter which species. You can pass many keys by passing occ_search in a call to an lapply-family function (see last example below).

- **scientificName**: A scientific name from the GBIF backbone. All included and synonym taxa are included in the search.

- **country**: The 2-letter country code (as per ISO-3166-1) of the country in which the occurrence was recorded. See here [http://en.wikipedia.org/wiki/ISO_3166-1_alpha-2](http://en.wikipedia.org/wiki/ISO_3166-1_alpha-2)

- **publishingCountry**: The 2-letter country code (as per ISO-3166-1) of the country in which the occurrence was recorded.

- **hasCoordinate**: (logical) Return only occurrence records with lat/long data (TRUE) or all records (FALSE, default).

- **typeStatus**: Type status of the specimen. One of many options. See `_typestatus`

- **recordNumber**: Number recorded by collector of the data, different from GBIF record number. See [http://rs.tdwg.org/dwc/terms/#recordNumber](http://rs.tdwg.org/dwc/terms/#recordNumber) for more info

- **lastInterpreted**: Date the record was last modified in GBIF, in ISO 8601 format: yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Supports range queries, smaller, larger (e.g., ’1990,1991’, whereas ’1991,1990’ wouldn’t work)

- **continent**: Continent. One of africa, antarctica, asia, europe, north_america (North America includes the Caribbean and reaches down and includes Panama), oceania, or south_america

- **geometry**: Searches for occurrences inside a polygon described in Well Known Text (WKT) format. A WKT shape written as either POINT, LINESTRING, LINEARRING POLYGON, or MULTIPOLYGON. Example of a polygon: POLYGON((30.1 10.1, 20, 20 40, 40 40, 30.1 10.1)) would be queried as [http://bit.ly/1BzNwDq](http://bit.ly/1BzNwDq). See also the section **WKT** below.

- **geom_big**: (character) One of "axe", "bbox", or "asis" (default). See Details.

- **geom_size**: (integer) An integer indicating size of the cell. Default: 40. See Details.

- **geom_n**: (integer) An integer indicating number of cells in each dimension. Default: 10. See Details.

- **recordedBy**: The person who recorded the occurrence.

- **basisOfRecord**: Basis of record, as defined in our BasisOfRecord enum here [http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/BasisOfRecord.html](http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/BasisOfRecord.html) Acceptable values are:
  - FOSSIL_SPECIMEN An occurrence record describing a fossilized specimen.
  - HUMAN_OBSERVATION An occurrence record describing an observation made by one or more people.
- LITERATURE An occurrence record based on literature alone.
- LIVING_SPECIMEN An occurrence record describing a living specimen, e.g.
- MACHINE_OBSERVATION An occurrence record describing an observation made by a machine.
- OBSERVATION An occurrence record describing an observation.
- PRESERVED_SPECIMEN An occurrence record describing a preserved specimen.
- UNKNOWN Unknown basis for the record.

**datasetKey**
The occurrence dataset key (a uuid)

**eventDate**
Occurrence date in ISO 8601 format: yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Supports range queries, smaller, larger (e.g., '1990,1991', whereas '1991,1990' wouldn't work)

**catalogNumber**
An identifier of any form assigned by the source within a physical collection or digital dataset for the record which may not be unique, but should be fairly unique in combination with the institution and collection code.

**year**
The 4 digit year. A year of 98 will be interpreted as AD 98. Supports range queries, smaller, larger (e.g., '1990,1991', whereas '1991,1990' wouldn't work)

**month**
The month of the year, starting with 1 for January. Supports range queries, smaller, larger (e.g., '1,2', whereas '2,1' wouldn't work)

**decimalLatitude**
Latitude in decimals between -90 and 90 based on WGS 84. Supports range queries, smaller, larger (e.g., '25,30', whereas '30,25' wouldn't work)

**decimalLongitude**
Longitude in decimals between -180 and 180 based on WGS 84. Supports range queries (e.g., '-0.4,-0.2', whereas '-0.2,-0.4' wouldn't work).

**elevation**
Elevation in meters above sea level. Supports range queries, smaller, larger (e.g., '5,30', whereas '30,5' wouldn't work)

**depth**
Depth in meters relative to elevation. For example 10 meters below a lake surface with given elevation. Supports range queries, smaller, larger (e.g., '5,30', whereas '30,5' wouldn't work)

**institutionCode**
An identifier of any form assigned by the source to identify the institution the record belongs to. Not guaranteed to be unique.

**collectionCode**
An identifier of any form assigned by the source to identify the physical collection or digital dataset uniquely within the text of an institution.

**hasGeospatialIssue**
(logical) Includes/excludes occurrence records which contain spatial issues (as determined in our record interpretation), i.e. hasGeospatialIssue=TRUE returns only those records with spatial issues while hasGeospatialIssue=FALSE includes only records without spatial issues. The absence of this parameter returns any record with or without spatial issues.

**issue**
(character) One or more of many possible issues with each occurrence record. See Details. Issues passed to this parameter filter results by the issue.
search  Query terms. The value for this parameter can be a simple word or a phrase.
mediaType  Media type. Default is NULL, so no filtering on mediatype. Options: NULL, 'MovingImage', 'Sound', and 'StillImage'.
subgenusKey  (numeric) Subgenus classification key.
repatriated  (character) Searches for records whose publishing country is different to the country where the record was recorded in.
phylumKey  (numeric) Phylum classification key.
kingdomKey  (numeric) Kingdom classification key.
classKey  (numeric) Class classification key.
orderKey  (numeric) Order classification key.
familyKey  (numeric) Family classification key.
genusKey  (numeric) Genus classification key.
establishmentMeans  (character) EstablishmentMeans, possible values include: INTRODUCED, INVASIVE, MANAGED, NATIVE, NATURALISED, UNCERTAIN
protocol  (character) Protocol or mechanism used to provide the occurrence record. See Details for possible values
license  (character) The type license applied to the dataset or record. Possible values: CC0_1_0, CC_BY_4_0, CC_BY_NC_4_0, UNSPECIFIED, and UNSUPPORTED
organismId  (numeric) An identifier for the Organism instance (as opposed to a particular digital record of the Organism). May be a globally unique identifier or an identifier specific to the data set.
publishingOrg  (character) The publishing organization key (a UUID).
stateProvince  (character) The name of the next smaller administrative region than country (state, province, canton, department, region, etc.) in which the Location occurs.
waterBody  (character) The name of the water body in which the locations occur.
locality  (character) The specific description of the place.
limit  Number of records to return. Default: 500. Note that the per request maximum is 300, but since we set it at 500 for the function, we do two requests to get you the 500 records (if there are that many). Note that there is a hard maximum of 200,000, which is calculated as the limit+start, so start=199,000 and limit=200 won't work
start  Record number to start at. Use in combination with limit to page through results. Note that we do the paging internally for you, but you can manually set the start parameter
spellCheck  (logical) If TRUE ask GBIF to check your spelling of the value passed to the search parameter. IMPORTANT: This only checks the input to the search parameter, and no others. Default: FALSE
skip_validate  (logical) whether to skip wicket::wkt_validate call or not. passed down to check_wkt(). Default: TRUE
curlopts  list of named curl options passed on to HttpClient. see curl_options for curl options
...  additional facet parameters
Details

**protocol parameter options:**

- **BIOCASE** - A BioCASe protocol compliant service.
- **DIGIR** - A DiGIR service endpoint.
- **DIGIR_MANIS** - A DiGIR service slightly modified for the MANIS network.
- **DWC_ARCHIVE** - A Darwin Core Archive as defined by the Darwin Core Text Guidelines.
- **EML** - A single EML metadata document in any EML version.
- **FEED** - Syndication feeds like RSS or ATOM of various flavors.
- **OAI_PMH** - The Open Archives Initiative Protocol for Metadata Harvesting.
- **OTHER** - Any other service not covered by this enum so far.
- **TAPIR** - A TAPIR service.
- **TCS_RDF** - Taxon Concept data given as RDF based on the TDWG ontology.
- **TCS_XML** - A Taxon Concept Schema document.
- **WFS** - An OGC Web Feature Service.
- **WMS** - An OGC Web Map Service.

**Multiple parameters:** Note that you can pass in a vector to one of taxonKey, scientificName, datasetKey, catalogNumber, recordedBy, geometry, country, publishingCountry, recordNumber, search, institutionCode, collectionCode, decimalLatitude, decimalLongitude, depth, year, typeS-status, lastInterpreted, continent, or mediatype parameters in a function call, but not a vector >1 of these parameters at the same time

**Hierarchies:** hierarchies are returned with each occurrence object. There is no option no to return them from the API. However, within the occ_search function you can select whether to return just hierarchies, just data, all of data and hierarchies and metadata, or just metadata. If all hierarchies are the same we just return one for you.

**Data:** By default only three data fields are returned: name (the species name), decimallatitude, and decimallongitude. Set parameter minimal=false if you want more data.

**Nerds:** You can pass parameters not defined in this function into the call to the GBIF API to control things about the call itself using . . . . See an example below that passes in the verbose function to get details on the http call.

**Scientific names vs. taxon keys:** In the previous GBIF API and the version of rgbif that wrapped that API, you could search the equivalent of this function with a species name, which was convenient. However, names are messy right. So it sorta makes sense to sort out the species key numbers you want exactly, and then get your occurrence data with this function. GBIF has added a parameter scientificName to allow searches by scientific names in this function - which includes synonym taxa. **Note:** that if you do use the scientificName parameter, we will check internally that it’s not a synonym of an accepted name, and if it is, we’ll search on the accepted name. If you want to force searching by a synonym do so by finding the GBIF identifier first with any name functions, then pass that ID to the taxonKey parameter.

**WKT:** Examples of valid WKT objects:

- 'POLYGON((-19.5 34.1, 27.8 34.1, 35.9 68.1, -25.3 68.1, -19.5 34.1))'
• 'MULTIPOLYGON(((-123 38,-116 38,-116 43,-123 43,-123 38)),((-97 41,-93 41,-93 45,-97 45,-97 41)))'
• 'POINT(-120 40)'
• 'LINESTRING(3 4,10 50,20 25)'
• 'LINEARRING' ???' - Not sure how to specify this. Anyone?

Note that GBIF expects counter-clockwise winding order for WKT. You can supply clockwise WKT, but GBIF treats it as an exclusion, so you get all data not inside the WKT area. `occ_download()` behaves differently in that you should simply get no data back at all with clockwise WKT.

**Long WKT**: Options for handling long WKT strings: Note that long WKT strings are specially handled when using `occ_search` or `occ_data`. Here are the three options for long WKT strings (> 1500 characters), set one of these three via the parameter `geom_big`:

- asis - the default setting. This means we don’t do anything internally. That is, we just pass on your WKT string just as we’ve done before in this package.
- axe - this option uses the `geoaxe` package to chop up your WKT string in to many polygons, which then leads to a separate data request for each polygon piece, then we combine all data back together to give to you. Note that if your WKT string is not of type polygon, we drop back to asis as there’s no way to chop up linestrings, etc. This option will in most cases be slower than the other two options. However, this polygon splitting approach won’t have the problem of the disconnect between how many records you want and what you actually get back as with the bbox option.

This method uses `chop`, which uses GridTopology from the `sp` package, which has two parameters `cellsize` and `cells.dim` that we use to chop up polygons. You can tweak those parameters here by tweaking `geom_size` and `geom_n`. `geom_size` seems to be more useful in toggling the number of WKT strings you get back.

See `wkt_parse` to manually break make WKT bounding box from a larger WKT string, or break a larger WKT string into many smaller ones.
- bbox - this option checks whether your WKT string is longer than 1500 characters, and if it is we create a bounding box from the WKT, do the GBIF search with that bounding box, then prune the resulting data to only those occurrences in your original WKT string. There is a big caveat however. Because we create a bounding box from the WKT, and the `limit` parameter determines some subset of records to get, then when we prune the resulting data to the WKT, the number of records you get could be less than what you set with your `limit` parameter. However, you could set the limit to be high enough so that you get all records back found in that bounding box, then you’ll get all the records available within the WKT.

**Range queries**: A range query is as it sounds - you query on a range of values defined by a lower and upper limit. Do a range query by specifying the lower and upper limit in a vector like `depth=’50,100’`. It would be more R like to specify the range in a vector like `c(50,100)`, but that sort of syntax allows you to do many searches, one for each element in the vector - thus range queries have to differ. The following parameters support range queries.

- `decimalLatitude`
- `decimalLongitude`
- `depth`
- `elevation`
• eventDate
• lastInterpreted
• month
• year

**Issue:** The options for the issue parameter (from http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/OccurrenceIssue.html):

- BASIS_OF_RECORD_INVALID The given basis of record is impossible to interpret or seriously different from the recommended vocabulary.
- CONTINENT_COUNTRY_MISMATCH The interpreted continent and country do not match up.
- CONTINENT_DERIVED_FROM_COORDINATES The interpreted continent is based on the coordinates, not the verbatim string information.
- CONTINENT_INVALID Uninterpretable continent values found.
- COORDINATE_INVALID Coordinate value given in some form but GBIF is unable to interpret it.
- COORDINATE_OUT_OF_RANGE Coordinate has invalid lat/lon values out of their decimal max range.
- COORDINATE_REPROJECTED The original coordinate was successfully reprojected from a different geodetic datum to WGS84.
- COORDINATE_REPROJECTION_FAILED The given decimal latitude and longitude could not be reprojected to WGS84 based on the provided datum.
- COORDINATE_REPROJECTION_SUSPICIOUS Indicates successful coordinate reprojec-tion according to provided datum, but which results in a datum shift larger than 0.1 decimal degrees.
- COORDINATE_ROUNDED Original coordinate modified by rounding to 5 decimals.
- COUNTRY_COORDINATE_MISMATCH The interpreted occurrence coordinates fall outside of the indicated country.
- COUNTRY_DERIVED_FROM_COORDINATES The interpreted country is based on the co-ordinates, not the verbatim string information.
- COUNTRY_INVALID Uninterpretable country values found.
- COUNTRY_MISMATCH Interpreted country for dwc:country and dwc:countryCode contradict each other.
- DEPTH_MIN_MAX_SWAPPED Set if supplied min>max
- DEPTH_NON_NUMERIC Set if depth is a non numeric value
- DEPTH_NOT_METRIC Set if supplied depth is not given in the metric system, for example using feet instead of meters
- DEPTH_UNLIKELY Set if depth is larger than 11.000m or negative.
- ELEVATION_MIN_MAX_SWAPPED Set if supplied min > max elevation
- ELEVATION_NON_NUMERIC Set if elevation is a non numeric value
- ELEVATION_NOT_METRIC Set if supplied elevation is not given in the metric system, for example using feet instead of meters
• **ELEVATION_UNLIKELY** Set if elevation is above the troposphere (17km) or below 11km (Mariana Trench).

• **GEODETIC_DATUM_ASSUMED_WGS84** Indicating that the interpreted coordinates assume they are based on WGS84 datum as the datum was either not indicated or interpretable.

• **GEODETIC_DATUM_INVALID** The geodetic datum given could not be interpreted.

• **IDENTIFIED_DATE_INVALID** The date given for dwc:dateIdentified is invalid and can't be interpreted at all.

• **IDENTIFIED_DATE_UNLIKELY** The date given for dwc:dateIdentified is in the future or before Linnean times (1700).

• **MODIFIED_DATE_INVALID** A (partial) invalid date is given for dc:modified, such as a non-existing date, invalid zero month, etc.

• **MODIFIED_DATE_UNLIKELY** The date given for dc:modified is in the future or predates Unix time (1970).

• **MULTIMEDIA_DATE_INVALID** An invalid date is given for dc:created of a multimedia object.

• **MULTIMEDIA_URI_INVALID** An invalid uri is given for a multimedia object.

• **PRESUMED_NEGATED_LATITUDE** Latitude appears to be negated, e.g. 32.3 instead of -32.3

• **PRESUMED_NEGATED_LONGITUDE** Longitude appears to be negated, e.g. 32.3 instead of -32.3

• **PRESUMED_SWAPPED_COORDINATE** Latitude and longitude appear to be swapped.

• **RECORDED_DATE_INVALID** A (partial) invalid date is given, such as a non-existing date, invalid zero month, etc.

• **RECORDED_DATE_MISMATCH** The recording date specified as the eventDate string and the individual year, month, day are contradicting.

• **RECORDED_DATE_UNLIKELY** The recording date is highly unlikely, falling either into the future or represents a very old date before 1600 that predates modern taxonomy.

• **REFERENCES_URI_INVALID** An invalid uri is given for dc:references.

• **TAXON_MATCH_FUZZY** Matching to the taxonomic backbone can only be done using a fuzzy, non exact match.

• **TAXON_MATCH_HIGHER_RANK** Matching to the taxonomic backbone can only be done on a higher rank and not the scientific name.

• **TAXON_MATCH_NONE** Matching to the taxonomic backbone cannot be done cause there was no match at all or several matches with too little information to keep them apart (homonyms).

• **TYPE_STATUS_INVALID** The given type status is impossible to interpret or seriously different from the recommended vocabulary.

• **ZERO_COORDINATE** Coordinate is the exact 0/0 coordinate, often indicating a bad null coordinate.

**Counts:** There is a slight difference in the way records are counted here vs. results from occ_count. For equivalent outcomes, in this function use hasCoordinate=TRUE, and hasGeospatialIssue=FALSE to have the same outcome using occ_count with isGeoreferenced=TRUE
This does nearly the same thing as `occ_search()`, but is a bit simplified for speed, and is for the most common use case where user just wants occurrence data, and not other information like taxon hierarchies and media (e.g., images). A lot of time in `occ_search()` is used parsing data to be more useable downstream. We do less of that in this function.

**Value**

An object of class `gbif_data`, which is a S3 class list, with slots for metadata (`meta`) and the occurrence data itself (`data`), and with attributes listing the user supplied arguments and whether it was a "single" or "many" search; that is, if you supply two values of the `datasetKey` parameter to searches are done, and it's a "many". `meta` is a list of length four with offset, limit, `endOfRecords` and count fields. `data` is a tibble (aka `data.frame`).

**References**

http://www.gbif.org/developer/occurrence#search

**See Also**

`downloads()`, `occ_search()`

**Examples**

```r
## Not run:
(key <- name_backbone(name='Encelia californica')$speciesKey)
occ_data(taxonKey = key, limit = 4)
(res <- occ_data(taxonKey = key, limit = 400))

# Return 20 results, this is the default by the way
(key <- name_suggest(q='Helianthus annuus', rank='species')$key[1])
occ_data(taxonKey=key, limit=20)

# Instead of getting a taxon key first, you can search for a name directly
# However, note that using this approach (with \code{scientificName="..."})
# you are getting synonyms too. The results for using \code{scientificName}
# and \code{taxonKey} parameters are the same in this case, but I wouldn't
# be surprised if for some names they return different results
occ_data(scientificName = 'Ursus americanus', curlopts=list(verbse=TRUE))
key <- name_backbone(name = 'Ursus americanus', rank='species')$usageKey
occ_data(taxonKey = key)

# Search by dataset key
occ_data(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', limit=10)

# Search by catalog number
occ_data(catalogNumber="49366", limit=10)
# separate requests: use a vector of strings
occ_data(catalogNumber=c("49366","Bird.27847588"), limit=10)
# one request, many instances of same parameter: use semi-colon sep. string
occ_data(catalogNumber="49366;Bird.27847588", limit=10)

# Use paging parameters (limit and start) to page. Note the different results
```
# for the two queries below.
occ_data(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', start=10, limit=5)
occ_data(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', start=20, limit=5)

# Many dataset keys
## separate requests: use a vector of strings
occ_data(datasetKey=c("50c9509d-22c7-4a22-a47d-8c48425ef4a7", "7b5d6a48-f762-11e1-a439-00145eb45e9a"), limit=20)
## one request, many instances of same parameter: use semi-colon sep. string
v="50c9509d-22c7-4a22-a47d-8c48425ef4a7;7b5d6a48-f762-11e1-a439-00145eb45e9a"
occ_data(datasetKey = v, limit=20)

# Search by recorder
occ_data(recordedBy="smith", limit=20)

# Many collector names
## separate requests: use a vector of strings
occ_data(recordedBy=c("smith", "BJ Stacey"), limit=10)
## one request, many instances of same parameter: use semi-colon sep. string
occ_data(recordedBy=recordedBy="smith; BJ Stacey", limit=10)

# Pass in curl options for extra fun
occ_data(taxonKey=2433407, limit=20, curlopts=list(verbosetrue))
occ_data(taxonKey=2433407, limit=20, curlopts = list(
  noprogress = FALSE,
  progressfunction = function(down, up) {
    cat(sprintf("up: %d | down %d\n", up, down))
    return(TRUE)
  }
)
ove_data(taxonKey=2433407, limit=20, curlopts=list(timeout_ms=1))

# Search for many species
splist <- c('Cyanocitta stelleri', 'Junco hyemalis', 'Aix sponsa')
keys <- sapply(splist, function(x) name_suggest(x)$key[1], USE.NAMES=FALSE)
## separate requests: use a vector of strings
occ_data(taxonKey = keys, limit=5)
## one request, many instances of same parameter: use semi-colon sep. string
occ_data(taxonKey = paste0(keys, collapse = ";"), limit=5)

# Search using a synonym name
# Note that you'll see a message printing out that the accepted name will
# be used
occ_data(scientificName = 'Pulsatilla patens', limit=5)

# Search on latitude and longitude
occ_data(decimallatitude=40, decimallongitude=-120, limit = 10)

# Search on a bounding box
## in well known text format
### polygon
### Search on a long WKT string - too long for a GBIF search API request

By default, a very long WKT string will likely cause a request failure as GBIF only handles strings up to about 1500 characters long. You can leave as is, or you can choose to break up your polygon into many, and do a separate request for each piece, and the output is put back together (see below)

#### Or, 2nd alternative, you could use the GBIF download API

```wkt
"POLYGON((-102.2 46.0,-93.9 46.0,-93.9 43.7,-102.2 43.7,-102.2 46.0)), "POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 40 10.1))"
```

### GBIF example query

```r
occ_data <- polygon(occ_data, geometry = "POLYGON((-123 38, -123 43, -116 43, -116 38, -123 38), 
(-97 41, -97 45, -93 45, -93 41, -97 41)))"
```

```r
occ_data(occ_data(occ_data, geometry = gsub("/n\s*", "", wkt), limit = 20)
```

```r
### polygon and taxonkey

```r
key <- name_suggest(q='Aesculus hippocastanum')$key1
```

```r
occ_data(occ_data, geometry = "POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 40 10.1)), 
```

```r
### or using bounding box, converted to WKT internally

```r
occ_data(occ_data, geometry = c(-125.0,38.4,-121.8,40.9), limit = 20)
```

```r
### you can search on many geometry objects

```r
### separate requests: use a vector of strings

```r
wkt <- c("POLYGON((-102.2 46.0,-93.9 46.0,-93.9 43.7,-102.2 43.7,-102.2 46.0)), "POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 40 10.1))"
```

```r
occ_data(occ_data, geometry = wkt, limit = 20)
```

```r
### one request, many instances of same parameter: use semi-colon sep. string

```r
occ_data(occ_data, geometry = paste0(wkt, collapse = ";"), limit = 20)
```
-2.732596993344635 46.25998980446569, -1.677989493444635 44.154980365192, -1.326346993444635 39.38493590580802, 2.189278080555365 41.44721797271696, 4.474434256555365 43.26556960428879, 2.18278080555365 46.7439686797322, 1.837715506555365 50.3492841273576, 6.935371756555365 49.67150849335254, 5.001778006555365 52.32557322465785, 7.814278080555365 51.6762709882223, 7.814278080555365 54.524591562317, 10.978340506555365 51.89375191441792, 10.978340506555365 55.43241335888528, 13.263496756555365 52.5399176118183)

wkt <- gsub("\n", " ", wkt)

### Default option with large WKT string fails
res <- occ_data(geom = wkt)

### if WKT too long, with 'geom_big=bbox': makes into bounding box
res <- occ_data(geom = wkt, geom_big = "bbox")

library("rgeos")
library("sp")
wktsp <- readWKT(wkt)
plot(wktsp)
coordinates(res$x$data) <- ~decimalLongitude+decimalLatitude
points(res$x$data)

### Or, use 'geom_big=axe'
(res <- occ_data(geom = wkt, geom_big = "axe"))

##### manipulate essentially number of polygons that result, so number of requests

##### default geom_size is 40

##### fewer calls
(res <- occ_data(geom = wkt, geom_big = "axe", geom_size=50))

##### more calls
(res <- occ_data(geom = wkt, geom_big = "axe", geom_size=30))

# Search on country
occ_data(country='US', limit=20)

isocodes[grepl("France", isocodes$name),"code"]

occ_data(country='FR', limit=20)

occ_data(country='DE', limit=20)

### separate requests: use a vector of strings

occ_data(country=c('US','DE'), limit=20)

### one request, many instances of same parameter: use semi-colon sep. string

occ_data(country = 'US;DE', limit=20)

# Get only occurrences with lat/long data
occ_data(taxonKey=key, hasCoordinate=TRUE, limit=20)

# Get only occurrences that were recorded as living specimens
occ_data(basisOfRecord="LIVING_SPECIMEN", hasCoordinate=TRUE, limit=20)

# Get occurrences for a particular eventDate
occ_data(taxonKey=key, eventDate="2013", limit=20)

occ_data(taxonKey=key, year="2013", limit=20)

occ_data(taxonKey=key, month="6", limit=20)

# Get occurrences based on depth
key <- name Backbone(name='Salmo salar', kingdom='animals')$speciesKey

occ_data(taxonKey=key, depth=1, limit=20)
# Get occurrences based on elevation
key <- name_backbone(name='Puma concolor', kingdom='animals')$speciesKey
occ_data(taxonKey=key, elevation=50, hasCoordinate=TRUE, limit=20)

# Get occurrences based on institutionCode
occ_data(institutionCode="TLMF", limit=20)
### separate requests: use a vector of strings
occ_data(institutionCode=c("TLMF","ArtDatabanken"), limit=20)
### one request, many instances of same parameter: use semi-colon sep. string
occ_data(institutionCode = "TLMF;ArtDatabanken", limit=20)

# Get occurrences based on collectionCode
occ_data(collectionCode="Floristic Databases MV - Higher Plants", limit=20)
### separate requests: use a vector of strings
occ_data(collectionCode=c("Floristic Databases MV - Higher Plants", 
    "Artport"), limit = 20)
### one request, many instances of same parameter: use semi-colon sep. string
occ_data(collectionCode = "Floristic Databases MV - Higher Plants;Artport", 
    limit = 20)

# Get only those occurrences with spatial issues
occ_data(taxonKey=key, hasGeospatialIssue=TRUE, limit=20)

# Search using a query string
occ_data(search="kingfisher", limit=20)
### spell check - only works with the 'search' parameter
### spelled correctly - same result as above call
occ_data(search = "kingfisher", limit=20, spellCheck = TRUE)
### spelled incorrectly - stops with suggested spelling
# occ_data(search = "kajsdkla", limit=20, spellCheck = TRUE)
### spelled incorrectly - stops with many suggested spellings
### and number of results for each
# occ_data(search = "helir", limit=20, spellCheck = TRUE)

# search on repatriated - doesn't work right now
# occ_data(repatriated = "")

# search on phylumKey
occ_data(phylumKey = 7707728, limit = 5)

# search on kingdomKey
occ_data(kingdomKey = 1, limit = 5)

# search on classKey
occ_data(classKey = 216, limit = 5)

# search on orderKey
occ_data(orderKey = 7192402, limit = 5)

# search on familyKey
occ_data(familyKey = 3925, limit = 5)
```
# search on genusKey
occ_data(genusKey = 1935496, limit = 5)

# search on establishmentMeans
occ_data(establishmentMeans = "INVASIVE", limit = 5)
occ_data(establishmentMeans = "NATIVE", limit = 5)
occ_data(establishmentMeans = "UNCERTAIN", limit = 5)
### separate requests: use a vector of strings
occ_data(establishmentMeans = c("INVASIVE", "NATIVE"), limit = 5)
### one request, many instances of same parameter: use semi-colon sep. string
occ_data(establishmentMeans = "INVASIVE;NATIVE", limit = 5)

# search on protocol
occ_data(protocol = "DIGIR", limit = 5)

# search on license
occ_data(license = "CC_BY_4.0", limit = 5)

# search on organismId
occ_data(organismId = "100", limit = 5)

# search on publishingOrg
occ_data(publishingOrg = "28eb1a3f-1c15-4a95-931a-4af90ecb574d", limit = 5)

# search on stateProvince
occ_data(stateProvince = "California", limit = 5)

# search on waterBody
occ_data(waterBody = "pacific ocean", limit = 5)

# search on locality
occ_data(locality = "Trondheim", limit = 5)
### separate requests: use a vector of strings
res <- occ_data(locality = c("Trondheim", "Hovekilen"), limit = 5)
res$Trondheim$data
res$Hovekilen$data
### one request, many instances of same parameter: use semi-colon sep. string
occ_data(locality = "Trondheim;Hovekilen", limit = 5)

# Range queries
### See Detail for parameters that support range queries
occ_data(depth = '50,100', limit = 20)
### this is not a range search, but does two searches for each depth
occ_data(depth = c(50,100), limit = 20)

# Range search with year
occ_data(year = '1999,2000', limit=20)

# Range search with latitude
occ_data(decimalLatitude = '29.59,29.6', limit = 20)

# Search by specimen type status
```
```r
## Look for possible values of the typeStatus parameter looking at the typestatus dataset
occ_data(typeStatus = 'allotype', limit = 20)$data[, c('name', 'typeStatus')]

# Search by specimen record number
## This is the record number of the person/group that submitted the data, not GBIF's numbers
## You can see that many different groups have record number 1, so not super helpful
occ_data(recordNumber = 1, limit = 20)$data[, c('name', 'recordNumber', 'recordedBy')]

# Search by last time interpreted: Date the record was last modified in GBIF
## The lastInterpreted parameter accepts ISO 8601 format dates, including
## yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Range queries are accepted for lastInterpreted
occ_data(lastInterpreted = '2016-04-02', limit = 20)

# Search for occurrences with images
occ_data(mediaType = 'StillImage', limit = 20)
occ_data(mediaType = 'MovingImage', limit = 20)
occ_data(mediaType = 'Sound', limit = 20)

# Search by continent
## One of africa, antarctica, asia, europe, north_america, oceania, or
## south_america
occ_data(continent = 'south_america', limit = 20)$meta
occ_data(continent = 'africa', limit = 20)$meta
occ_data(continent = 'oceania', limit = 20)$meta
occ_data(continent = 'antarctica', limit = 20)$meta

### separate requests: use a vector of strings
occ_data(continent = c('south_america', 'oceania'), limit = 20)
### one request, many instances of same parameter: use semi-colon sep. string
occ_data(continent = 'south_america;oceania', limit = 20)

# Query based on issues - see Details for options
## one issue
x <- occ_data(taxonKey=1, issue='DEPTH_UNLIKELY', limit = 20)
x$data[, c('name', 'key', 'decimalLatitude', 'decimalLongitude', 'depth')]

## two issues
occ_data(taxonKey=1, issue=c('DEPTH_UNLIKELY', 'COORDINATE_ROUNDED'), limit = 20)

# Show all records in the Arizona State Lichen Collection that cant be matched to the GBIF
# backbone properly:
occ_data(datasetKey='84c8e1a0-f762-11e1-a439-00145eb45e9a',
         issue=c('TAXON_MATCH_NONE','TAXON_MATCH_HIGHERRANK'), limit = 20)

# Parsing output by issue
(res <- occ_data(geometry='POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))', limit = 50))
## what do issues mean, can print whole table, or search for matches
head(gbif_issues())
gbif_issues()[ gbif_issues()$code %in% c('cdround', 'cudc', 'gassXT', 'txmathi'), ]
## or parse issues in various ways
### remove data rows with certain issue classes
library('magrittr')
res %>% occ_issues(gass84)
### split issues into separate columns
res %>% occ_issues(mutate = "split")
### expand issues to more descriptive names
```
**occ_download**

Spin up a download request for GBIF occurrence data.

**Description**

Spin up a download request for GBIF occurrence data.

**Usage**

```r
occ_download(..., body = NULL, type = "and", format = "DWCA",
user = NULL, pwd = NULL, email = NULL, curlopts = list())

occ_download_prep(..., body = NULL, type = "and", format = "DWCA",
user = NULL, pwd = NULL, email = NULL, curlopts = list())
```

**Arguments**

- `...` One or more of query arguments to kick off a download job. If you use this, don’t use `body` parameter. All inputs must be character strings. See Details.
- `body` if you prefer to pass in the payload yourself, use this parameter. if use this, don’t pass anything to the dots. accepts either an R list, or JSON. JSON is likely easier, since the JSON library `jsonlite` requires that you unbox strings that shouldn’t be auto-converted to arrays, which is a bit tedious for large queries. optional
- `type` (character) One of equals (=), and (&), or (|), lessThan (<), lessThanOrEquals (<=), greaterThan (>), greaterThanOrEquals (>=), in, within, not (!), like
- `format` (character) The download format. One of DWCA (default), SIMPLE_CSV, or SPECIES_LIST
- `user` (character) User name within GBIF’s website. Required. See Details.
- `pwd` (character) User password within GBIF’s website. Required. See Details.
- `email` (character) Email address to receive download notice done email. Required. See Details.
- `curlopts` list of named curl options passed on to `HttpClient`. see `curl_options` for curl options
Details

Argument passed have to be passed as character (e.g., 'country = US'), with a space between key ('country'), operator ('='), and value ('US'). See the type parameter for possible options for the operator. This character string is parsed internally.

The value can be comma separated, in which case we’ll turn that into a predicate combined with the OR operator, for example, "taxonKey = 2480946,5229208" will turn into

```
{
  "type": "or",
  "predicates": [
    {
      "type": "equals",
      "key": "TAXON_KEY",
      "value": "2480946"
    },
    {
      "type": "equals",
      "key": "TAXON_KEY",
      "value": "5229208"
    }
  ]
}
```

Acceptable arguments to . . . are:

- taxonKey = 'TAXON_KEY'
- scientificName = 'SCIENTIFIC_NAME'
- country = 'COUNTRY'
- publishingCountry = 'PUBLISHING_COUNTRY'
- hasCoordinate = 'HAS_COORDINATE'
- hasGeospatialIssue = 'HAS_GEOSpatial_ISSUE'
- typeStatus = 'TYPE_STATUS'
- recordNumber = 'RECORD_NUMBER'
- lastInterpreted = 'LAST_INTERPRETED'
- continent = 'CONTINENT'
- geometry = 'GEOMETRY'
- basisOfRecord = 'BASIS_OF_RECORD'
- datasetKey = 'DATASET_KEY'
- eventDate = 'EVENT_DATE'
- catalogNumber = 'CATALOG_NUMBER'
- year = 'YEAR'
- month = 'MONTH'
- decimalLatitude = 'DECIMAL_LATITUDE'
• decimalLongitude = 'DECIMAL_LONGITUDE'
• elevation = 'ELEVATION'
• depth = 'DEPTH'
• institutionCode = 'INSTITUTION_CODE'
• collectionCode = 'COLLECTION_CODE'
• issue = 'ISSUE'
• mediatype = 'MEDIA_TYPE'
• recordedBy = 'RECORDED_BY'

geometry

When using the geometry parameter, make sure that your well known text (WKT) is formatted as GBIF expects it. They expect WKT to have a counter-clockwise winding order. For example, the following is clockwise
```
polygonHHMQYNU STNQL MRUNS VXNQL SUNY VXNQL RWNX STNQL MQYNU STNQII
```
whereas they expect the other order:
```
polygonHHMQYNU STNQL RWNX STNQL SUNY VXNQL MRUNS VXNQL MQYNU STNQII
```
Note that coordinate pairs are longitude latitude, longitude first, then latitude.
You should not get any results if you supply WKT that has clockwise winding order.
Also note that `occ_search()`/`occ_data()` behave differently with respect to WKT in that you can supply counter-clockwise WKT to those functions but they treat it as an exclusion, so get all data not inside the WKT area.

Methods

- `occ_download_prep`: prepares a download request, but DOES NOT execute it. Meant for use with `occ_download_queue()`
- `occ_download`: prepares a download request and DOES execute it

Authentication

For user, pwd, and email parameters, you can set them in one of three ways:

- Set them in your `.Rprofile` file with the names `gbif_user`, `gbif_pwd`, and `gbif_email`
- Set them in your `.Renviron`, `bash_profile` (or similar) file with the names `GBIF_USER`, `GBIF_PWD`, and `GBIF_EMAIL`
- Simply pass strings to each of the parameters in the function call

We strongly recommend the second option - storing your details as environment variables as it’s the most widely used way to store secrets.
See `?Startup` for help.

Query length

GBIF has a limit of 12,000 characters for a download query. This means that you can have a pretty long query, but at some point it may lead to an error on GBIF's side and you'll have to split your query into a few.
Note

see downloads for an overview of GBIF downloads methods

References

See the API docs http://www.gbif.org/developer/occurrence#download for more info, and the predicates docs http://www.gbif.org/developer/occurrence#predicates

Examples

```r
## Not run:
# occ_download("basisOfRecord = LITERATURE")
# occ_download("taxonKey = 3119195")
# occ_download('decimalLatitude > 50')
# occ_download('elevation >= 9000')
# occ_download('decimalLatitude >= 65')
# occ_download("country = US")
# occ_download("institutionCode = TLMF")
# occ_download("catalogNumber = Bird.27847588")

# download format
# z <- occ_download('decimalLatitude >= 75', format = "SPECIES_LIST")

# res <- occ_download('taxonKey = 7264332', 'hasCoordinate = TRUE')

# pass output directly, or later, to occ_download_meta for more information
# occ_download('decimalLatitude > 75') %>% occ_download_meta

# Multiple queries
# occ_download('decimalLatitude >= 65', 'decimalLatitude <= -65', type="or")
# gg <- occ_download('depth = 80', 'taxonKey = 2343454', type="or")

# complex example with many predicates
# shows example of how to do date ranges for both year and month
# res <- occ_download(
#   "taxonKey = 2480946.5229208",
#   "basisOfRecord = HUMAN_OBSERVATION, OBSERVATION, MACHINE_OBSERVATION",
#   "country = US",
#   "hasCoordinate = true",
#   "hasGeospatialIssue = false",
#   "year >= 1999",
#   "year <= 2011",
#   "month >= 3",
#   "month <= 8"
# )

# Using body parameter - pass in your own complete query
## as JSON
query1 <- '{"creator":"sckott",
 "notification_address":["myrmecocystus@gmail.com"],
 "predicate":{"type":"and","predicates":[
 {"type":"equals","key":"TAXON_KEY","value":"7264332"},
 ```
### occ_download_cancel

*Cancel a download creation process.*

#### Description

Cancel a download creation process.

#### Usage

```r
occ_download_cancel(key = NULL, user = NULL, pwd = NULL, curlopts = list())
```

```r
occ_download_cancel_staged(user = NULL, pwd = NULL, limit = 20, start = 0, curlopts = list())
```

#### Arguments

- **key** (character) A key generated from a request, like that from `occ_download`. Required.
- **user** (character) User name within GBIF's website. Required. See Details.
- **pwd** (character) User password within GBIF's website. Required. See Details.
occ_download_datasets

`curlopts` list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

`limit` Number of records to return. Default: 20

`start` Record number to start at. Default: 0

**Details**

Note, these functions only cancel a job in progress. If your download is already prepared for you, this won’t do anything to change that.

occ_download_cancel cancels a specific job by download key - returns success message

occ_download_cancel_staged cancels all jobs with status RUNNING or PREPARING - if none are found, returns a message saying so - if some found, they are cancelled, returning message saying so

**Note**

see downloads for an overview of GBIF downloads methods

**Examples**

```r
## Not run:
# occ_download_cancel(key="0003984-140910143529206")
# occ_download_cancel_staged()

## End(Not run)
```

---

occ_download_datasets  *List datasets for a download*

**Description**

List datasets for a download

**Usage**

```r
occ_download_datasets(key, curlopts = list())
```

**Arguments**

- **key** A key generated from a request, like that from `occ_download`
- **curlopts** list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

**Value**

a list with slots of offset, limit, endOfRecords, count, and results. results has an array of the datasets
Note
see downloads for an overview of GBIF downloads methods

Examples
```r
## Not run:
occ_download_datasets(key="0003983-140910143529206")
## End(Not run)
```

```
occ_download_dataset_activity
  Lists the downloads activity of a dataset
```

Description
Lists the downloads activity of a dataset

Usage
```r
occ_download_dataset_activity(dataset, curlopts = list())
```

Arguments
- `dataset` (character) A dataset key
- `curlopts` list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

Value
a list with slots of offset, limit, endOfRecords, count, and results. results has an array of the downloads for the dataset

Note
see downloads for an overview of GBIF downloads methods

Examples
```r
## Not run:
res <- occ_download_dataset_activity("7f2edc10-f762-11e1-a439-00145eb45e9a")
res
res$count
## End(Not run)
```
Occ_download_get

Get a download from GBIF.

Description

Get a download from GBIF.

Usage

```r
occ_download_get(key, path = ".", overwrite = FALSE,
curlopts = list())
```

Arguments

- **key**
  A key generated from a request, like that from `occ_download`

- **path**
  Path to write zip file to. Default: ".", with a .zip appended to the end.

- **overwrite**
  Will only overwrite existing path if TRUE.

- **curlopts**
  List of named curl options passed on to `HttpClient`. See `curl_options` for curl options.

Details

Downloads the zip file to a directory you specify on your machine. `crl::HttpClient()` is used internally to write the zip file to disk. See `crl::writing-options`. This function only downloads the file. See `occ_download_import` to open a downloaded file in your R session. The speed of this function is of course proportional to the size of the file to download. For example, a 58 MB file on my machine took about 26 seconds.

Note

See `downloads` for an overview of GBIF downloads methods.

Examples

```r
## Not run:
occ_download_get("0000006-140928181241064")
occ_download_get("0003983-140910143529206", overwrite = TRUE)

## End(Not run)
```
import a downloaded file from GBIF.

Usage

occ_download_import(x = NULL, key = NULL, path = ".", fill = TRUE, ...)

as.download(path = ".", key = NULL)

## S3 method for class 'character'
as.download(path = ".", key = NULL)

## S3 method for class 'download'
as.download(path = ".", key = NULL)

Arguments

x The output of a call to occ_download_get
key A key generated from a request, like that from occ_download
path Path to unzip file to. Default: "." Writes to folder matching zip file name
fill (logical) (default: FALSE). If TRUE then in case the rows have unequal length,
blank fields are implicitly filled, passed on to fill parameter in data.table::fread.
If you get problems with this function crashing it could be due to data.table
failing, in which case try setting fill=FALSE

... parameters passed on to data.table::fread()

Details

You can provide either x as input, or both key and path. We use data.table::fread() internally
to read data.

Value

a tibble (data.frame)

Note

see downloads for an overview of GBIF downloads methods
occ_download_list

_lists the downloads created by a user.

Description

Lists the downloads created by a user.

Usage

occ_download_list(user = NULL, pwd = NULL, limit = 20, start = 0, curlopts = list())

Arguments

user (character) User name within GBIF’s website. Required. See Details.
pwd (character) User password within GBIF’s website. Required. See Details.
limit Number of records to return. Default: 20
start Record number to start at. Default: 0
curlopts list of named curl options passed on to HttpClient. see curl_options for curl options
Note

see downloads for an overview of GBIF downloads methods

Examples

```r
## Not run:
occ_download_list(user="sckott")
occ_download_list(user="sckott", limit = 5)
occ_download_list(user="sckott", start = 21)

## End(Not run)
```

---

**occ_download_meta**

Retrieves the occurrence download metadata by its unique key.

**Description**

Retrieves the occurrence download metadata by its unique key.

**Usage**

```
occ_download_meta(key, curlopts = list())
```

**Arguments**

- **key**: A key generated from a request, like that from `occ_download`
- **curlopts**: list of named curl options passed on to `HttpClient`. see `curl_options` for curl options

**Note**

see downloads for an overview of GBIF downloads methods

**Examples**

```r
## Not run:
occ_download_meta(key="0003983-140910143529206")
occ_download_meta("0000066-140928181241064")

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

*Download requests in a queue*

**Description**

Download requests in a queue

**Usage**

```
occ_download_queue(..., .list = list(), status_ping = 10)
```

**Arguments**

- `...`: any number of `occ_download()` requests
- `.list`: any number of `occ_download_prep()` requests
- `status_ping`: (integer) seconds between pings checking status of the download request. Generally larger numbers for larger requests. Default: 10 (i.e., 10 seconds). Must be 10 or greater.

**Details**

This function is a convenience wrapper around `occ_download()`, allowing the user to kick off any number of requests, while abiding by GBIF rules of 3 concurrent requests per user.

**Value**

A list of `occ_download` class objects, see `occ_download_get()` to fetch data.

**How it works**

It works by using lazy evaluation to collect your requests into a queue. Then it kicks off the first 3 requests. Then in a while loop, we check status of those requests, and when any request finishes, we kick off the next, and so on. So in theory, there may not always strictly be 3 running concurrently, but the function will usually provide for 3 running concurrently.

**Beware**

This function is still in development. There’s a lot of complexity to this problem. We’ll be rolling out fixes and improvements in future versions of the package, so expect to have to adjust your code with new versions.

**Note**

See downloads for an overview of GBIF downloads methods.
Examples

```r
## Not run:
# passing occ_download() requests via ...
out <- occ_download_queue(
  occ_download('taxonKey = 3119195', "year = 1976"),
  occ_download('taxonKey = 3119195', "year = 2001"),
  occ_download('taxonKey = 3119195', "year = 2001", "month <= 8"),
  occ_download('taxonKey = 5229208', "year = 2011"),
  occ_download('taxonKey = 2480946', "year = 2015"),
  occ_download("country = NZ", "year = 1999", "month = 3"),
  occ_download("catalogNumber = Bird.27847588", "year = 1998", "month = 2")
)

# supports <= 3 requests too
out <- occ_download_queue(
  occ_download("country = NZ", "year = 1999", "month = 3"),
  occ_download("catalogNumber = Bird.27847588", "year = 1998", "month = 2")
)

# using pre-prepared requests via .list
keys <- c(7905507, 5384395, 8911082)
queries <- list()
for (i in seq_along(keys)) {
  queries[[i]] <- occ_download_prep(
    paste0("taxonKey = ", keys[i]),
    "basisOfRecord = HUMAN_OBSERVATION, OBSERVATION",
    "hasCoordinate = true",
    "hasGeospatialIssue = false",
    "year = 1993"
  )
}
out <- occ_download_queue(.list = queries)
out

# another pre-prepared example
yrs <- 1930:1934
length(yrs)
queries <- list()
for (i in seq_along(yrs)) {
  queries[[i]] <- occ_download_prep(
    "taxonKey = 2877951",
    "basisOfRecord = HUMAN_OBSERVATION, OBSERVATION",
    "hasCoordinate = true",
    "hasGeospatialIssue = false",
    paste0("year = ", yrs[i])
  )
}
out <- occ_download_queue(.list = queries)
out
## End(Not run)
```
Description

Facet GBIF occurrences

Usage

occ_facet(facet, facetMincount = NULL, curlopts = list(), ...)

Arguments

- **facet** (character) a character vector of length 1 or greater. Required.
- **facetMincount** (numeric) minimum number of records to be included in the faceting results
- **curlopts** list of named curl options passed on to HttpClient. see curl_options for curl options
- **...** Facet parameters, such as for paging based on each facet variable, e.g., country.facetLimit

Details

All fields can be faceted on except for last "lastInterpreted", "eventDate", and "geometry"

If a faceted variable is not found, it is silently dropped, returning nothing for that query

Value

A list of tibbles (data.frame's) for each facet (each element of the facet parameter).

See Also

occ_search() also has faceting ability, but can include occurrence data in addition to facets

Examples

```r
## Not run:
occ_facet(facet = "country")

# facetMincount - minimum number of records to be included
# in the faceting results
occ_facet(facet = "country", facetMincount = 3000000L)
occ_facet(facet = c("country", "basisOfRecord"))

# paging with many facets
occ_facet(
    facet = c("country", "basisOfRecord", "hasCoordinate"),
    country.facetLimit = 3,
    basisOfRecord.facetLimit = 6
)
```
# paging
## limit
occ_facet(facet = "country", country.facetLimit = 3)

## offset
occ_facet(facet = "country", country.facetLimit = 3,
          country.facetOffset = 3)

# Pass on curl options
occ_facet(facet = "country", country.facetLimit = 3,
curlopts = list(verbose = TRUE))

## End(Not run)

---

**occ_fields**

*Vector of fields in the output for the function* `occ_search()`

---

**occ_get**

*Get data for specific GBIF occurrences.*

---

**Description**

Get data for specific GBIF occurrences.

**Usage**

```r
occ_get(key = NULL, return = "all", verbatim = FALSE,
        fields = "minimal", curlopts = list())
```

**Arguments**

- **key**: Occurrence key
- **return**: One of data, hier, meta, or all. If "data", a data.frame with the data. "hier" returns the classifications in a list for each record. meta returns the metadata for the entire call. 'all' gives all data back in a list. Ignored if `verbatim=TRUE`.
- **verbatim**: Return verbatim object (TRUE) or cleaned up object (FALSE, default).
- **fields**: (character) Default ("minimal") will return just taxon name, key, latitude, and longitude. 'all' returns all fields. Or specify each field you want returned by name, e.g. fields = c('name', 'decimalLatitude', 'altitude').
- **curlopts**: list of named curl options passed on to `HttpClient`. see `curl_options` for curl options.
occ_issues

Value

A data.frame or list of data.frame’s.

References

https://www.gbif.org/developer/occurrence#occurrence

Examples

```r
## Not run:
occ_get(key=855998194, return="data")
occ_get(key=855998194, "hier")
occ_get(key=855998194, 'all')

# many occurrences
occc_get(key=c(101010, 240713150, 855998194), return="data")

# Verbatim data
occc_get(key=855998194, verbatim=TRUE)
occc_get(key=855998194, fields='all', verbatim=TRUE)
occc_get(key=855998194, fields=c('scientificName', 'lastCrawled', 'county'),
  verbatim=TRUE)
occc_get(key=c(855998194, 620594291), verbatim=TRUE)
occc_get(key=c(855998194, 620594291),
  fields=c('scientificName', 'decimalLatitude', 'basisOfRecord'),
  verbatim=TRUE)

# Pass in curl options
occc_get(key=855998194, curlopts = list(verb=TRUE))

## End(Not run)
```

---

**occ_issues**

*Parse and examine further GBIF issues on a dataset*

**Description**

Parse and examine further GBIF issues on a dataset

**Usage**

`occ_issues(.data, ..., mutate = NULL)`
Arguments

.data  Output from a call to `occ_search()`, `occ_data()`, or `occ_download_import()`, but only if `return="all"`, or `return="data"`, otherwise function stops with error. The data from `occ_download_import` is just a regular data.frame so you can pass in a data.frame to this function, but if it doesn’t have certain columns it will fail.

... Named parameters to only get back (e.g., `cdround`), or to remove (e.g. `-cdround`).

mutate  (character) One of:

- `split` Split issues into new columns
- `split_expand` Split into new columns, and expand issue names
- `expand` Expand issue abbreviated codes into descriptive names. for downloads datasets, this is not super useful since the issues come to you as expanded already.

For `split` and `split_expand`, values in cells become y ("yes") or n ("no")

Details

See also the vignette Cleaning data using GBIF issues

Note that you can also query based on issues, e.g., `occ_search(taxonKey=1, issue='DEPTH_UNLIKELY')`. However, I imagine it’s more likely that you want to search for occurrences based on a taxonomic name, or geographic area, not based on issues, so it makes sense to pull data down, then clean as needed using this function.

This function only affects the data element in the gbif class that is returned from a call to `occ_search()`. Maybe in a future version we will remove the associated records from the hierarchy and media elements as they are remove from the data element.

You’ll notice that we sort columns to make it easier to glimpse the important parts of your data, namely taxonomic name, taxon key, latitude and longitude, and the issues. The columns are unchanged otherwise.

References


Examples

```r
## Not run:
## what do issues mean, can print whole table, or search for matches
head(gbif_issues())
iss <- c('cdround','cudc','gass84','txmathi')
gbif_issues()[ gbif_issues()$code %in% iss, ]

# compare out data to after occ_issues use
(out <- occ_search(limit=100))
out %>% occ_issues(cround)

# occ_data
```
(out <- occ_data(limit=100))
out %>% occ_issues(cround)

# Parsing output by issue
(res <- occ_data(
    geometry='POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))',
    limit = 600))

## or parse issues in various ways
### include only rows with cround issue
gg <- res %>% occ_issues(cround)
NROW(res$data)
NROW(gg$data)
head(res$data)[,c(1:5)]
head(gg$data)[,c(1:5)]

### remove data rows with certain issue classes
res %>% occ_issues(-cround, -cudc)

### split issues into separate columns
res %>% occ_issues(mutate = "split")
res %>% occ_issues(-cudc, -mdatunl, mutate = "split")
res %>% occ_issues(gass84, mutate = "split")

### expand issues to more descriptive names
res %>% occ_issues(mutate = "expand")

### split and expand
res %>% occ_issues(mutate = "split_expanding")

### split, expand, and remove an issue class
res %>% occ_issues(-cround, mutate = "split_expanding")

## Or you can use occ_issues without the pipe
occ_issues(res, -cround, mutate = "split_expanding")

# from GBIF downloaded data via occ_download and friends
res <- occ_download_get(key="0000066-149281248124812", overwrite=TRUE)
x <- occ_download_import(res)
occ_issues(x, -txmathi) occ_issues(x, txmathi) occ_issues(x, gass84) occ_issues(x, zerocond) occ_issues(x, gass84, txmathi) occ_issues(x, mutate = "split") occ_issues(x, -gass84, mutate = "split") occ_issues(x, mutate = "expand") occ_issues(x, mutate = "split_expanding")

# occ_search/occ_data with many inputs - give slightly different output
# format than normal 2482598, 2498387
xyz <- occ_data(taxonKey = c(9362842, 2492483, 2435099), limit = 300)
xyz
occ_issues_lookup  
Lookup occurrence issue definitions and short codes

Description
Lookup occurrence issue definitions and short codes

Usage
occ_issues_lookup(issue = NULL, code = NULL)

Arguments
issue  
Full name of issue, e.g., CONTINENT_COUNTRY_MISMATCH

code  
an issue short code, e.g., ccm

Examples
occ_issues_lookup(issue = 'CONTINENT_COUNTRY_MISMATCH')
occ_issues_lookup(issue = 'MULTIMEDIA_DATE_INVALID')
occ_issues_lookup(issue = 'ZERO_COORDINATE')
occ_issues_lookup(code = 'cdiv')

occ_metadata  
Search for catalog numbers, collection codes, collector names, and institution codes.

Description
Search for catalog numbers, collection codes, collector names, and institution codes.

Usage
occ_metadata(type = "catalogNumber", q = NULL, limit = 5,
        pretty = TRUE, curlopts = list())
Arguments

- **type**: Type of data, one of catalogNumber, collectionCode, recordedBy, or institutionCode. Unique partial strings work too, like 'cat' for catalogNumber.
- **q**: Search term
- **limit**: Number of results, default=5
- **pretty**: Pretty as true (Default) uses cat to print data, FALSE gives character strings.
- **curlopts**: list of named curl options passed on to HttpClient. see curl_options for curl options.

References

http://www.gbif.org/developer/occurrence#search

Examples

```r
## Not run:
# catalog number
occ_metadata(type = "catalogNumber", q=122)

# collection code
occ_metadata(type = "collectionCode", q=12)

# institution code
occ_metadata(type = "institutionCode", q='GB')

# recorded by
occ_metadata(type = "recordedBy", q='scott')

# data as character strings
occ_metadata(type = "catalogNumber", q=122, pretty=FALSE)

# Change number of results returned
occ_metadata(type = "catalogNumber", q=122, limit=10)

# Partial unique type strings work too
occ_metadata(type = "cat", q=122)

# Pass on curl options
occ_metadata(type = "cat", q=122, curlopts = list(verbos = TRUE))

## End(Not run)
```

occ_search  

Search for GBIF occurrences

Description

Search for GBIF occurrences
Usage

```r
occ_search(taxonKey = NULL, scientificName = NULL, country = NULL,
        publishingCountry = NULL, hasCoordinate = NULL, typeStatus = NULL,
        recordNumber = NULL, lastInterpreted = NULL, continent = NULL,
        geometry = NULL, geom_big = "asis", geom_size = 40, geom_n = 10,
        recordedBy = NULL, basisOfRecord = NULL, datasetKey = NULL,
        eventDate = NULL, catalogNumber = NULL, year = NULL,
        month = NULL, decimalLatitude = NULL, decimalLongitude = NULL,
        elevation = NULL, depth = NULL, institutionCode = NULL,
        collectionCode = NULL, hasGeospatialIssue = NULL, issue = NULL,
        search = NULL, mediaType = NULL, subgenusKey = NULL,
        repatriated = NULL, phylumKey = NULL, kingdomKey = NULL,
        classKey = NULL, orderKey = NULL, familyKey = NULL,
        genusKey = NULL, establishmentMeans = NULL, protocol = NULL,
        license = NULL, organismId = NULL, publishingOrg = NULL,
        stateProvince = NULL, waterBody = NULL, locality = NULL,
        limit = 500, start = 0, fields = "all", return = "all",
        spellCheck = NULL, facet = NULL, facetMinCount = NULL,
        facetMultiSelect = NULL, skip_validate = TRUE, curlopts = list(),
        ...)```

Arguments

taxonKey (numeric) A taxon key from the GBIF backbone. All included and synonym taxa are included in the search, so a search for aves with taxononKey=212 (i.e. /occurrence/search?taxonKey=212) will match all birds, no matter which species. You can pass many keys by passing occ_search in a call to an lapply-family function (see last example below).

scientificName A scientific name from the GBIF backbone. All included and synonym taxa are included in the search.

country The 2-letter country code (as per ISO-3166-1) of the country in which the occurrence was recorded. See here [http://en.wikipedia.org/wiki/ISO_3166-1_alpha-2](http://en.wikipedia.org/wiki/ISO_3166-1_alpha-2)

country publishingCountry The 2-letter country code (as per ISO-3166-1) of the country in which the occurrence was recorded.

hasCoordinate (logical) Return only occurrence records with lat/long data (TRUE) or all records (FALSE, default).

typeStatus Type status of the specimen. One of many options. See ?typestatus

recordNumber Number recorded by collector of the data, different from GBIF record number. See [http://rs.tdwg.org/dwc/terms/#recordNumber](http://rs.tdwg.org/dwc/terms/#recordNumber) for more info

lastInterpreted Date the record was last modified in GBIF, in ISO 8601 format: yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Supports range queries, smaller,larger (e.g., ’1990,1991’, whereas ’1991,1990’ wouldn’t work)
continent

Continent. One of africa, antarctica, asia, europe, north_america (North America includes the Caribbean and reaches down and includes Panama), oceania, or south_america

geometry

Searches for occurrences inside a polygon described in Well Known Text (WKT) format. A WKT shape written as either POINT, LINSTRING, LINERARRING, POLYGON, or MULTIPOLYGON. Example of a polygon: POLYGON((30.1 10.1, 20, 20 40, 40 40, 30.1 10.1)) would be queried as http://bit.ly/1BzNw0q. See also the section WKT below.

geom_big

(character) One of "axe", "bbox", or "asis" (default). See Details.

geom_size

(integer) An integer indicating size of the cell. Default: 40. See Details.

geom_n

(integer) An integer indicating number of cells in each dimension. Default: 10. See Details.

recordedBy

The person who recorded the occurrence.

basisOfRecord

Basis of record, as defined in our BasisOfRecord enum here http://gbif.github.io/gbif-api/apidocs/org/gbif/api/vocabulary/BasisOfRecord.html Acceptable values are:

- FOSSIL_SPECIMEN An occurrence record describing a fossilized specimen.
- HUMAN_OBSERVATION An occurrence record describing an observation made by one or more people.
- LITERATURE An occurrence record based on literature alone.
- LIVING_SPECIMEN An occurrence record describing a living specimen, e.g.
- MACHINE_OBSERVATION An occurrence record describing an observation made by a machine.
- OBSERVATION An occurrence record describing an observation.
- PRESERVED_SPECIMEN An occurrence record describing a preserved specimen.
- UNKNOWN Unknown basis for the record.

datasetKey

The occurrence dataset key (a uuid)

eventDate

Occurrence date in ISO 8601 format: yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Supports range queries, smaller,larger (e.g., '1990,1991', whereas '1991,1990' wouldn't work)

catalogNumber

An identifier of any form assigned by the source within a physical collection or digital dataset for the record which may not unique, but should be fairly unique in combination with the institution and collection code.

year

The 4 digit year. A year of 98 will be interpreted as AD 98. Supports range queries, smaller,larger (e.g., '1990,1991', whereas '1991,1990' wouldn't work)

month

The month of the year, starting with 1 for January. Supports range queries, smaller,larger (e.g., '1,2', whereas '2,1' wouldn't work)

decimalLatitude

Latitude in decimals between -90 and 90 based on WGS 84. Supports range queries, smaller,larger (e.g., '25,30', whereas '30,25' wouldn't work)
decimalLongitude
Longitud in decimals between -180 and 180 based on WGS 84. Supports range queries (e.g., '-0.4,-0.2', whereas '-0.2,-0.4' wouldn’t work).

elevation
Elevation in meters above sea level. Supports range queries, smaller,larger (e.g., '5,30', whereas '30,5' wouldn’t work)

depth
Depth in meters relative to elevation. For example 10 meters below a lake surface with given elevation. Supports range queries, smaller,larger (e.g., '5,30', whereas '30,5' wouldn’t work)

institutionCode
An identifier of any form assigned by the source to identify the institution the record belongs to. Not guaranteed to be unique.

collectionCode
An identifier of any form assigned by the source to identify the physical collection or digital dataset uniquely within the text of an institution.

hasGeospatialIssue
(logical) Includes/excludes occurrence records which contain spatial issues (as determined in our record interpretation), i.e. hasGeospatialIssue=TRUE returns only those records with spatial issues while hasGeospatialIssue=FALSE includes only records without spatial issues. The absence of this parameter returns any record with or without spatial issues.

issue
(character) One or more of many possible issues with each occurrence record. See Details. Issues passed to this parameter filter results by the issue.

search
Query terms. The value for this parameter can be a simple word or a phrase.

mediaType
Media type. Default is NULL, so no filtering on mediatype. Options: NULL, 'MovingImage', 'Sound', and 'StillImage'.

subgenusKey
(numeric) Subgenus classification key.

repatriated
(character) Searches for records whose publishing country is different to the country where the record was recorded in.

phylumKey
(numeric) Phylum classification key.

kingdomKey
(numeric) Kingdom classification key.

classKey
(numeric) Class classification key.

orderKey
(numeric) Order classification key.

familyKey
(numeric) Family classification key.

genusKey
(numeric) Genus classification key.

establishmentMeans
(character) EstablishmentMeans, possible values include: INTRODUCED, INVASIVE, MANAGED, NATIVE, NATURALISED, UNCERTAIN

protocol
(character) Protocol or mechanism used to provide the occurrence record. See Details for possible values

license
(character) The type license applied to the dataset or record. Possible values: CC0_1_0, CC_BY_4_0, CC_BY_NC_4_0, UNSPECIFIED, and UNSUPPORTED

organismId
(numeric) An identifier for the Organism instance (as opposed to a particular digital record of the Organism). May be a globally unique identifier or an identifier specific to the data set.
Occurrence Search (occ_search)

- **publishingOrg** (character) The publishing organization key (a UUID).
- **stateProvince** (character) The name of the next smaller administrative region than country (state, province, canton, department, region, etc.) in which the Location occurs.
- **waterBody** (character) The name of the water body in which the locations occur.
- **locality** (character) The specific description of the place.
- **limit** Number of records to return. Default: 500. Note that the per request maximum is 300, but since we set it at 500 for the function, we do two requests to get you the 500 records (if there are that many). Note that there is a hard maximum of 200,000, which is calculated as the limit+start, so start=199,000 and limit=2000 won't work.
- **start** Record number to start at. Use in combination with limit to page through results. Note that we do the paging internally for you, but you can manually set the start parameter.
- **fields** (character) Default ('all') returns all fields. 'minimal' returns just taxon name, key, latitude, and longitude. Or specify each field you want returned by name, e.g. fields = c('name','latitude','elevation').
- **return** One of data, hier, meta, or all. If data, a data.frame with the data. hier returns the classifications in a list for each record. meta returns the metadata for the entire call. all gives all data back in a list.
- **spellCheck** (logical) If TRUE ask GBIF to check your spelling of the value passed to the search parameter. IMPORTANT: This only checks the input to the search parameter, and no others. Default: FALSE.
- **facet** (character) a character vector of length 1 or greater. Required.
- **facetMincount** (numeric) minimum number of records to be included in the faceting results.
- **facetMultiselect** (logical) Set to TRUE to still return counts for values that are not currently filtered. See examples. Default: FALSE.

**Faceting:** All fields can be faceted on except for last "lastInterpreted", "eventDate", and "geometry". You can do facet searches alongside searching occurrence data, and return both, or only return facets, or only occurrence data, etc.

- **skip_validate** (logical) whether to skip wicket::wkt_validate call or not. passed down to check_wkt(). Default: TRUE.
- **curlopts** list of named curl options passed on to HttpClient. see curl_options for curl options.

... additional facet parameters

**Details**

**protocol parameter options:**

- **BIOCASE** - A BioCASe protocol compliant service.
- **DIGIR** - A DiGIR service endpoint.
- **DIGIR_MANIS** - A DiGIR service slightly modified for the MANIS network.
• DWC_ARCHIVE - A Darwin Core Archive as defined by the Darwin Core Text Guidelines.
• EML - A single EML metadata document in any EML version.
• FEED - Syndication feeds like RSS or ATOM of various flavors.
• OAI_PMH - The Open Archives Initiative Protocol for Metadata Harvesting.
• OTHER - Any other service not covered by this enum so far.
• TAPIR - A TAPIR service.
• TCS_RDF - Taxon Concept data given as RDF based on the TDWG ontology.
• TCS_XML - A Taxon Concept Schema document.
• WFS - An OGC Web Feature Service.
• WMS - An OGC Web Map Service.

Multiple parameters: Note that you can pass in a vector to one of taxonKey, scientificName, datasetKey, catalogNumber, recordedBy, geometry, country, publishingCountry, recordNumber, search, institutionCode, collectionCode, decimalLatitude, decimalLongitude, depth, year, typeStatus, lastInterpreted, continent, or mediatype parameters in a function call, but not a vector >1 of these parameters at the same time.

Hierarchies: hierarchies are returned with each occurrence object. There is no option no to return them from the API. However, within the occ_search function you can select whether to return just hierarchies, just data, all of data and hierarchies and metadata, or just metadata. If all hierarchies are the same we just return one for you.

Data: By default only three data fields are returned: name (the species name), decimallatitude, and decimallongitude. Set parameter minimal=FALSE if you want more data.

Nerds: You can pass parameters not defined in this function into the call to the GBIF API to control things about the call itself using . . . . See an example below that passes in the verbose function to get details on the http call.

Scientific names vs. taxon keys: In the previous GBIF API and the version of rgbif that wrapped that API, you could search the equivalent of this function with a species name, which was convenient. However, names are messy right. So it sorts makes sense to sort out the species key numbers you want exactly, and then get your occurrence data with this function. GBIF has added a parameter scientificName to allow searches by scientific names in this function - which includes synonym taxa. Note: that if you do use the scientificName parameter, we will check internally that it’s not a synonym of an accepted name, and if it is, we’ll search on the accepted name. If you want to force searching by a synonym do so by finding the GBIF identifier first with any name_* functions, then pass that ID to the taxonKey parameter.

WKT: Examples of valid WKT objects:
  "POLYGON((-19.5 34.1, 27.8 34.1, 35.9 68.1, -25.3 68.1, -19.5 34.1))"
  "MULTIPOLYGON(((123 38,-116 38,-116 43,-123 43,-123 38)),((-97 41,-93 41,-93 45,-97 45,-97 41)))"
  "POINT(-120 40)"
  "LINESTRING(3 4,10 50,20 25)"
  "LINEARRING" - Not sure how to specify this. Anyone?
Note that GBIF expects counter-clockwise winding order for WKT. You can supply clockwise WKT, but GBIF treats it as an exclusion, so you get all data not inside the WKT area. `occ_download()` behaves differently in that you should simply get no data back at all with clockwise WKT.

**Long WKT**: Options for handling long WKT strings: Note that long WKT strings are specially handled when using `occ_search` or `occ_data`. Here are the three options for long WKT strings (> 1500 characters), set one of these three via the parameter `geom_big`:

- **asis** - the default setting. This means we don’t do anything internally. That is, we just pass on your WKT string just as we’ve done before in this package.
- **axe** - this option uses the `geoaxe` package to chop up your WKT string in to many polygons, which then leads to a separate data request for each polygon piece, then we combine all dat back together to give to you. Note that if your WKT string is not of type polygon, we drop back to asis as there’s no way to chop up linestrings, etc. This option will in most cases be slower than the other two options. However, this polygon splitting approach won’t have the problem of the disconnect between how many records you want and what you actually get back as with the bbox option.

This method uses `chop`, which uses `gridTopology` from the `sp` package, which has two parameters `cellsize` and `cells.dim` that we use to chop up polygons. You can tweak those parameters here by tweaking `geom_size` and `geom_n`. `geom_size` seems to be more useful in toggling the number of WKT strings you get back.

See `wkt_parse` to manually break make WKT bounding box from a larger WKT string, or break a larger WKT string into many smaller ones.

- **bbox** - this option checks whether your WKT string is longer than 1500 characters, and if it is we create a bounding box from the WKT, do the GBIF search with that bounding box, then prune the resulting data to only those occurrences in your original WKT string. There is a big caveat however. Because we create a bounding box from the WKT, and the `limit` parameter determines some subset of records to get, then when we prune the resulting data to the WKT, the number of records you get could be less than what you set with your `limit` parameter. However, you could set the limit to be high enough so that you get all records back found in that bounding box, then you’ll get all the records available within the WKT.

**Range queries**: A range query is as it sounds - you query on a range of values defined by a lower and upper limit. Do a range query by specifying the lower and upper limit in a vector like `depth='50,100'`. It would be more R like to specify the range in a vector like `c(50,100)`, but that sort of syntax allows you to do many searches, one for each element in the vector - thus range queries have to differ. The following parameters support range queries.

- `decimalLatitude`
- `decimalLongitude`
- `depth`
- `elevation`
- `eventDate`
- `lastInterpreted`
- `month`
- `year`

- BASIS_OF_RECORD_INVALID The given basis of record is impossible to interpret or seriously different from the recommended vocabulary.
- CONTINENT_COUNTRY_MISMATCH The interpreted continent and country do not match up.
- CONTINENT_DERIVED_FROM_COORDINATES The interpreted continent is based on the coordinates, not the verbatim string information.
- CONTINENT_INVALID Uninterpretable continent values found.
- COORDINATE_INVALID Coordinate value given in some form but GBIF is unable to interpret it.
- COORDINATE_OUT_OF_RANGE Coordinate has invalid lat/lon values out of their decimal max range.
- COORDINATE_REPROJECTED The original coordinate was successfully reprojected from a different geodetic datum to WGS84.
- COORDINATE_REPROJECTION_FAILED The given decimal latitude and longitude could not be reprojected to WGS84 based on the provided datum.
- COORDINATE_REPROJECTION_SUSPICIOUS Indicates successful coordinate reprojec-
tion according to provided datum, but which results in a datum shift larger than 0.1 decimal degrees.
- COORDINATE_ROUNDED Original coordinate modified by rounding to 5 decimals.
- COUNTRY_COORDINATE_MISMATCH The interpreted occurrence coordinates fall outside of the indicated country.
- COUNTRY_DERIVED_FROM_COORDINATES The interpreted country is based on the coordinates, not the verbatim string information.
- COUNTRY_INVALID Uninterpretable country values found.
- COUNTRY_MISMATCH Interpreted country for dwc:country and dwc:countryCode con-
tradict each other.
- DEPTH_MIN_MAX_SWAPPED Set if supplied min > max
- DEPTH_NON_NUMERIC Set if depth is a non numeric value
- DEPTH_NOT_METRIC Set if supplied depth is not given in the metric system, for example using feet instead of meters
- DEPTH_UNLIKELY Set if depth is larger than 11.000m or negative.
- ELEVATION_MIN_MAX_SWAPPED Set if supplied min > max elevation
- ELEVATION_NON_NUMERIC Set if elevation is a non numeric value
- ELEVATION_NOT_METRIC Set if supplied elevation is not given in the metric system, for ex-
ample using feet instead of meters
- ELEVATION_UNLIKELY Set if elevation is above the troposphere (17km) or below 11km (Mariana Trench).
- GEODETIC_DATUM_ASSUMED_WGS84 Indicating that the interpreted coordinates assume they are based on WGS84 datum as the datum was either not indicated or interpretable.
- GEODETIC_DATUM_INVALID The geodetic datum given could not be interpreted.
- IDENTIFIED_DATE_INVALID The date given for dwc:dateIdentified is invalid and can’t be interpreted at all.
• IDENTIFIED_DATE_UNLIKELY  The date given for dwc:dateIdentified is in the future or before Linnean times (1700).

• MODIFIED_DATE_INVALID  A (partial) invalid date is given for dc:modified, such as a non existing date, invalid zero month, etc.

• MODIFIED_DATE_UNLIKELY  The date given for dc:modified is in the future or predates unix time (1970).

• MULTIMEDIA_DATE_INVALID  An invalid date is given for dc:created of a multimedia object.

• MULTIMEDIA_URI_INVALID  An invalid uri is given for a multimedia object.

• PRESUMED_NEGATED_LATITUDE  Latitude appears to be negated, e.g. 32.3 instead of -32.3.

• PRESUMED_NEGATED_LONGITUDE  Longitude appears to be negated, e.g. 32.3 instead of -32.3.

• PRESUMED_SWAPPED_COORDINATE  Latitude and longitude appear to be swapped.

• RECORDED_DATE_INVALID  A (partial) invalid date is given, such as a non existing date, invalid zero month, etc.

• RECORDED_DATE_MISMATCH  The recording date specified as the eventDate string and the individual year, month, day are contradicting.

• RECORDED_DATE_UNLIKELY  The recording date is highly unlikely, falling either into the future or represents a very old date before 1600 that predates modern taxonomy.

• REFERENCES_URI_INVALID  An invalid uri is given for dc:references.

• TAXON_MATCH_FUZZY  Matching to the taxonomic backbone can only be done using a fuzzy, non exact match.

• TAXON_MATCH_HIGHER_RANK  Matching to the taxonomic backbone can only be done on a higher rank and not the scientific name.

• TAXON_MATCH_NONE  Matching to the taxonomic backbone cannot be done cause there was no match at all or several matches with too little information to keep them apart (homonyms).

• TYPE_STATUS_INVALID  The given type status is impossible to interpret or seriously different from the recommended vocabulary.

• ZERO_COORDINATE  Coordinate is the exact 0/0 coordinate, often indicating a bad null coordinate.

Counts:  There is a slight difference in the way records are counted here vs. results from occ_count. For equivalent outcomes, in this function use hasCoordinate=TRUE, and hasGeospatialIssue=FALSE to have the same outcome using occ_count with isGeoreferenced=TRUE.

Value

An object of class gbif, which is a S3 class list, with slots for metadata (meta), the occurrence data itself (data), the taxonomic hierarchy data (hier), and media metadata (media). In addition, the object has attributes listing the user supplied arguments and whether it was a "single" or "many" search; that is, if you supply two values of the datasetKey parameter to searches are done, and it’s a "many". meta is a list of length four with offset, limit, endOfRecords and count fields. data is a tibble (aka data.frame). hier is a list of data.frame’s of the unique set of taxa found, where
each data.frame is its taxonomic classification. media is a list of media objects, where each element holds a set of metadata about the media object. If the return parameter is set to something other than default you get back just the meta, data, hier, or media.

References

http://www.gbif.org/developer/occurrence#search

See Also

downloads(), occ_data(), occ_facet()

Examples

```r
## Not run:
# Search by species name, using \code{name_backbone} first to get key
(key <- name_suggest(q='Helianthus annuus', rank='species')$key[[1]])
occ_search(taxonKey=key, limit=2)

# Return 20 results, this is the default by the way
occ_search(taxonKey=key, limit=20)

# Return just metadata for the search
occ_search(taxonKey=key, limit=0, return='meta')

# Instead of getting a taxon key first, you can search for a name directly
## However, note that using this approach (with \code{scientificName}='')
## you are getting synonyms too. The results for using \code{scientificName} and
## \code{taxonKey} parameters are the same in this case, but I wouldn't be surprised if for some
## names they return different results
occ_search(scientificName = 'Ursus americanus')
key <- name_backbone(name = 'Ursus americanus', rank='species')$usageKey
occ_search(taxonKey = key)

# Search by dataset key
occ_search(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', return='data', limit=20)

# Search by catalog number
occ_search(catalogNumber="49366", limit=20)
## separate requests: use a vector of strings
occ_search(catalogNumber=c("49366","Bird.27847588"), limit=10)
## one request, many instances of same parameter: use semi-colon sep. string
occ_search(catalogNumber="49366;Bird.27847588", limit=10)

# Get all data, not just lat/long and name
occ_search(taxonKey=key, fields='all', limit=20)

# Or get specific fields. Note that this isn't done on GBIF's side of things. This
# is done in R, but before you get the return object, so other fields are garbage
# collected
occ_search(taxonKey=key, fields=c('name','basisOfRecord','protocol'), limit=20)
```
# Use paging parameters (limit and start) to page. Note the different results # for the two queries below.
occ_search(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', start=10, limit=5, return="data")
occ_search(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a', start=20, limit=5, return="data")

# Many dataset keys
## separate requests: use a vector of strings
occ_search(datasetKey=c("50c9509d-22c7-4a22-a47d-8c48425ef4a7", "7b5d6a48-f762-11e1-a439-00145eb45e9a"), limit=20)
## one request, many instances of same parameter: use semi-colon sep. string
v="50c9509d-22c7-4a22-a47d-8c48425ef4a7;7b5d6a48-f762-11e1-a439-00145eb45e9a"
occ_search(datasetKey = v, limit=20)

# Occurrence data: lat/long data, and associated metadata with occurrences
## If return='data' the output is a data.frame of all data together
## for easy manipulation
occ_search(taxonKey=key, return='data', limit=20)

# Taxonomic hierarchy data
## If return='meta' the output is a list of the hierarch for each record
occ_search(taxonKey=key, return='hier', limit=10)

# Search by recorder
occ_search(recordedBy="smith", limit=20)

# Many collector names
occ_search(recordedBy=c("smith","BJ Stacey"), limit=20)

# Pass in curl options for extra fun
occ_search(taxonKey=2433407, limit=20, return='hier',
curlopts=list(verbose=TRUE))
occ_search(taxonKey=2433407, limit=20, return='hier',
curlopts = list(
  noprogress = FALSE,
  progressfunction = function(down, up) {
    cat(sprintf("up: %d | down %d\n", up, down))
    return(TRUE)
  }
)

# occ_search(taxonKey=2433407, limit=20, return='hier',
# curlopts = list(timeout_ms = 1))

# Search for many species
splist <- c("Cyanocitta stelleri", 'Junco hyemalis', 'Aix sponsa')
keys <- sapply(splist, function(x) name_suggest(x)$key[]), USE.NAMES=FALSE)
## separate requests: use a vector of strings
occ_search(taxonKey = keys, limit=5)
## one request, many instances of same parameter: use semi-colon sep. string
occ_search(taxonKey = paste0(keys, collapse = ";"), limit=5)
# Search using a synonym name
# Note that you'll see a message printing out that the accepted name will be used
occ_search(scienceName='Pulsatilla patens', fields=['name', 'scientificName'], limit=5)

# Search on latitude and longitude
occ_search(decimalLatitude=48, decimalLongitude=10)

# Search on a bounding box
## in well known text format
### polygon
occ_search(geometries='POLYGON((30.1 10.1, 10 20, 40 40, 30.1 10.1))', limit=20)
### multipolygon
wkt <- 'MULTIPOLYGON(((123 38, -123 43, -116 43, -116 38, -123 38),
                   ((97 41, -97 45, -93 45, -93 41, -97 41)))'
occ_search(geometries = gsub('"n\\s*"', '', wkt), limit = 20)
## or using bounding box, converted to WKT internally
occ_search(geometries='(-125.0 38.4, -121.8 40.9)', limit=20)

# Search on a long WKT string - too long for a GBIF search API request
## We internally convert your WKT string to a bounding box
## then do the query
## - Alternatively, you can set the parameter `geom_big` to `bbox`
## - An additional alternative is to use the GBIF download API, see ?downloads
```r
39.30493590580082, 2.18927800655365 41.44721797271696, 4.47443425655365 43.26556960420879, 2.18927800655365 46.7439668697322, 1.83771556555365 50.3492841273576, 6.9353775655365 49.67150954335254, 5.00778006555365 52.32557322466785, 7.81427800655365 51.67627099882223, 7.81427800655365 54.5245591562317, 10.97834050655365 51.89375191441792, 10.97834050655365 55.43241335888528, 13.263496756555365 52.539917561181831))

wkt <- gsub("\"", "", wkt)

### Default option with large WKT string fails
# res <- occ_search(geometry = wkt)

### if WKT too long, with 'geom_big=bbox': makes into bounding box
res <- occ_search(geom = wkt, geom_big = "bbox")
library("rgeos")
library("sp")
wktstr <- readWKT(wkt)
plot(wktstr)
coordinates(res) <- c(decimalLongitude+decimalLatitude
points(res)

### Or, use 'geom_big=axe'
(res <- occ_search(geom = wkt, geom_big = "axe"))

### manipulate essentially number of polygons that result, so number of requests

### default geom_size is 40
### fewer calls
(res <- occ_search(geom = wkt, geom_big = "axe", geom_size=50))
### more calls
(res <- occ_search(geom = wkt, geom_big = "axe", geom_size=30))

# Search on country
occ_search(taxonkey = taxonKey, hasCoordinate=TRUE, limit=20)

# Get only occurrences with lat/long data
occ_search(taxonKey=taxonKey, hasCoordinate=TRUE, limit=20)

# Get only occurrences that were recorded as living specimens
occ_search(taxonKey=taxonKey, basisOfRecord="LIVING_SPECIMEN", hasCoordinate=TRUE, limit=20)

# Get occurrences for a particular eventdate
occ_search(taxonKey=taxonKey, eventDate="2013", limit=20)
occ_search(taxonKey=taxonKey, year="2013", limit=20)
occ_search(taxonKey=taxonKey, month="6", limit=20)

# Get occurrences based on depth
occ_search(taxonKey=taxonKey, depth="5", limit=20)
```

```
# Get occurrences based on elevation
key <- name_backbone(name='Puma concolor', kingdom='animals')$speciesKey
occ_search(taxonKey=key, elevation=50, hasCoordinate=TRUE, limit=20)

# Get occurrences based on institutionCode
occ_search(institutionCode="TLMF", limit=20)
### separate requests: use a vector of strings
occ_search(institutionCode=c("TLMF","ArtDatabanken"), limit=20)
### one request, many instances of same parameter: use semi-colon sep. string
occ_search(institutionCode = "TLMF;ArtDatabanken", limit=20)

# Get occurrences based on collectionCode
occ_search(collectionCode="Floristic Databases MV - Higher Plants", limit=20)
occ_search(collectionCode=c("Floristic Databases MV - Higher Plants","Artport"))

# Get only those occurrences with spatial issues
occ_search(taxonKey=key, hasGeospatialIssue=TRUE, limit=20)

# Search using a query string
# occ_search(search = "kingfisher", limit=20)
## spell check - only works with the 'search' parameter
## spelled correctly - same result as above call
# occ_search(search = "kingfisher", limit=20, spellCheck = TRUE)
## spelled incorrectly - stops with suggested spelling
# occ_search(search = "kajsdkla", limit=20, spellCheck = TRUE)
## spelled incorrectly - stops with many suggested spellings
### and number of results for each
# occ_search(search = "helir", limit=20, spellCheck = TRUE)

# search on repatriated - doesn't work right now
# occ_search(repatriated = "")

# search on phylumKey
occ_search(phylumKey = 7707728, limit = 5)

# search on kingdomKey
occ_search(kingdomKey = 1, limit = 5)

# search on classKey
occ_search(classKey = 216, limit = 5)

# search on orderKey
occ_search(orderKey = 7192402, limit = 5)

# search on familyKey
occ_search(familyKey = 3925, limit = 5)

# search on genusKey
occ_search(genusKey = 1935496, limit = 5)
# search on establishmentMeans
occ_search(establishmentMeans = "INVASIVE", limit = 5)
occ_search(establishmentMeans = "NATIVE", limit = 5)
occ_search(establishmentMeans = "UNCERTAIN", limit = 5)

# search on protocol
occ_search(protocol = "DIGIR", limit = 5)

# search on license
occ_search(license = "CC_BY_4_0", limit = 5)

# search on organismId
occ_search(organismId = "100", limit = 5)

# search on publishingOrg
occ_search(publishingOrg = "28eb1a3f-1c15-4a95-931a-4af90ecb574d", limit = 5)

# search on stateProvince
occ_search(stateProvince = "California", limit = 5)

# search on waterBody
occ_search(waterBody = "AMAZONAS BASIN, RIO JURUA", limit = 5)

# search on locality
res <- occ_search(locality = c("Trondheim", "Hovekilen"), limit = 5)
res$Trondheim$data
data

res$Hovekilen$data

# Range queries
## See Detail for parameters that support range queries
occ_search(depth="50,100") # this is a range depth, with lower/upper limits in character string
occ_search(depth=c(50,100)) # this is not a range search, but does two searches for each depth

## Range search with year
occ_search(year='1999,2000', limit=20)

## Range search with latitude
occ_search(decimallatitude='29.59,29.6')

# Search by specimen type status
## Look for possible values of the typeStatus parameter looking at the typestatus dataset
occ_search(typeStatus = 'allotype', fields = c('name','typeStatus'))

# Search by specimen record number
## This is the record number of the person/group that submitted the data, not GBIF's numbers
## You can see that many different groups have record number 1, so not super helpful
occ_search(recordNumber = 1, fields = c('name','recordNumber','recordedBy'))

# Search by last time interpreted: Date the record was last modified in GBIF
## The lastInterpreted parameter accepts ISO 8601 format dates, including
## yyyy, yyyy-MM, yyyy-MM-dd, or MM-dd. Range queries are accepted for lastInterpreted
occ_search(lastInterpreted = '2014-04-02', fields = c('name', 'lastInterpreted'))

# Search by continent
## One of africa, antarctica, asia, europe, north_america, oceania, or south_america
occ_search(continent = 'south_america', return = 'meta')
occ_search(continent = 'africa', return = 'meta')
occ_search(continent = 'oceania', return = 'meta')
occ_search(continent = 'antarctica', return = 'meta')

# Search for occurrences with images
occ_search(mediaType = 'StillImage', return = 'media')
occ_search(mediaType = 'MovingImage', return = 'media')
occ_search(mediaType = 'Sound', return = 'media')

# Query based on issues - see Details for options
## one issue
occ_search(taxonKey = 1, issue = 'DEPTH_UNLIKELY', fields = c('name', 'key', 'decimalLatitude', 'decimalLongitude', 'depth'))
## two issues
occ_search(taxonKey = 1, issue = c('DEPTH_UNLIKELY', 'COORDINATE_ROUNDED'))

# Show all records in the Arizona State Lichen Collection that can't be matched to the GBIF backbone properly:
occ_search(datasetKey = '84c0e1a0-f762-11e1-a439-00145eb45e9a',
            issue = c('TAXON_MATCH.NONE', 'TAXON_MATCH_HIGHER_RANK'))

# Parsing output by issue
(res <- occ_search(geometry = 'POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))', limit = 50))

## what do issues mean, can print whole table, or search for matches
head(gbif_issues())

## or parse issues in various ways
### remove data rows with certain issue classes
library('magrittr')
res %>% occ_issues(gass84)

### split issues into separate columns
res %>% occ_issues(mutate = "split")

### expand issues to more descriptive names
res %>% occ_issues(mutate = "expand")

### split and expand
res %>% occ_issues(mutate = "split_expand")

### split, expand, and remove an issue class
res %>% occ_issues(-cudc, mutate = "split_expand")

# If you try multiple values for two different parameters you are wacked on the hand
# occ_search(taxonKey = c(2482598, 2492010), recordedBy = c("smith", "BJ Stacey"))

# Get a lot of data, here 1500 records for Helianthus annuus
# out <- occ_search(taxonKey = key, limit = 1500, return = "data")
# nrow(out)

# If you pass in an invalid polygon you get hopefully informative errors

### the WKT string is fine, but GBIF says bad polygon

# occ_search(geom = gsub("\\n", ",", wkt))

### unable to parse due to last number pair needing two numbers, not one
# wkt <- 'POLYGON((-178.5 64.8, -165.9 59.2, -147.3 59.0, -130.7 51.0, -125.8))'
# occ_search(geom = wkt)

### unable to parse due to unclosed string
# wkt <- 'POLYGON((-178.5 64.8, -165.9 59.2, -147.3 59.0, -130.7 51.0))'
# occ_search(geom = wkt)

### another of the same
# wkt <- 'POLYGON((-178.5 64.8, -165.9 59.2, -147.3 59.0, -130.7 51.0, -125.8 36.7))'
# occ_search(geom = wkt)

### returns no results
# wkt <- 'LINESTRING(3 4,10 50,20 25)'
# occ_search(geom = wkt)

### Apparently a point is allowed, but errors
# wkt <- 'POINT(45 -122)'
# occ_search(geom = wkt)

## Faceting
x <- occ_search(facet = "country", limit = 0)
x$facets
x <- occ_search(facet = "establishmentMeans", limit = 10)
x$facets
x$data
x <- occ_search(facet = c("country", "basisOfRecord"), limit = 10)
x$data
x$facets
x$facets$country
x$facets$basisOfRecord
x$facets$basisOfRecord$count
x <- occ_search(facet = "country", facetMincount = 300000000L, limit = 10)
x$facets
x$data

# paging per each faceted variable
(x <- occ_search(facet = c("country", "basisOfRecord", "hasCoordinate"),
  country.facetLimit = 3,
  basisOfRecord.facetLimit = 6,
  limit = 0)
Occurrence spellcheck

Occurrence spellcheck

Description

Spell check search term for occurrence searches

Usage

occ_spellcheck(search, curlopts = list())

Arguments

- **search** (character) query term
- **curlopts** list of named curl options passed on to HttpClient. See curl_options for curl options

Value

A boolean if search term spelled correctly, or if not spelled correctly with no suggested alternatives. If spelled incorrectly and suggested alternatives given, we give back a list with slots "correctlySpelled" (boolean) and "suggestions" (list)

Examples

## Not run:
# incorrectly spelled, with suggested alternative
occ_spellcheck(search = "kajskdla")

# incorrectly spelled, without > 1 suggested alternative
occ_spellcheck(search = "helir")

# incorrectly spelled, without no alternatives
occ_spellcheck(search = "asdfadfasdf")

# correctly spelled, alternatives
occ_spellcheck(search = "helianthus")

## End(Not run)
organizations

Organizations metadata.

Description

Organizations metadata.

Usage

organizations(data = "all", uuid = NULL, query = NULL, limit = 100,
start = NULL, curlopts = list())

Arguments

data  (character) The type of data to get. One or more of: 'organization', 'contact', 'endpoint', 'identifier', 'tag', 'machineTag', 'comment', 'hostedDataset', 'ownedDataset', 'deleted', 'pending', 'nonPublishing', or the special 'all'. Default: 'all'

uuid  (character) UUID of the data node provider. This must be specified if data is anything other than 'all'.

query  (character) Query nodes. Only used when data='all'

limit  Number of records to return. Default: 100. Maximum: 1000.

start  Record number to start at. Default: 0. Use in combination with limit to page through results.

curlopts  list of named curl options passed on to HttpClient. see curl_options for curl options

Value

A list of length one or two. If uuid is NULL, then a data.frame with call metadata, and a data.frame, but if uuid given, then a list.

References

http://www.gbif.org/developer/registry#organizations

Examples

## Not run:
organizations(limit=5)
organizations(query="france", limit=5)
organizations(uuid="4b4b2111-ee51-45f5-bf5e-f535f4a1c9dc")
organizations(data='contact', uuid="4b4b2111-ee51-45f5-bf5e-f535f4a1c9dc")
organizations(data='pending')
organizations(data=c('contact','endpoint'),
    uuid="4b4b2111-ee51-45f5-bf5e-f535f4a1c9dc")
parsenames

Parse taxon names using the GBIF name parser.

Description
Parse taxon names using the GBIF name parser.

Usage
parsenames(scientificname, curlopts = list())

Arguments
- scientificname: A character vector of scientific names.
- curlopts: list of named curl options passed on to HttpClient. see curl_options for curl options

Value
A data.frame containing fields extracted from parsed taxon names. Fields returned are the union of fields extracted from all species names in scientificname.

Author(s)
John Baumgartner (johnbb@student.unimelb.edu.au)

References
http://www.gbif.org/developer/species#parser

Examples
## Not run:
parsenames(c('Arrhenatherum elatius var. elatius',
              'Secale cereale subsp. cereale', 'Secale cereale ssp. cereale',
              'Vanessa atalanta (Linnaeus, 1758)'))
parsenames("Ajuga pyramidata")
parsenames("Ajuga pyramidata x reptans")

# Pass on curl options
# res <- parsenames(c('Arrhenatherum elatius var. elatius',
#                      'Secale cereale subsp. cereale', 'Secale cereale ssp. cereale',
#                      'Vanessa atalanta (Linnaeus, 1758)'), curlopts=list(verbos TRUE))
Defunct functions in rgbif

Description

- `density_spplist()`: service no longer provided
- `densitylist()`: service no longer provided
- `gbifdata()`: service no longer provided
- `gbifmap_dens()`: service no longer provided
- `gbifmap_list()`: service no longer provided
- `occurrence_density()`: service no longer provided
- `providers()`: service no longer provided
- `resources()`: service no longer provided
- `taxoncount()`: service no longer provided
- `taxonget()`: service no longer provided
- `taxonsearch()`: service no longer provided
- `style_geojson()`: moving this functionality to spocc package, will be removed soon
- `togeojson()`: moving this functionality to spocc package, will be removed soon
- `gist()`: moving this functionality to spocc package, will be removed soon

Details

The above functions have been removed. See https://github.com/ropensci/rgbif and poke around the code if you want to find the old functions in previous versions of the package, or email Scott at <myrmecocystus@gmail.com>

Look up 2 character ISO country codes

Description

Look up 2 character ISO country codes

Usage

`rgb_country_codes(country_name, fuzzy = FALSE, ...)"
Arguments

- **country_name**: Name of country to look up
- **fuzzy**: If TRUE, uses agrep to do fuzzy search on names.
- **...**: Further arguments passed on to agrep or grep

Examples

```r
taxrank()
```

---

### taxrank

*Get the possible values to be used for (taxonomic) rank arguments in GBIF API methods.*

**Description**

Get the possible values to be used for (taxonomic) rank arguments in GBIF API methods.

**Usage**

```r
taxrank()
```

**Examples**

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

## End(Not run)
```

---

### typestatus

*Type status options for GBIF searching*

**Description**

- **name**: Name of type.
- **description**: Description of the type.
**wkt_parse**  
parse wkt into smaller bits

**Description**
parse wkt into smaller bits

**Usage**

```r
wkt_parse(wkt, geom_big, geom_size = 40, geom_n = 10)
```

**Arguments**

- **wkt** (character) A WKT string. Required.
- **geom_big** (character) One of "axe" or "bbox". Required.
- **geom_size** (integer) An integer indicating size of the cell. Default: 40. See Details.
- **geom_n** (integer) An integer indicating number of cells in each dimension. Default: 10. See Details.

**Examples**

```r
"
7.81427800655365 54.5245591562317, 10.97834050655365 51.89375191441792, 10.97834050655365 55.43241335888528, 13.263496756555365 52.53991761181831))

wkt <- gsub("\n", " ", wkt)

# to a bounding box in wkt format
wkt_parse(wkt, geom_big = "bbox")

# to many wkt strings, chopped up from input
wkt_parse(wkt, geom_big = "axe")
wkt_parse(wkt, geom_big = "axe", 60)
wkt_parse(wkt, geom_big = "axe", 30)
wkt_parse(wkt, geom_big = "axe", 20)
wkt_parse(wkt, geom_big = "axe", 10)
wkt_parse(wkt, geom_big = "axe", 5)
Index

+Topic **GBIF**
  - `map_fetch`, 26
+Topic **data**
  - `isocodes`, 25
  - `occ_fields`, 76
  - `typestatus`, 102
+Topic **map**
  - `map_fetch`, 26
+Topic **tile**
  - `map_fetch`, 26
+Topic **web**
  - `map_fetch`, 26
  - `asNdownload()`, 70
  - `cat`, 9, 11
  - `check_wkt`, 4
  - `check_wkt()`, 50, 85
  - `chop`, 52, 87
  - `count_facet`, 5
  - `crul::HttpClient`, 28
  - `crul::HttpClient()`, 69
  - `crul::verb=GET`, 15
  - `crul::writing-options`, 69
  - `curl::curl_options()`, 15
  - `curl_options`, 6, 7, 9, 11, 17, 24, 30, 34, 37, 39, 41, 42, 45, 50, 62, 67–69, 71, 72, 75, 76, 81, 85, 98–100
  - `datasets`, 6
  - `density_spplist()`, 101
  - `densitylist()`, 101
  - `downloads`, 13, 65, 67–70, 72, 73
  - `downloads()`, 55, 90
  - `elevation`, 14
  - `enumeration`, 16
  - `enumeration_country (enumeration)`, 16
  - `gbif_bbox2wkt`, 17
  - `gbif_citation`, 18
  - `gbif_issues`, 20
  - `gbif_issues()`, 31
  - `gbif_names`, 20
  - `gbif_oai`, 21
  - `gbif_oai_get_records (gbif_oai)`, 21
  - `gbif_oai_identify (gbif_oai)`, 21
  - `gbif_oai_list_identifiers (gbif_oai)`, 21
  - `gbif_oai_list_metadataformats (gbif_oai)`, 21
  - `gbif_oai_list_records (gbif_oai)`, 21
  - `gbif_oai_list_sets (gbif_oai)`, 21
  - `gbif_photos`, 23
  - `gbif_wkt2bbox (gbif_bbox2wkt)`, 17
  - `gbifdata()`, 101
  - `gbifmap_dens()`, 101
  - `gbifmap_list()`, 101
  - `gist()`, 101

  `HttpClient`, 6, 7, 9, 11, 17, 24, 30, 34, 37, 39, 41, 42, 45, 50, 62, 67–69, 71, 72, 75, 76, 81, 85, 98–100

  `installations`, 24
  - `isocodes`, 25
  - `many-values`, 4, 26, 37
  - `map_fetch`, 26
  - `name_backbone`, 29
  - `name_issues`, 31
  - `name_issues()`, 20, 39
  - `name_lookup`, 32
  - `name_lookup()`, 26, 39
name_suggest, 36
name_suggest(), 26
name_usage, 38
name_usage(), 26
networks, 40
dnodes, 42
occ_count, 44, 54, 89
occ_data, 47, 52, 87
occ_data(), 26, 64, 78, 90
occ_download, 62
occ_download(), 13, 14, 52, 73, 87
occ_download_cancel, 66
occ_download_cancel(), 14
occ_download_cancel_staged
   (occ_download_cancel), 66
occ_download_cancel_staged(), 14
occ_download_dataset_activity, 68
occ_download_dataset_activity(), 14
occ_download_datasets, 67
occ_download_datasets(), 14
occ_download_get, 69
occ_download_get(), 14, 18, 73
occ_download_import, 70
occ_download_import(), 14, 78
occ_download_list, 71
occ_download_list(), 14
occ_download_meta, 72
occ_download_meta(), 14, 18
occ_download_prep(occ_download), 62
occ_download_prep(), 14, 73
occ_download_queue, 73
occ_download_queue(), 14, 64
occ_facet, 75
occ_facet(), 90
occ_fields, 76
occ_get, 76
occ_issues, 77
occ_issues_lookup, 80
occ_metadata, 80
occ_search, 52, 81, 87
occ_search(), 13, 18, 26, 44, 45, 55, 64, 75, 76, 78
occ_spellcheck, 98
occurrencedensity(), 101
options(), 13
organizations, 8, 11, 99
parsenames, 100

providers(), 101
resources(), 101
rgb_country_codes, 101
rgbif (rgbif-package), 3
rgbif-defunct, 101
rgbif-package, 3
stylegeojson(), 101
Sys.setenv(), 13
taxoncount(), 101
taxonget(), 101
taxonsearch(), 101
taxrank, 102
togeojson(), 101
typestatus, 102
typestatus(), 44
wkt_parse, 52, 87, 103