Package 'rgbif'

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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 3.9.0

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

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rgbif-package *Interface to the Global Biodiversity Information Facility API.*

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 https://www.gbif.org/ via their API.

Documentation for the GBIF API

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

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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 wk::wk_problems call or not. Default: FALSE

Examples

```
## 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)
```

---

collection_search *Search GRSciColl collections*

Description

Search GRSciColl collections

Usage

```
collection_search(
  query = NULL,
  name = NULL,
  fuzzyName = NULL,
  preservationType = NULL,
  contentType = NULL,
  numberSpecimens = NULL,
  occurrenceCount = NULL,
  typeSpecimenCount = NULL,
  accessionStatus = NULL,
  personalCollection = NULL,
  sourceId = NULL,
  source = NULL,
```

```
  code = NULL,
  alternativeCode = NULL,
  contact = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  institutionKey = NULL,
  country = NULL,
  city = NULL,
  gbifRegion = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  identifier = NULL,
  identifierType = NULL,
  active = NULL,
  displayOnNHCPortal = NULL,
  masterSourceType = NULL,
  replacedBy = NULL,
  sortBy = NULL,
  sortOrder = NULL,
  offset = NULL,
  limit = NULL,
  format = NULL,
  curlopts = list(http_version = 2)
)

collection_export(
  query = NULL,
  name = NULL,
  fuzzyName = NULL,
  preservationType = NULL,
  contentType = NULL,
  numberSpecimens = NULL,
  occurrenceCount = NULL,
  typeSpecimenCount = NULL,
  accessionStatus = NULL,
  personalCollection = NULL,
  sourceId = NULL,
  source = NULL,
  code = NULL,
  alternativeCode = NULL,
  contact = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  institution = NULL,
  institutionKey = NULL,
  country = NULL,
  city = NULL,
```

```
  gbifRegion = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  identifier = NULL,
  identifierType = NULL,
  active = NULL,
  displayOnNHCPortal = NULL,
  masterSourceType = NULL,
  replacedBy = NULL,
  sortBy = NULL,
  sortOrder = NULL,
  offset = NULL,
  limit = NULL,
  format = "TSV",
  curlopts = list()
)
```

Arguments

query	Simple full text search parameter. The value for this parameter can be a simple word or a phrase. Wildcards are not supported.
name	Name of a GrSciColl institution or collection.
fuzzyName	It searches by name fuzzily so the parameter doesn't have to be the exact name.
preservationType	Preservation type of a GrSciColl collection. Accepts multiple values.
contentType	Content type of a GrSciColl collection. See here for accepted values : https://techdocs.gbif.org/en/openapi
numberSpecimens	Number of specimens. It supports ranges and a * can be used as a wildcard.
occurrenceCount	(character) Count of occurrences linked. It supports ranges and a * can be used as a wildcard. Optional parameter for filtering results.
typeSpecimenCount	(character) Count of type specimens linked. It supports ranges and a * can be used as a wildcard. Optional parameter for filtering results.
accessionStatus	Accession status of a GrSciColl collection. Accepted values : INSTITUTIONAL, PROJECT
personalCollection	Flag for personal GRSciColl collections.
sourceId	sourceId of MasterSourceMetadata.
source	Source attribute of MasterSourceMetadata. Accepted values : DATASET, ORGANIZATION, IH_IRN
code	Code of a GrSciColl institution or collection.
alternativeCode	Alternative code of a GrSciColl institution or collection.

`contact` Filters collections and institutions whose contacts contain the person key specified.

`contactUserId` (numeric) Filters collections by the user ID of a contact. Optional parameter for filtering results.

`contactEmail` (character) Filters collections by the email of a contact. Optional parameter for filtering results.

`institutionKey` Keys of institutions to filter by.

`country` Filters by country given as a ISO 639-1 (2 letter) country code.

`city` Filters by the city of the address. It searches in both the physical and the mailing address.

`gbifRegion` Filters by a gbif region Available values : AFRICA, ASIA, EUROPE, NORTH_AMERICA, OCEANIA, LATIN_AMERICA, ANTARCTICA.

`machineTagNamespace` Filters for entities with a machine tag in the specified namespace.

`machineTagName` Filters for entities with a machine tag with the specified name (use in combination with the machineTagNamespace parameter).

`machineTagValue` Filters for entities with a machine tag with the specified value (use in combination with the machineTagNamespace and machineTagName parameters).

`identifier` An identifier of the type given by the identifierType parameter, for example a DOI or UUID.

`identifierType` An identifier type for the identifier parameter. Available values : URL, LSID, HANDLER, DOI, UUID, FTP, URI, UNKNOWN, GBIF_PORTAL, GBIF_NODE, GBIF_PARTICIPANT, GRSCICOLL_ID, GRSCICOLL_URI, IH_IRN, ROR, GRID, CITES, SYMBIOTA_UUID, WIKIDATA, NCBI_BIOCOLLECTION, ISIL, CLB_DATASET_KEY.

`active` Active status of a GrSciColl institution or collection.

`displayOnNHCPortal` Flag to show this record in the NHC portal.

`masterSourceType` The master source type of a GRSciColl institution. or collection. Available values : GRSCICOLL, GBIF_REGISTRY, IH.

`replacedBy` Key of the entity that replaced another entity.

`sortBy` Field to sort the results by. It only supports the fields contained in the enum. Available values : NUMBER_SPECIMENS.

`sortOrder` Sort order to use with the sortBy parameter. Available values : ASC, DESC.

`offset` Determines the offset for the search results.

`limit` Controls the number of results in the page. Default 20.

`format` (character) Format of the export. Default is "TSV". Only used for collection_export.

`curlopts` curlopts options passed on to crul::HttpClient.

`institution` Name of institutions hosting collections.

Details

Will return GRSciColl collections data. collection_export will return all of the results in a single `tibble`, while collection_search will return a sample of results.

Value

a `list`

References

https://scientific-collections.gbif.org/connected-systems#grscicoll-data-coming-from-other-sources

Examples

```
## Not run:
  collection_search(query="insect",limit=2)
  collection_search(name="Insects;Entomology", limit=2)
  collection_search(numberSpecimens = "0,100", limit=1)
  collection_search(institutionKey = "6a6ac6c5-1b8a-48db-91a2-f8661274ff80"
  , limit = 1)
  collection_search(query = "insect", country = "US;GB", limit=1)

## End(Not run)
```

`count_facet` *Facetted count occurrence search.*

Description

Facetted count occurrence search.

Usage

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

Arguments

`keys`	(numeric) GBIF keys, a vector. optional
`by`	(character) One of georeferenced, basisOfRecord, country, or publishingCountry. default: country
`countries`	(numeric) Number of countries to facet on, or a vector of country names. default: 10
`removezeros`	(logical) remove zeros or not? default: `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)
count_facet(keys, by='basisOfRecord', countries=5, 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)
```

`dataset` *Search for more obscure dataset metadata.*

Description

Search for more obscure dataset metadata.

Usage

```
dataset(
  country = NULL,
  type = NULL,
  identifierType = NULL,
  identifier = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  modified = NULL,
```

```
  query = NULL,
  deleted = FALSE,
  limit = NULL,
  start = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

country	The 2-letter country code (as per ISO-3166-1) of the country publishing the dataset.
type	The primary type of the dataset. Available values : OCCURRENCE, CHECKLIST, METADATA, SAMPLING_EVENT, MATERIAL_ENTITY.
identifierType	An identifier type for the identifier parameter. Available values : URL, LSID, HANDLER, DOI, UUID, FTP, URI, UNKNOWN, GBIF_PORTAL, GBIF_NODE, GBIF_PARTICIPANT, GRSCICOLL_ID, GRSCICOLL_URI, IH_IRN, ROR, GRID, CITES, SYMBIOTA_UUID, WIKIDATA, NCBI_BIOCOLLECTION.
identifier	An identifier of the type given by the identifierType parameter.
machineTagNamespace	Filters for entities with a machine tag in the specified namespace.
machineTagName	Filters for entities with a machine tag with the specified name (use in combination with the machineTagNamespace parameter).
machineTagValue	Filters for entities with a machine tag with the specified value (use in combination with the machineTagNamespace and machineTagName parameters).
modified	The modified date of the dataset. Accepts ranges and a ” can be used as a wildcard, e.g.:modified=2023-04-01,
query	Simple full text search parameter. The value for this parameter can be a simple word or a phrase. Wildcards are not supported.
deleted	Logical specifying whether to return only deleted datasets.
limit	Controls the number of results in the page.
start	Determines the start for the search results.
curlopts	options passed on to crul::HttpClient.

Details

This function allows you to search for some more obscure dataset metadata that might not be possible with `dataset_search()`. For example, searching through registry machinetags.

Value

A `list`.

Examples

```
## Not run:
dataset(limit=3)
dataset(country="US",limit=3)
dataset(type="CHECKLIST",limit=3)
dataset(identifierType = "URL",limit=3)
dataset(identifier = 168,limit=3)
dataset(machineTagNamespace = "metasync.gbif.org",limit=3)
dataset(machineTagName = "datasetTitle",limit=3)
dataset(machineTagValue = "Borkhart",limit=3)
dataset(modified = "2023-04-01", limit=3)
dataset(q = "dog", limit=3)
dataset(deleted=TRUE,limit=3)

## End(Not run)
```

`datasets` *Search for datasets and dataset metadata.*

Description

Search for datasets and dataset metadata.

Usage

```
datasets(
  data = "all",
  type = NULL,
  uuid = NULL,
  query = NULL,
  id = NULL,
  limit = 100,
  start = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

`data`	The type of data to get. One or more of: 'organization', 'contact', 'endpoint', 'identifier', 'tag', 'machinetag', '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::curl_options for curl options

Value

A list.

References

https://www.gbif.org/developer/registry#datasets

Examples

```
## Not run:
datasets(limit=5)
datasets(type="occurrence", limit=10)
datasets(uuid="a6998220-7e3a-485d-9cd6-73076bd85657")
datasets(data='contact', uuid="a6998220-7e3a-485d-9cd6-73076bd85657")
datasets(data='metadata', uuid="a6998220-7e3a-485d-9cd6-73076bd85657")
datasets(data='metadata', uuid="a6998220-7e3a-485d-9cd6-73076bd85657",
  id=598)
datasets(data=c('deleted','duplicate'))
datasets(data=c('deleted','duplicate'), limit=1)

# curl options
datasets(data=c('deleted','duplicate'), curlopts = list(verbose=TRUE))

## End(Not run)
```

---

dataset_doi *Get a GBIF dataset from a doi*

Description

Get a GBIF dataset from a doi

Usage

```
dataset_doi(
  doi = NULL,
  limit = 20,
  start = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

doi	the doi of the dataset you wish to lookup.
limit	Controls the number of results in the page.
start	Determines the offset for the search results.
curlopts	options passed on to crul::HttpClient.

Details

This function allows for dataset lookup using a doi. Be aware that some doi have more than one dataset associated with them.

Value

A list.

Examples

```
## Not run:
dataset_doi('10.15468/igasai')

## End(Not run)
```

---

dataset_gridded *Check if a dataset is gridded*

Description

Check if a dataset is gridded

Usage

```
dataset_gridded(
  uuid = NULL,
  min_dis = 0.05,
  min_per = 50,
  min_dis_count = 30,
  return = "logical",
  warn = TRUE
)
```

Arguments

uuid	(vector) A character vector of GBIF datasetkey uuids.
min_dis	(numeric) (default 0.02) Minimum distance in degrees to accept as gridded.
min_per	(integer)(default 50%) Minimum percentage of points having same nearest neighbor distance to be considered gridded.

min_dis_count	(default 30) Minimum number of unique points to accept an assessment of 'griddyness'.
return	(character) (default "logical"). Choice of "data" will return a data.frame of more information or "logical" will return just TRUE or FALSE indicating whether a dataset is considered 'gridded".
warn	(logical) indicates whether to warn about missing values or bad values.

Details

Gridded datasets are a known problem at GBIF. Many datasets have equally-spaced points in a regular pattern. These datasets are usually systematic national surveys or data taken from some atlas ("so-called rasterized collection designs"). This function uses the percentage of unique lat-long points with the most common nearest neighbor distance to identify gridded datasets.

https://data-blog.gbif.org/post/finding-gridded-datasets/

I recommend keeping the default values for the parameters.

Value

A logical vector indicating whether a dataset is considered gridded. Or if return="data", a data.frame of more information.

Examples

```
## Not run:

dataset_gridded("9070a460-0c6e-11dd-84d2-b8a03c50a862")
dataset_gridded(c("9070a460-0c6e-11dd-84d2-b8a03c50a862",
               "13b70480-bd69-11dd-b15f-b8a03c50a862"))



## End(Not run)
```

---

dataset_list_funs *List datasets that are deleted or have no endpoint.*

Description

List datasets that are deleted or have no endpoint.

Usage

```
dataset_duplicate(limit = 20, start = NULL, curlopts = list(http_version = 2))

dataset_noendpoint(limit = 20, start = NULL, curlopts = list(http_version = 2))
```

Arguments

limit	Controls the number of results in the page.
start	Determines the start for the search results.
curlopts	options passed on to crul::HttpClient.

Details

Get a list of deleted datasets or datasets with no endpoint. You get the full and no parameters aside from limit and start are accepted.

Value

A list.

Examples

```
## Not run:
dataset_noendpoint(limit=3)

## End(Not run)
```

---

dataset_search *Search for dataset metadata.*

Description

Search for dataset metadata.

Usage

```
dataset_export(
  query = NULL,
  type = NULL,
  publishingCountry = NULL,
  subtype = NULL,
  license = NULL,
  keyword = NULL,
  publishingOrg = NULL,
  hostingOrg = NULL,
  endorsingNodeKey = NULL,
  decade = NULL,
  projectId = NULL,
  hostingCountry = NULL,
  networkKey = NULL,
  doi = NULL,
  installationKey = NULL,
  endpointType = NULL,
```

```
  category = NULL,
  continent = NULL,
  taxonKey = NULL,
  recordCount = NULL,
  modifiedDate = NULL,
  createdDate = NULL,
  contactUserId = NULL,
  contactEmail = NULL
)

dataset_search(
  query = NULL,
  type = NULL,
  publishingCountry = NULL,
  subtype = NULL,
  license = NULL,
  keyword = NULL,
  publishingOrg = NULL,
  hostingOrg = NULL,
  endorsingNodeKey = NULL,
  decade = NULL,
  projectId = NULL,
  hostingCountry = NULL,
  networkKey = NULL,
  doi = NULL,
  installationKey = NULL,
  endpointType = NULL,
  category = NULL,
  continent = NULL,
  taxonKey = NULL,
  recordCount = NULL,
  modifiedDate = NULL,
  createdDate = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  facet = NULL,
  facetLimit = NULL,
  facetOffset = NULL,
  facetMincount = NULL,
  facetMultiselect = NULL,
  limit = 100,
  start = NULL,
  description = FALSE,
  curlopts = list(http_version = 2)
)

dataset_suggest(
  query = NULL,
```

```
  type = NULL,
  publishingCountry = NULL,
  subtype = NULL,
  license = NULL,
  keyword = NULL,
  publishingOrg = NULL,
  hostingOrg = NULL,
  endorsingNodeKey = NULL,
  decade = NULL,
  projectId = NULL,
  hostingCountry = NULL,
  networkKey = NULL,
  doi = NULL,
  installationKey = NULL,
  endpointType = NULL,
  category = NULL,
  continent = NULL,
  taxonKey = NULL,
  recordCount = NULL,
  modifiedDate = NULL,
  createdDate = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  limit = 100,
  start = NULL,
  description = FALSE,
  curlopts = list(http_version = 2)
)
```

Arguments

query	Simple full text search parameter. The value for this parameter can be a simple word or a phrase. Wildcards are not supported.
type	The primary type of the dataset. Available values: "OCCURRENCE", "CHECKLIST", "METADATA", "SAMPLING_EVENT", "MATERIAL_ENTITY".
publishingCountry	Filters datasets by their owning organization's country given as a ISO 639-1 (2 letter) country code.
subtype	The sub-type of the dataset.The sub-type of the dataset. Available values: "TAXONOMIC_AUTHORITY", "NOMENCLATOR_AUTHORITY", "INVENTORY_THEMATIC", "INVENTORY_REGIONAL", "GLOBAL_SPECIES_DATASET", "DERIVED_FROM_OCCURRENC "SPECIMEN", "OBSERVATION".
license	The dataset's licence. Available values: "CC0_1_0", "CC_BY_4_0", "CC_BY_NC_4_0", "UNSPECIFIED", "UNSUPPORTED".
keyword	Filters datasets by a case insensitive plain text keyword. The search is done on the merged collection of tags, the dataset keywordCollections and temporalCoverages.

`publishingOrg` Filters datasets by their publishing organization UUID key.

`hostingOrg` Filters datasets by their hosting organization UUID key

`endorsingNodeKey`
Node UUID key that endorsed this dataset's publisher.

`decade` 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. Ranges can be used like this "1800,1900".

`projectId` Filter or facet based on the project ID of a given dataset. A dataset can have a project id if it is the result of a project. Multiple datasets can have the same project id.

`hostingCountry` Filters datasets by their hosting organization's country given as a ISO 639-1 (2 letter) country code.

`networkKey` Filters network UUID associated to a dataset.

`doi` DOI of the dataset.

`installationKey`
Filters datasets by their installation UUID key.

`endpointType` Filters datasets by their endpoint type. Available values : EML, FEED, WFS, WMS, TCS_RDF, TCS_XML, DWC_ARCHIVE, DIGIR, DIGIR_MANIS, TAPIR, BIOCASE, BIOCASE_XML_ARCHIVE, OAI_PMH, COLDP, CAMTRAP_DP, BIOM_1_0, BIOM_2_1, ACEF, TEXT_TREE, OTHER

`category` Filters datasets by their dataset category tag. For example "eDNA", "Citizen-Science", "Tracking".

`continent` Filters datasets by the continent of their spatial coverage. Available values: "AFRICA", "ANTARCTICA", "ASIA", "EUROPE", "NORTH_AMERICA", "OCEANIA", "SOUTH_AMERICA".

`taxonKey` Filters datasets by a taxon key from the GBIF backbone. The dataset must index records linked to this taxon or any of its descendants.

`recordCount` Filters datasets by number of occurrence records. Accepts ranges, e.g. "1000,5000".

`modifiedDate` Filters datasets by their last modified date. Accepts date ranges, e.g. "2020-01-01,2021-01-01".

`createdDate` Filters datasets by their created date. Accepts date ranges, e.g. "2020-01-01,2021-01-01".

`contactUserId` Filters datasets by the user ID of a dataset contact.

`contactEmail` Filters datasets by the email of a dataset contact.

`facet` A facet name used to retrieve the most frequent values for a field.

`facetLimit` Facet parameters allow paging requests using the parameters facetOffset and facetLimit.

`facetOffset` Facet parameters allow paging requests using the parameters facetOffset and facetLimit

`facetMincount` Used in combination with the facet parameter.

`facetMultiselect`
Used in combination with the facet parameter.

limit	Controls the number of results in the page. Using too high a value will be overwritten with the default maximum threshold, depending on the service. Sensible defaults are used so this may be omitted.
start	Determines the offset for the search results. A limit of 20 and offset of 40 will get the third page of 20 results. Some services have a maximum offset.
description	Logical whether to return descriptions.
curlopts	options passed on to crul::HttpClient.

Details

`dataset_search()` searches and returns metadata on GBIF datasets from the registry. This function does not search occurrence data, only metadata on the datasets that contain may contain occurrence data. It also searches over other dataset types, such checklist and metadata datasets. Only a sample of results is returned.

`dataset_export()` function will download a `tibble` of the results of a `dataset_search()`. This function is primarily useful if you want the full results of a `dataset_search()`.

Use `dataset_search(facet="x",limit=0)$facets` to get simple group by counts for different parameters.

Value

A `list` for `dataset_search()`. A `tibble` for `dataset_export()`.

References

https://techdocs.gbif.org/en/openapi/v1/registry#/Datasets/searchDatasets

Examples

```
## Not run:
# search metadata on all datasets and return a sample
dataset_search()
# dataset_export() # download info on all +90K datasets

dataset_search(publishingCountry = "US")
dataset_search(type = "OCCURRENCE")
dataset_search(keyword = "bird")
dataset_search(subtype = "TAXONOMIC_AUTHORITY")
dataset_search(license = "CC0_1_0")
dataset_search(query = "frog")
dataset_search(publishingCountry = "UA")
dataset_search(publishingOrg = "e2e717bf-551a-4917-bdc9-4fa0f342c530")
dataset_search(hostingOrg = "7ce8aef0-9e92-11dc-8738-b8a03c50a862")
dataset_search(decade="1890,1990",limit=5)
dataset_search(projectId = "GRIIS")
dataset_search(hostingCountry = "NO")
dataset_search(networkKey = "99d66b6c-9087-452f-a9d4-f15f2c2d0e7e")
dataset_search(doi='10.15468/aomfnb')

# search multiple values
```

```
dataset_search(projectId = "GRIIS;BID-AF2020-140-REG")
dataset_search(hostingCountry = "NO;SE")
dataset_search(doi="10.15468/aomfnb;10.15468/igasai")
dataset_search(installationKey = "d209e552-7e6e-4840-b13c-c0596ef36e55")
dataset_search(category = "eDNA")
dataset_search(recordCount = "10000,100000", limit = 5)
dataset_search(modifiedDate = "2020-01-01,2021-01-01", limit = 5)
dataset_search(createdDate = "2015-01-01,2016-01-01", limit = 5)
dataset_search(contactEmail = "helpdesk@gbif.org", limit = 5)

# multiple filters
dataset_search(license = "CC0_1_0",subtype = "TAXONOMIC_AUTHORITY")
# dataset_export(license = "CC0_1_0",subtype = "TAXONOMIC_AUTHORITY")

# using dataset export to get all datasets
dataset_export(decade="1800,1900")
dataset_export(projectId="GRIIS")

# get simple group by counts
dataset_search(facet="type",limit=0,facetLimit=5)$facets
dataset_search(facet="publishingCountry",limit=0,facetLimit=5)$facets
dataset_search(facet="license",limit=0,facetLimit=5, facetMincount=10000)


## End(Not run)
```

`dataset_uuid_funs` *Get dataset metadata using a datasetkey*

Description

Get dataset metadata using a datasetkey

Usage

```
dataset_get(uuid = NULL, curlopts = list(http_version = 2))

dataset_process(
  uuid = NULL,
  limit = 20,
  start = NULL,
  curlopts = list(http_version = 2)
)

dataset_networks(
  uuid = NULL,
  limit = 20,
  start = NULL,
  curlopts = list(http_version = 2)
```

```
)

dataset_constituents(
  uuid = NULL,
  limit = 20,
  start = NULL,
  curlopts = list(http_version = 2)
)

dataset_comment(uuid = NULL, curlopts = list(http_version = 2))

dataset_contact(uuid = NULL, curlopts = list(http_version = 2))

dataset_endpoint(uuid = NULL, curlopts = list(http_version = 2))

dataset_identifier(uuid = NULL, curlopts = list(http_version = 2))

dataset_machinetag(uuid = NULL, curlopts = list(http_version = 2))

dataset_tag(uuid = NULL, curlopts = list(http_version = 2))

dataset_metrics(uuid = NULL, curlopts = list(http_version = 2))
```

Arguments

uuid	A GBIF datasetkey uuid.
curlopts	options passed on to crul::HttpClient.
limit	Number of records to return.
start	Record number to start at.

Details

`dataset_metrics()` can only be used with checklist type datasets.

Value

A `tibble` or a `list`.

References

https://techdocs.gbif.org/en/openapi/v1/registry

Examples

```
## Not run:
dataset_get("38b4c89f-584c-41bb-bd8f-cd1def33e92f")
dataset_process("38b4c89f-584c-41bb-bd8f-cd1def33e92f",limit=3)
dataset_networks("3dab037f-a520-4bc3-b888-508755c2eb52")
dataset_constituents("7ddf754f-d193-4cc9-b351-99906754a03b",limit=3)
```

```
dataset_comment("2e4cc37b-302e-4f1b-bbbb-1f674ff90e14")
dataset_contact("7ddf754f-d193-4cc9-b351-99906754a03b")
dataset_endpoint("7ddf754f-d193-4cc9-b351-99906754a03b")
dataset_identifier("7ddf754f-d193-4cc9-b351-99906754a03b")
dataset_machinetag("7ddf754f-d193-4cc9-b351-99906754a03b")
dataset_tag("c47f13c1-7427-45a0-9f12-237aad351040")
dataset_metrics("7ddf754f-d193-4cc9-b351-99906754a03b")

## End(Not run)
```

`derived_dataset` *Register a derived dataset for citation.*

Description

Register a derived dataset for citation.

Usage

```
derived_dataset(
  citation_data = NULL,
  title = NULL,
  description = NULL,
  source_url = NULL,
  gbif_download_doi = NULL,
  user = NULL,
  pwd = NULL,
  curlopts = list(http_version = 2)
)

derived_dataset_prep(
  citation_data = NULL,
  title = NULL,
  description = NULL,
  source_url = NULL,
  gbif_download_doi = NULL,
  user = NULL,
  pwd = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

`citation_data`	(required) A data.frame with **two columns**. The first column should be GBIF **datasetkey uuids** and the second column should be **occurrence counts** from each of your datasets, representing the contribution of each dataset to your final derived dataset.
`title`	(required) The title for your derived dataset.

description	(required) A description of the dataset. Perhaps describing how it was created.
source_url	(required) A link to where the dataset is stored.
gbif_download_doi	(optional) A DOI from an original GBIF download.
user	(required) Your GBIF username.
pwd	(required) Your GBIF password.
curlopts	a list of arguments to pass to curl.

Value

A list.

Usage

Create a **citable DOI** for a dataset derived from GBIF mediated occurrences.

Use-case (1) your dataset was obtained with `occ_search()` and never returned a **citable DOI**, but you want to cite the data in a research paper.

Use-case (2) your dataset was obtained using `occ_download()` and you got a DOI, but the data underwent extensive filtering using `CoordinateCleaner` or some other cleaning pipeline. In this case be sure to fill in your original `gbif_download_doi`.

Use-case (3) your dataset was generated using a GBIF cloud export but you want a DOI to cite in your research paper.

Use `derived_dataset` to create a custom citable meta-data description and most importantly a DOI link between an external archive (e.g. Zenodo) and the datasets involved in your research or analysis.

All fields (except `gbif_download_doi`) are required for the registration to work.

We recommend that you run `derived_dataset_prep()` to check registration details before making it final with `derived_dataset()`.

Authentication

Some `rgbif` functions require your **GBIF credentials**.

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

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

We strongly recommend the **first option** - storing your details as environment variables - as it's the most widely used way to store secrets.

You can edit your `.Renviron` with `usethis::edit_r_environ()`.

After editing, your `.Renviron` file should look something like this...

GBIF_USER="jwaller"
GBIF_PWD="fakepassword123"

GBIF_EMAIL="jwaller@gbif.org"

See ?Startup for help.

References

https://data-blog.gbif.org/post/derived-datasets/ https://www.gbif.org/derived-dataset/about

Examples

```
## Not run:
data <- data.frame(
 datasetKey = c(
 "3ea36590-9b79-46a8-9300-c9ef0bfed7b8",
 "630eb55d-5169-4473-99d6-a93396aeae38",
 "806bf7d4-f762-11e1-a439-00145eb45e9a"),
 count = c(3, 1, 2781)
 )

## If output looks ok, run derived_dataset to register the dataset
 derived_dataset_prep(
 citation_data = data,
 title = "Test for derived dataset",
 description = "This data was filtered using a fake protocol",
 source_url = "https://zenodo.org/record/4246090#.YPGS2OgzZPY"
 )

#  derived_dataset(
#  citation_data = data,
#  title = "Test for derived dataset",
#  description = "This data was filtered using a fake protocol",
#  source_url = "https://zenodo.org/record/4246090#.YPGS2OgzZPY"
#  )

## Example with occ_search and dplyr
# library(dplyr)

# citation_data <- occ_search(taxonKey="Q2M4", limit=20)$data %>%
#   group_by(datasetKey) %>%
#   count()

# # You would still need to upload your data to Zenodo or something similar
# derived_dataset_prep(
#   citation_data = citation_data,
#   title= "data downloaded for test",
#   description="This data was downloaded using rgbif::occ_search and was
#   later uploaded to Zenodo.",
#   source_url="https://zenodo.org/record/4246090#.YPGS2OgzZPY",
#   gbif_download_doi = NULL,
# )
```

```
## End(Not run)
```

`downloads` *Downloads interface*

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_cached()` - Check for downloads already in your GBIF account
- `occ_download_wait()` - Re-run `occ_download_meta()` until ready
- `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_countries()` - List countries for a download
- `occ_download_organizations()` - List organizations for a download
- `occ_download_dataset_activity()` - Lists the downloads activity of a dataset

Download query composer methods:

See download_predicate_dsl

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.

Download status

The following statuses can be found with any download:

- PREPARING: just submitted by user and awaiting processing (typically only a few seconds)
- RUNNING: being created (takes typically 1-15 minutes)
- FAILED: something unexpected went wrong
- KILLED: user decided to abort the job while it was in PREPARING or RUNNING phase
- SUCCEEDED: The download was created and the user was informed
- FILE_ERASED: The download was deleted according to the retention policy, see https://www.gbif.org/faq?question=fo how-long-will-does-gbif-store-downloads

---

`download_predicate_dsl`

Download predicate DSL (domain specific language)

Description

Download predicate DSL (domain specific language)

Usage

```
pred(key, value, checklistKey = NULL)

pred_gt(key, value)

pred_gte(key, value)

pred_lt(key, value)

pred_lte(key, value)

pred_not(...)

pred_like(key, value)

pred_within(value)

pred_isnull(key)

pred_notnull(key)

pred_or(..., .list = list())

pred_and(..., .list = list())

pred_in(key, value, checklistKey = NULL)

pred_default()
```

Arguments

key	(character) the key for the predicate. See "Keys" below
value	(various) the value for the predicate
checklistKey	(character) A checklistKey to use for downloading using alternative taxonomies. Can be used with any taxonomic rank key (taxonKey, classKey, phylumKey, orderKey, familyKey, genusKey, subgenusKey, speciesKey, acceptedTaxonKey, kingdomKey). The default is COL (Catalogue of Life) Extended Release ("7ddf754f-d193-4cc9-b351-9 To use GBIF Backbone Taxonomy, pass "d7dddbf4-2cf0-4f39-9b2a-bb099caae36c".
..., .list	For pred_or() or pred_and(), one or more objects of class occ_predicate, created by any pred* function

predicate methods and their equivalent types

pred* functions are named for the 'type' of operation they do, following the terminology used by GBIF, see https://www.gbif.org/developer/occurrence#predicates

Function names are given, with the equivalent GBIF type value (e.g., pred_gt and greaterThan)

The following functions take one key and one value:

- `pred`: equals
- `pred_lt`: lessThan
- `pred_lte`: lessThanOrEquals
- `pred_gt`: greaterThan
- `pred_gte`: greaterThanOrEquals
- `pred_like`: like

The following function is only for geospatial queries, and only accepts a WKT string:

- `pred_within`: within

The following function is only for stating the you don't want a key to be null, so only accepts one key:

- `pred_notnull`: isNotNull

The following function is only for stating that you want a key to be null.

- `pred_isnull` : isNull

The following two functions accept multiple individual predicates, separating them by either "and" or "or":

- `pred_and`: and
- `pred_or`: or

The not predicate accepts one predicate; that is, this negates whatever predicate is passed in, e.g., not the taxonKey of 12345:

- `pred_not`: not

The following function is special in that it accepts a single key but many values; stating that you want to search for all the values:

- `pred_in`: in

The following function will apply commonly used **defaults**.

- `pred_default`

Using `pred_default()` is equivalent to running:

```
pred_and(
 pred("HAS_GEOSPATIAL_ISSUE",FALSE),
 pred("HAS_COORDINATE",TRUE),
 pred("OCCURRENCE_STATUS","PRESENT"),
 pred_not(pred_in("BASIS_OF_RECORD",
  c("FOSSIL_SPECIMEN","LIVING_SPECIMEN")))
)
```

What happens internally

Internally, the input to `pred*` functions turns into JSON to be sent to GBIF. For example ...

`pred_in("taxonKey", c("9WLSS", "Q2N2"))` gives:

```
{
   "type": "in",
   "key": "TAXON_KEY",
   "values": ["9WLSS", "Q2N2"]
 }
```

`pred_gt("elevation", 5000)` gives:

```
{
   "type": "greaterThan",
   "key": "ELEVATION",
   "value": "5000"
}
```

`pred_or(pred("taxonKey", "Q2M4"), pred("taxonKey", "Q2KZ"))` gives:

```
{
  "type": "or",
  "predicates": [
     {
       "type": "equals",
       "key": "TAXON_KEY",
       "value": "Q2M4"
     },
     {
       "type": "equals",
       "key": "TAXON_KEY",
       "value": "Q2KZ"
     }
  ]
}
```

Keys

Acceptable arguments to the `key` parameter are (with the version of the key in parens that must be sent if you pass the query via the `body` parameter; see below for examples). You can also use the 'ALL_CAPS' version of a key if you prefer. Open an issue in the GitHub repository for this package if you know of a key that should be supported that is not yet.

- taxonKey (TAXON_KEY)
- acceptedTaxonKey (ACCEPTED_TAXON_KEY)
- kingdomKey (KINGDOM_KEY)
- phylumKey (PHYLUM_KEY)

- classKey (CLASS_KEY)
- orderKey (ORDER_KEY)
- familyKey (FAMILY_KEY)
- genusKey (GENUS_KEY)
- subgenusKey (SUBGENUS_KEY)
- speciesKey (SPECIES_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)
- modified (MODIFIED)
- continent (CONTINENT)
- geometry (GEOMETRY)
- basisOfRecord (BASIS_OF_RECORD)
- datasetKey (DATASET_KEY)
- datasetID/datasetId (DATASET_ID)
- eventDate (EVENT_DATE)
- catalogNumber (CATALOG_NUMBER)
- otherCatalogNumbers (OTHER_CATALOG_NUMBERS)
- 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)
- recordedById/recordedByID (RECORDED_BY_ID)
- establishmentMeans (ESTABLISHMENT_MEANS)
- coordinateUncertaintyInMeters (COORDINATE_UNCERTAINTY_IN_METERS)

- gadm (GADM_GID) (for the Database of Global Administrative Areas)
- level0Gid (GADM_LEVEL_0_GID)
- level1Gid (GADM_LEVEL_1_GID)
- level2Gid (GADM_LEVEL_2_GID)
- level3Gid (GADM_LEVEL_3_GID)
- stateProvince (STATE_PROVINCE)
- occurrenceStatus (OCCURRENCE_STATUS)
- publishingOrg (PUBLISHING_ORG)
- occurrenceId/occurrenceID (OCCURRENCE_ID)
- eventId/eventID (EVENT_ID)
- parentEventId/parentEventID (PARENT_EVENT_ID)
- identifiedBy (IDENTIFIED_BY)
- identifiedById/identifiedByID (IDENTIFIED_BY_ID)
- license (LICENSE) - Note: Use underscores, not spaces (e.g., "CC_BY_4_0" not "CC BY 4.0")
- locality(LOCALITY)
- pathway (PATHWAY)
- preparations (PREPARATIONS)
- networkKey (NETWORK_KEY)
- organismId/organismID (ORGANISM_ID)
- organismQuantity (ORGANISM_QUANTITY)
- organismQuantityType (ORGANISM_QUANTITY_TYPE)
- protocol (PROTOCOL)
- relativeOrganismQuantity (RELATIVE_ORGANISM_QUANTITY)
- repatriated (REPATRIATED)
- sampleSizeUnit (SAMPLE_SIZE_UNIT)
- sampleSizeValue (SAMPLE_SIZE_VALUE)
- samplingProtocol (SAMPLING_PROTOCOL)
- verbatimScientificName (VERBATIM_SCIENTIFIC_NAME)
- taxonID/taxonId (TAXON_ID)
- taxonomicStatus (TAXONOMIC_STATUS)
- waterBody (WATER_BODY)
- iucnRedListCategory (IUCN_RED_LIST_CATEGORY)
- degreeOfEstablishment (DEGREE_OF_ESTABLISHMENT)
- isInCluster (IS_IN_CLUSTER)
- lifeStage (LIFE_STAGE)
- distanceFromCentroidInMeters (DISTANCE_FROM_CENTROID_IN_METERS)
- gbifId (GBIF_ID)
- institutionKey (INSTITUTION_KEY)

References

Download predicates docs: https://www.gbif.org/developer/occurrence#predicates

See Also

Other downloads: occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dat occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

```
# Uses COL (Catalogue of Life) Extended Release alpha-numeric keys by default
pred("taxonKey", "Q2M4") # Calopteryx splendens
pred_gt("elevation", 5000)
pred_gte("elevation", 5000)
pred_lt("elevation", 1000)
pred_lte("elevation", 1000)
pred_within("POLYGON((-14 42, 9 38, -7 26, -14 42))")
pred_and(pred_within("POLYGON((-14 42, 9 38, -7 26, -14 42))"),
  pred_gte("elevation", 5000))
pred_or(pred_lte("year", 1989), pred("year", 2000))
pred_and(pred_lte("year", 1989), pred("year", 2000))
pred_in("taxonKey", c("Q2M4", "9WLSS", "Q2N2")) # COL XR alpha-numeric keys
pred_in("basisOfRecord", c("MACHINE_OBSERVATION", "HUMAN_OBSERVATION"))
pred_not(pred("taxonKey", "Q2M4"))
pred_like("catalogNumber", "PAPS5-560%")
pred_notnull("issue")
pred("basisOfRecord", "LITERATURE")
pred("hasCoordinate", TRUE)
pred("stateProvince", "California")
pred("hasGeospatialIssue", FALSE)
pred_within("POLYGON((-14 42, 9 38, -7 26, -14 42))")
pred_or(pred("taxonKey", "Q2M4"), pred("taxonKey", "9WLSS"),
  pred("taxonKey", "Q2N2"))
pred_in("taxonKey", c("Q2M4", "9WLSS", "Q2N2", "Q2KZ"))
pred("license", "CC_BY_4_0")
pred_in("license", c("CC_BY_4_0", "CC_BY_NC_4_0"))

# Using checklistKey with different taxonomic rank keys
pred("classKey", "B8V3Z")  # Uses COL XR by default
pred("orderKey", "C4PL")   # Uses COL XR by default
# Override to use GBIF Backbone
pred("classKey", "220", checklistKey = "d7dddbf4-2cf0-4f39-9b2a-bb099caae36c")
```

`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 = list(http_version = 2),
  ...
)
```

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, curlopts	defunct. see docs
...	curl options passed on to crul::verb-GET see `curl::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.

Deprecation Notice

This function is deprecated as of rgbif 3.9.0 and will be removed in a future version. It relies on a non-GBIF web service (GeoNames) and is not core to the package's purpose of interacting with GBIF data.

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 (http://www.geonames.org/manageaccount). 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

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

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

# Pass in a vector of lat's and a vector of long's
elevation(latitude = dat$data$decimalLatitude[1:10],
  longitude = dat$data$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$data$decimalLatitude[1:5]
lons <- dat$data$decimalLongitude[1:5]
elevation(latitude = lats, longitude = lons, elevation_model = "srtm3")
elevation(latitude = lats, longitude = lons, elevation_model = "srtm1")
elevation(latitude = lats, longitude = lons, elevation_model = "astergdem")
elevation(latitude = lats, longitude = lons, elevation_model = "gtopo30")

## End(Not run)
```

`enumeration` *Enumerations.*

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

```
enumeration(x = NULL, curlopts = list(http_version = 2))

enumeration_country(curlopts = list(http_version = 2))
```

Arguments

`x`	A given enumeration.
`curlopts`	list of named curl options passed on to `HttpClient`. see `curl::curl_options` for curl options

Value

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

Examples

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

```
# country enumeration
enumeration_country()

# curl options
enumeration(curlopts = list(verbose=TRUE))

## End(Not run)
```

---

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

```
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 charactere, 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

```
## 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` *Get citation for datasets used*

Description

Get citation for datasets used

Usage

```
gbif_citation(x)
```

Arguments

x	(character) Result of call to `occ_download_get()`, `occ_download_meta()`.

Details

The function is deprecated for use with `occ_search()` and `occ_data()` results, and is deprecated for use with datasetKeys and gbifids. Instead, we encourage you to use `derived_dataset()` instead.

`occ_download_get()` and `occ_download_meta()` results are still supported.

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

```
## Not run:
# Downloads
## occ_download_get()
# d1 <- occ_download(pred("country", "BG"), pred_gte("year", 2020))
# occ_download_meta(d1) # wait until status = succeeded
# d1 <- occ_download_get(d1, overwrite = TRUE)
# gbif_citation(d1)

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

## End(Not run)
```

gbif_geocode *Geocode lat-lon point(s) with GBIF's set of geo-polygons (experimental)*

Description

Geocode lat-lon point(s) with GBIF's set of geo-polygons (experimental)

Usage

```
gbif_geocode(
  latitude = NULL,
  longitude = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

latitude	a vector of numeric latitude values between -90 and 90.
longitude	a vector of numeric longitude values between -180 and 180.
curlopts	A list of curl options to pass to the request.

Value

A data.frame of results from the GBIF gecoding service.

- **latitude** : The input latitude
- **longitude** : The input longitude
- **index** : The original input rownumber
- **id** : The polygon id from which the geocode comes from
- **type** : One of the following : "Political" (county codes), "IHO" (marine regions), "SeaVox" (marine regions), "WGSRPD" (tdwg regions), "EEZ", (in national waters) or "GADM0","GADM1","GADM2","GADM
- **title** : The name of the source polygon
- **distance** : distance to the polygon boarder

This function uses the GBIF geocoder API which is not guaranteed to be stable and is undocumented. As such, this may return different data over time, may be rate-limited or may stop working if GBIF change the service. Use this function with caution.

References

http://gadm.org/ http://marineregions.org/ http://www.tdwg.org/standards/ http://api.gbif.org/v1/geocode/reverse?lat=0&lng=0

Examples

```
## Not run:
# one pair
gbif_geocode(0,0)
# or multiple pairs of points
gbif_geocode(c(0,50),c(0,20))


## End(Not run)
```

---

gbif_issues *List all GBIF issues and their codes.*

Description

Returns a data.frame of all GBIF issues with the following columns:

- code: issue short code, e.g. gass84
- code: issue full name, e.g. GEODETIC_DATUM_ASSUMED_WGS84
- description: issue description
- type: issue type, either related to occurrence or name

Usage

```
gbif_issues()
```

Source

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

---

gbif_issues_lookup *Lookup issue definitions and short codes*

Description

Lookup issue definitions and short codes

Usage

```
gbif_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

```
gbif_issues_lookup(issue = 'CONTINENT_COUNTRY_MISMATCH')
gbif_issues_lookup(code = 'ccm')
gbif_issues_lookup(issue = 'COORDINATE_INVALID')
gbif_issues_lookup(code = 'cdiv')
```

---

gbif_names *View highlighted terms in name results from GBIF.*

Description

View highlighted terms in name results from GBIF.

Usage

```
gbif_names(input, output = NULL, browse = TRUE)
```

Arguments

input	Input output from occ_search
output	Output folder path. If not given uses temporary folder.
browse	(logical) Browse output (default: TRUE)

Examples

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

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

# or not highlight
gbif_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

```
gbif_oai_identify(...)

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

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

gbif_oai_list_metadataformats(id = NULL, ...)

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

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

Arguments

...	Curl options passed on to `httr::GET`
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 datestamp to be used as lower bound for datestamp-based selective harvesting (i.e., only harvest records with datestamps 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/

Value

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

Examples

```
## 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

```
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

```
## Not run:
res <- occ_search(mediaType = 'StillImage', limit = 100)
gbif_photos(res)
gbif_photos(res, which='map')

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

## End(Not run)
```

gbif_to_col *Convert GBIF Backbone taxon keys to COL Extended Release keys*

Description

Convert GBIF Backbone taxon keys to COL Extended Release keys

Usage

```
gbif_to_col(
  key,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  curlopts = list(http_version = 2)
)
```

Arguments

key	(integer or character) One or more GBIF Backbone numeric taxon keys to convert to COL Extended Release alpha-numeric keys. Can be a single value or a vector of values.
checklistKey	(character) The key of the COL checklist to use. Defaults to COL Extended Release. Generally should not need to change this.
curlopts	A list of curl options passed on to `httr::GET()`.

Details

This function uses the GBIF species matching API with the `scientificNameID` parameter to resolve GBIF Backbone taxonomy keys to COL Extended Release keys. This is useful when migrating existing code from numeric GBIF Backbone keys to the new COL XR alpha-numeric keys.

Value

A list containing the full API response for each input key. Each element includes:

- `gbif_key` - The input GBIF Backbone key
- `usage` - The matched COL taxon usage details (including the COL key)
- `classification` - Full taxonomic classification path
- `diagnostics` - Match quality information (matchType, confidence, etc.)
- `additionalStatus` - Additional status information (e.g., IUCN status)
- `synonym` - Whether the match is a synonym

If only one key is provided, returns an object of class `gbif_to_col` with a custom print method. If multiple keys are provided, returns an object of class `gbif_to_col_list`. The full API response data is always accessible in the returned list structure.

References

https://techdocs.gbif.org/en/openapi/v1/species

Examples

```
## Not run:
# Convert a single GBIF Backbone key to COL XR
result <- gbif_to_col(5231190)  # Calopteryx splendens

# The print method shows a clean summary:
# <<GBIF to COL key conversion>>
#   GBIF Backbone key: 5231190
#   COL Extended Release key: Q2M4
#   Scientific name: Calopteryx splendens
#   Rank: SPECIES
#   Match type: EXACT
#   Confidence: 100

# Access the full data structure:
result$usage$key                # COL XR key: "Q2M4"
result$usage$name               # Scientific name
result$classification           # Full taxonomic hierarchy
result$diagnostics$matchType    # Quality of match
result$diagnostics$confidence   # Confidence score

# Convert multiple keys at once
results <- gbif_to_col(c(5231190, 2435099, 2877951))
results  # Shows summary for all matches

# Extract specific data from multiple results:
sapply(results, function(x) x$usage$key)  # Extract all COL keys
sapply(results, function(x) x$usage$name) # Extract all names

## 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(http_version = 2)
)
```

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::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.
- URI No description.
- URL No description.
- UUID No description.

References

https://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(verbose=TRUE))

## End(Not run)
```

---

installation_search *Search for installations*

Description

Search for installations

Usage

```
installation_search(
  query = NULL,
  type = NULL,
  identifierType = NULL,
  identifier = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  modified = NULL,
  limit = 20,
  offset = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

query	A search query string.
type	Choose from : IPT_INSTALLATION, DGIR INSTALLATION, TAPIR_INSTALLATION, BIOCASE_INSTALLATION, HTTP_INSTALLATION, SYMBIOTA_INSTALLATION, EARTHCAPE_INSTALLATION, MDT_INSTALLATION. Only accepts one value.

identifierType Choose from : URL, LSID, HANDLER, DOI, UUID, FTP, URI, UNKNOWN, GBIF_PORTAL, GBIF_NODE, GBIF_PARTICIPANT, GRSCICOLL_ID, GRSCICOLL_URI, IH_IRN, ROR, GRID, CITES, SYMBIOTA_UUID, WIKIDATA, NCBI_BIOCOLLECTION, ISIL, CLB_DATASET_KEY.

identifier An identifier of the type given by the identifierType parameter, for example a DOI or UUID.

machineTagNamespace Filters for entities with a machine tag in the specified namespace.

machineTagName Filters for entities with a machine tag with the specified name (use in combination with the machineTagNamespace parameter).

machineTagValue Filters for entities with a machine tag with the specified value (use in combination with the machineTagNamespace and machineTagName parameters).

modified The modified date of the dataset. Accepts ranges and a * can be used as a wildcard, e.g. modified=2023-04-01,*

limit The maximum number of results to return. Defaults to 20.

offset The offset of the first result to return.

curlopts A list of curl options to pass to the request.

Value

A list

Examples

```
## Not run:
installation_search()
installation_search(query="Estonia")
installation_search(type="IPT_INSTALLATION")
installation_search(modified="2023-04-01,*")


## End(Not run)
```

---

installation_uuid_funs

Get installation metadata using an installation key

Description

Get installation metadata using an installation key

Usage

```
installation_dataset(
  uuid = NULL,
  limit = 20,
  start = NULL,
  curlopts = list(http_version = 2)
)

installation_comment(uuid = NULL, curlopts = list(http_version = 2))

installation_contact(uuid = NULL, curlopts = list(http_version = 2))

installation_endpoint(uuid = NULL, curlopts = list(http_version = 2))

installation_identifier(uuid = NULL, curlopts = list(http_version = 2))

installation_machinetag(uuid = NULL, curlopts = list(http_version = 2))

installation_tag(uuid = NULL, curlopts = list(http_version = 2))
```

Arguments

uuid	A GBIF installationKey uuid.
limit	The number of results to return. Default is 20.
start	The offset of the first result to return.
curlopts	A list of curl options to pass to the request.

Value

A tibble or a list.

Examples

```
## Not run:
# Get all datasets for a given installation
installation_dataset(uuid="d209e552-7e6e-4840-b13c-c0596ef36e55", limit=10)
installation_comment(uuid="a0e05292-3d09-4eae-9f83-02ae3516283c")
installation_contact(uuid="896898e8-c0ac-47a0-8f38-0f792fbe3343")
installation_endpoint(uuid="896898e8-c0ac-47a0-8f38-0f792fbe3343")
installation_identifier(uuid="896898e8-c0ac-47a0-8f38-0f792fbe3343")
installation_machinetag(uuid="896898e8-c0ac-47a0-8f38-0f792fbe3343")

## End(Not run)
```

`institution_search` *Search GRSciColl institutions*

Description

Search GRSciColl institutions

Usage

```
institution_search(
  query = NULL,
  type = NULL,
  institutionalGovernance = NULL,
  disciplines = NULL,
  discipline = NULL,
  name = NULL,
  fuzzyName = NULL,
  numberSpecimens = NULL,
  occurrenceCount = NULL,
  typeSpecimenCount = NULL,
  sourceId = NULL,
  source = NULL,
  code = NULL,
  alternativeCode = NULL,
  contact = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  institutionKey = NULL,
  country = NULL,
  city = NULL,
  gbifRegion = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  identifier = NULL,
  identifierType = NULL,
  active = NULL,
  displayOnNHCPortal = NULL,
  masterSourceType = NULL,
  replacedBy = NULL,
  sortBy = NULL,
  sortOrder = NULL,
  offset = NULL,
  limit = NULL,
  format = NULL,
  curlopts = list(http_version = 2)
)
```

```
institution_export(
  query = NULL,
  type = NULL,
  institutionalGovernance = NULL,
  disciplines = NULL,
  name = NULL,
  fuzzyName = NULL,
  numberSpecimens = NULL,
  occurrenceCount = NULL,
  typeSpecimenCount = NULL,
  institution = NULL,
  contentType = NULL,
  preservationType = NULL,
  accessionStatus = NULL,
  personalCollection = NULL,
  sourceId = NULL,
  source = NULL,
  code = NULL,
  alternativeCode = NULL,
  contact = NULL,
  contactUserId = NULL,
  contactEmail = NULL,
  institutionKey = NULL,
  country = NULL,
  city = NULL,
  gbifRegion = NULL,
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  identifier = NULL,
  identifierType = NULL,
  active = NULL,
  displayOnNHCPortal = NULL,
  masterSourceType = NULL,
  replacedBy = NULL,
  sortBy = NULL,
  sortOrder = NULL,
  offset = NULL,
  limit = NULL,
  format = "TSV",
  curlopts = list()
)
```

Arguments

query	(character) Simple full text search parameter. The value for this parameter can be a simple word or a phrase. Wildcards are not supported

type (character) Type of a GrSciColl institution Available values : BIOMEDICAL_RESEARCH_INSTITUTE, BOTANICAL_GARDEN, HERBARIUM, LIVING_ORGANISM_COLLECTION, MEDICAL_RESEARCH_INSTITUTE, MUSEUM, MUSEUM_HERBARIUM_PRIVATE_NON_PROF OTHER_INSTITUTIONAL_TYPE, OTHER_TYPE_RESEARCH_INSTITUTION_BIOREPOSITORY UNIVERSITY_COLLEGE, ZOO_AQUARIUM

institutionalGovernance (character) Instutional governance of a GrSciColl institution Available values : ACADEMIC_FEDERAL, ACADEMIC_FOR_PROFIT, ACADEMIC_LOCAL, ACADEMIC_NON_PROFIT, ACADEMIC_STATE, FEDERAL, FOR_PROFIT, LOCAL, NON_PROFIT, OTHER, STATE.

disciplines (character) Discipline of a GrSciColl institution. Check available values : https://techdocs.gbif.org/en/ope

discipline (character) Discipline of a GrSciColl institution. Optional parameter for filtering results.

name (character) Name of a GrSciColl institution or collection

fuzzyName (character) It searches by name fuzzily so the parameter doesn't have to be the exact name.

numberSpecimens (character) Number of specimens. It supports ranges and a * can be used as a wildcard.

occurrenceCount (character) Count of occurrences linked. It supports ranges and a * can be used as a wildcard.

typeSpecimenCount (character) Count of type specimens linked. It supports ranges and a * can be used as a wildcard.

sourceId (character) sourceId of MasterSourceMetadata

source (character) Source attribute of MasterSourceMetadata Available values : DATASET, ORGANIZATION, IH_IRN

code (character) Code of a GrSciColl institution or collection.

alternativeCode (character) Alternative code of a GrSciColl institution.

contact (character) Filters collections and institutions whose contacts contain the person key specified.

contactUserId (numeric) Filters institutions by the user ID of a contact. Optional parameter for filtering results.

contactEmail (character) Filters institutions by the email of a contact. Optional parameter for filtering results.

institutionKey (character) Keys of institutions to filter by.

country (character) Filters by country given as a ISO 639-1 (2 letter) country code.

city (character) Filters by the city of the address. It searches in both the physical and the mailing address.

gbifRegion (character) Filters by a gbif region. Available values : AFRICA, ASIA, EUROPE, NORTH_AMERICA, OCEANIA, LATIN_AMERICA, ANTARCTICA.

machineTagNamespace
: (character) Filters for entities with a machine tag in the specified namespace.

machineTagName
: (character) Filters for entities with a machine tag with the specified name (use in combination with the machineTagNamespace parameter).

machineTagValue
: (character) Filters for entities with a machine tag with the specified value (use in combination with the machineTagNamespace and machineTagName parameters).

identifier
: (character) An identifier of the type given by the identifierType parameter, for example a DOI or UUID.

identifierType
: (character) An identifier type for the identifier parameter. Available values : URL, LSID, HANDLER, DOI, UUID, FTP, URI, UNKNOWN, GBIF_PORTAL, GBIF_NODE, GBIF_PARTICIPANT, GRSCICOLL_ID, GRSCICOLL_URI, IH_IRN, ROR, GRID, CITES, SYMBIOTA_UUID, WIKIDATA, NCBI_BIOCOLLECTION, ISIL, CLB_DATASET_KEY.

active
: (logical) Active status of a GrSciColl institution or collection.

displayOnNHCPortal
: (logical) Flag to show this record in the NHC portal.

masterSourceType
: (character) The master source type of a GRSciColl institution or collection. Available values : GRSCICOLL, GBIF_REGISTRY, IH.

replacedBy
: (character) Key of the entity that replaced another entity.

sortBy
: (character) Field to sort the results by. It only supports the fields contained in the enum. Available values : NUMBER_SPECIMENS.

sortOrder
: (character) Sort order to use with the sortBy parameter. Available values : ASC, DESC.

offset
: (numeric) Determines the offset for the search results.

limit
: (numeric) Controls the number of results in the page. Default 20.

format
: (character) Format of the export. Default is "TSV". Only used for institution_export.

curlopts
: (list) curlopts options passed on to crul::HttpClient.

institution
: (character) Filters collections by institution key or name. Optional parameter for filtering results. Only used for institution_export.

contentType
: (character) Content type of a GrSciColl collection. Optional parameter for filtering results. Only used for institution_export.

preservationType
: (character) Preservation type of a GrSciColl collection. Optional parameter for filtering results. Only used for institution_export.

accessionStatus
: (character) Accession status of a GrSciColl collection. Optional parameter for filtering results. Only used for institution_export.

personalCollection
: (logical) Whether the collection is a personal collection. Optional parameter for filtering results. Only used for institution_export.

Details

Will return GRSciColl collections data. institution_export will return all of the results in a single `tibble`, while institution_search will return a sample of results.

Value

A `list`

Examples

```
## Not run:
institution_search(query="Kansas",limit=1)
institution_search(numberSpecimens = "1000,*",limit=2)
institution_search(source = "IH_IRN")
institution_search(country = "US;GB")
institution_search(typeSpecimenCount = "10,100")


## End(Not run)
```

---

lit_search *Search for literature that cites GBIF mediated data*

Description

Search for literature that cites GBIF mediated data

Usage

```
lit_search(
  q = NULL,
  countriesOfResearcher = NULL,
  countriesOfCoverage = NULL,
  literatureType = NULL,
  relevance = NULL,
  year = NULL,
  topics = NULL,
  datasetKey = NULL,
  publishingOrg = NULL,
  peerReview = NULL,
  openAccess = NULL,
  downloadKey = NULL,
  doi = NULL,
  journalSource = NULL,
  journalPublisher = NULL,
  flatten = TRUE,
  abstract = FALSE,
  limit = NULL,
```

```
  curlopts = list(http_version = 2)
)

lit_count(...)

lit_export(
  q = NULL,
  countriesOfResearcher = NULL,
  countriesOfCoverage = NULL,
  literatureType = NULL,
  relevance = NULL,
  year = NULL,
  topics = NULL,
  datasetKey = NULL,
  publishingOrg = NULL,
  peerReview = NULL,
  openAccess = NULL,
  downloadKey = NULL,
  doi = NULL,
  journalSource = NULL,
  journalPublisher = NULL,
  flatten = NULL,
  abstract = FALSE,
  limit = NULL,
  curlopts = list()
)
```

Arguments

q	(character) Simple full text search parameter. The value for this parameter can be a simple word or a phrase. Wildcards are not supported.
countriesOfResearcher	(character) Country of institution with which author is affiliated, e.g. DK (for Denmark). Country codes are listed in enumeration_country().
countriesOfCoverage	(character) Country of focus of study, e.g. BR (for Brazil). Country codes are listed in enumeration_country().
literatureType	(character) Type of literature ("JOURNAL", "BOOK_SECTION", "WORKING_PAPER", "REPORT", "GENERIC", "THESIS", "CONFERENCE_PROCEEDINGS", "WEB_PAGE").
relevance	(character) How is the publication relate to GBIF. See details ("GBIF_USED", "GBIF_MENTIONED", "GBIF_PUBLISHED", "GBIF_CITED", "GBIF_CITED", "GBIF_PUBLISHED", "GBIF_ACKNOWLEDGED", "GBIF_AUTHOR").
year	(integer) Year of publication.
topics	(character) Topic of publication.
datasetKey	(character) GBIF dataset uuid referenced in publication.
publishingOrg	(character) Publisher uuid whose dataset is referenced in publication.

peerReview	(logical) Has publication undergone peer-review?
openAccess	(logical) Is publication Open Access?
downloadKey	(character) Download referenced in publication.
doi	(character) Digital Object Identifier (DOI).
journalSource	(character) Journal of publication.
journalPublisher	(character) Publisher of journal.
flatten	(logical) should any lists in the resulting data be flattened into comma-seperated strings? Ignored in lit_export.
abstract	(logical) should the abstract be included in the results. Ignored for lit_search.
limit	how many records to return. limit=NULL will fetch up to 10,000.
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options.
...	additional parameters passed to lit_search

Details

This function enables you to search for literature indexed by GBIF, including peer-reviewed papers, citing GBIF datasets and downloads. The literature API powers the literature search on GBIF.

The GBIF Secretariat maintains an ongoing literature tracking programme, which identifies research uses and citations of biodiversity information accessed through GBIF's global infrastructure.

In the literature database, **relevance** refers to how publications relate to GBIF following these definitions:

- GBIF_USED : makes substantive use of data in a quantitative analysis (e.g. ecological niche modelling)
- GBIF_CITED : cites a qualitative fact derived in data (e.g. a given species is found in a given country)
- GBIF_DISCUSSED : discusses GBIF as an infrastructure or the use of data
- GBIF_PRIMARY : GBIF is the primary source of data (no longer applied)
- GBIF_ACKNOWLEDGED : acknowledges GBIF (but doesn't use or cite data)
- GBIF_PUBLISHED : describes or talks about data published to GBIF
- GBIF_AUTHOR : authored by GBIF staff
- GBIF_MENTIONED : unspecifically mentions GBIF or the GBIF portal
- GBIF_FUNDED : funded by GBIF or a GBIF-managed funding programme

The following arguments can take multiple values:

- relevance
- countriesOfResearcher
- countriesOfCoverage
- literatureType

- topics
- datasetKey
- publishingOrg
- downloadKey
- doi
- journalSource
- journalPublisher

If `flatten=TRUE`, then **data** will be returned as flat data.frame with no complex column types (i.e. no lists or data.frames).

`limit=NULL` will return up to 10,000 records. The maximum value for `limit` is 10,000. If no filters are used, only the first 1,000 records will be returned, limit must be explicitly set to `limit=10000`, to get the first 10,000 records in this case.

`lit_count()` is a convenience wrapper, which will return the number of literature references for a certain `lit_search()` query. This is the same as running `lit_search()$meta$count`.

Value

A named list with two values: `$data` and `$meta`. `$data` is a `data.frame` of literature references.

Examples

```
## Not run:
lit_search(q="bats")$data
lit_search(datasetKey="50c9509d-22c7-4a22-a47d-8c48425ef4a7")
lit_search(year=2020)
lit_search(year="2011,2020") # year ranges
lit_search(relevance=c("GBIF_CITED","GBIF_USED")) # multiple values
lit_search(relevance=c("GBIF_USED","GBIF_CITED"),
topics=c("EVOLUTION","PHYLOGENETICS"))
lit_count() # total number of literature referencing GBIF
lit_count(peerReview=TRUE)
# number of citations of iNaturalist
lit_count(datasetKey="50c9509d-22c7-4a22-a47d-8c48425ef4a7")
# number of peer-reviewed articles used GBIF mediated data
lit_count(peerReview=TRUE,literatureType="JOURNAL",relevance="GBIF_USED")

# Typically what is meant by "literature that uses GBIF"
lit_search(peerReview=TRUE,literatureType="JOURNAL",relevance="GBIF_USED")
lit_count(peerReview=TRUE,literatureType="JOURNAL",relevance="GBIF_USED")

## End(Not run)
```

`map_fetch` *Fetch 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 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

Usage

```
map_fetch(
  source = "density",
  x = 0:1,
  y = 0,
  z = 0,
  format = "@1x.png",
  srs = "EPSG:4326",
  bin = NULL,
  hexPerTile = NULL,
  squareSize = NULL,
  style = NULL,
  taxonKey = NULL,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  datasetKey = NULL,
  country = NULL,
  publishingOrg = NULL,
  publishingCountry = NULL,
  year = NULL,
  basisOfRecord = NULL,
  return = "png",
  base_style = NULL,
  plot_terra = TRUE,
  curlopts = list(http_version = 2),
  ...
)
```

Arguments

`source`	(character) Either `density` for fast, precalculated tiles, or `adhoc` for any search. Default: `density`
`x`	(integer sequence) the column. Default: 0:1
`y`	(integer sequence) the row. Default: 0

`z` (integer) the zoom. Default: 0

`format` (character) The data format, one of:

- `@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.

`hexPerTile` (integer) sets the size of the hexagons (the number horizontally across a tile).

`squareSize` (integer) sets the size of the squares. Choose a factor of 4096 so they tessalate correctly: probably from 8, 16, 32, 64, 128, 256, 512.

`style` (character) for raster tiles, choose from the available styles. Defaults to classic.point for source="density" and "scaled.circle" for source="adhoc".

`taxonKey` (integer/numeric/character) search by taxon key, can only supply 1.

`checklistKey` (character) The key of a checklist to use for taxonomy. Defaults to COL (Catalogue of Life) Extended Release (`"7ddf754f-d193-4cc9-b351-99906754a03b"`). Set to `NULL` to use the GBIF Backbone Taxonomy.

`datasetKey` (character) search by taxon key, can only supply 1.

`country` (character) search by taxon key, can only supply 1.

`publishingOrg` (character) search by taxon key, can only supply 1.

`publishingCountry` (character) search by taxon key, can only supply 1.

`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")`.

`return` (character) Either "png" or "terra".

`base_style` (character) The style of the base map.

`plot_terra` (logical) Set whether the terra map be default plotted.

`curlopts` options passed on to crul::HttpClient

`...` additional arguments passed to the adhoc interface.

Details

The default settings, `return='png'`, will return a `magick-image` png. This image will be a composite image of the the occurrence tiles fetched and a base map. This map is primarily useful as a high quality image of occurrence records.

The args `x` and `y` can both be integer sequences. For example, `x=0:3` or `y=0:1`. Note that the tile index starts at 0. Higher values of `z`, will will produce more tiles that can be fetched and stitched together. Selecting a too high value for `x` or `y` will produce a blank image.

Setting `return='terra'` will return a `terra::SpatRaster` object. This is primarily useful if you were interested in the underlying aggregated occurrence density data.

See the article

Value

a `magick-image` or `terra::SpatRaster` object.

Author(s)

John Waller and Laurens Geffert <laurensgeffert@gmail.com>

References

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

https://api.gbif.org/v2/map/demo.html

https://api.gbif.org/v2/map/demo13.html

See Also

`mvt_fetch()`

Examples

```
## Not run:

# all occurrences
map_fetch()
# get artic map
map_fetch(srs='EPSG:3031')
# only preserved specimens
map_fetch(basisOfRecord="PRESERVED_SPECIMEN")

# Map of occ in Great Britain
map_fetch(z=3,y=1,x=7:8,country="GB")
# Penguins with artic projection using COL XR key
map_fetch(srs='EPSG:3031',taxonKey="623RM",style='glacier.point',
base_style="gbif-dark")

# occ from a long time ago
map_fetch(year=1600)
# polygon style
```

```
map_fetch(style="iNaturalist.poly",bin="hex")
# iNaturalist dataset plotted
map_fetch(datasetKey="50c9509d-22c7-4a22-a47d-8c48425ef4a7",
  style="iNaturalist.poly")

# use source="adhoc" for more filters
map_fetch(z=1,
  source="adhoc",
  iucn_red_list_category="CR",
  style="scaled.circles",
  base_style='gbif-light')

# cropped map of Hawaii
map_fetch(z=5,x=3:4,y=12,source="adhoc",gadmGid="USA.12_1")



## End(Not run)
```

`mvt_fetch` *Fetch Map Vector Tiles (MVT)*

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 maps vector tiles 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

Usage

```
mvt_fetch(
  source = "density",
  x = 0,
  y = 0,
  z = 0,
  srs = "EPSG:4326",
  bin = NULL,
  hexPerTile = NULL,
  squareSize = NULL,
  style = "classic.point",
  taxonKey = NULL,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  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 column. Default: 0
y	(integer) the row. Default: 0
z	(integer) the zoom. Default: 0
srs	(character) Spatial reference system for the output (input srs for mvt from GBIF is always EPSG:3857). 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 tessalate correctly: probably from 8, 16, 32, 64, 128, 256, 512. optional
style	(character) for raster tiles, choose from the available styles. Defaults to classic.point. optional. THESE DON'T WORK YET.
taxonKey	(integer/numeric/character) search by taxon key, can only supply 1. optional
checklistKey	(character) The key of a checklist to use for taxonomy. Defaults to COL (Catalogue of Life) Extended Release ("7ddf754f-d193-4cc9-b351-99906754a03b"). Set to NULL to use the GBIF Backbone Taxonomy. 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
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 crul::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 sf object

References

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

See Also

map_fetch()

Examples

```
## Not run:
if (
 requireNamespace("sf", quietly = TRUE) &&
 requireNamespace("protolite", quietly = TRUE)
) {
  # Using COL XR taxon key (default)
  x <- mvt_fetch(taxonKey = "V2", year = 2007:2011)
  x

  # gives an sf object
  class(x)

  # different srs
  ## 3857
  y <- mvt_fetch(taxonKey = "V2", year = 2010, srs = "EPSG:3857")
  y
  ## 3031
  z <- mvt_fetch(taxonKey = "V2", year = 2010, srs = "EPSG:3031", verbose = TRUE)
  z
  # 3575
  z <- mvt_fetch(taxonKey = "V2", year = 2010, srs = "EPSG:3575")
  z

  # bin
  x <- mvt_fetch(taxonKey = "V2", year = 1998, bin = "hex",
     hexPerTile = 30, style = "classic-noborder.poly")
  x

  # query with basisOfRecord
```

```
  mvt_fetch(taxonKey = "V2", year = 2010,
    basisOfRecord = "HUMAN_OBSERVATION")
  mvt_fetch(taxonKey = "V2", year = 2010,
    basisOfRecord = c("HUMAN_OBSERVATION", "LIVING_SPECIMEN"))
 }

## End(Not run)
```

---

name_backbone *Match names to GBIF backbone and other checklists.*

Description

Match names to GBIF backbone and other checklists.

Usage

```
name_backbone(
  name = NULL,
  rank = NULL,
  kingdom = NULL,
  phylum = NULL,
  class = NULL,
  order = NULL,
  superfamily = NULL,
  family = NULL,
  subfamily = NULL,
  tribe = NULL,
  subtribe = NULL,
  genus = NULL,
  subgenus = NULL,
  species = NULL,
  usageKey = NULL,
  taxonID = NULL,
  taxonConceptID = NULL,
  scientificNameID = NULL,
  scientificNameAuthorship = NULL,
  genericName = NULL,
  specificEpithet = NULL,
  infraspecificEpithet = NULL,
  verbatimTaxonRank = NULL,
  exclude = NULL,
  strict = NULL,
  verbose = FALSE,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  start = NULL,
  limit = NULL,
  curlopts = list(http_version = 2)
```

```
)

name_backbone_verbose(
  name = NULL,
  rank = NULL,
  kingdom = NULL,
  phylum = NULL,
  class = NULL,
  order = NULL,
  superfamily = NULL,
  family = NULL,
  subfamily = NULL,
  tribe = NULL,
  subtribe = NULL,
  genus = NULL,
  subgenus = NULL,
  species = NULL,
  usageKey = NULL,
  taxonID = NULL,
  taxonConceptID = NULL,
  scientificNameID = NULL,
  scientificNameAuthorship = NULL,
  genericName = NULL,
  specificEpithet = NULL,
  infraspecificEpithet = NULL,
  verbatimTaxonRank = NULL,
  exclude = NULL,
  strict = NULL,
  checklistKey = NULL,
  start = NULL,
  limit = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

name	(character) Full scientific name potentially with authorship (required)
rank	(character) Filter by taxonomic rank. See API reference for available values.
kingdom	(character) Kingdom to match.
phylum	(character) Phylum to match.
class	(character) Class to match.
order	(character) Order to match.
superfamily	(character) Superfamily to match.
family	(character) Family to match.
subfamily	(character) Subfamily to match.
tribe	(character) Tribe to match.

subtribe	(character) Subtribe to match.
genus	(character) Genus to match.
subgenus	(character) Subgenus to match.
species	(character) Species to match.
usageKey	(character) The usage key to look up. When provided, all other fields are ignored.
taxonID	(character) The taxon ID to look up. Matches to a taxonID will take precedence over scientificName values supplied. A comparison of the matched scientific and taxonID is performed tocheck for inconsistencies.
taxonConceptID	(character) The taxonConceptID to match. Matches to a taxonConceptID will take precedence over scientificName values supplied. A comparison of the matched scientific and taxonConceptID is performed to check for inconsistencies.
scientificNameID	(character) Matches to a scientificNameID will take precedence over scientificName values supplied. A comparison of the matched scientific and scientificNameID is performed to check for inconsistencies.
scientificNameAuthorship	(character) The scientific name authorship to match against.
genericName	(character) Generic part of the name to match when given as atomised parts instead of the full name parameter.
specificEpithet	(character) Specific epithet to match.
infraspecificEpithet	(character) Infraspecific epithet to match.
verbatimTaxonRank	(character) Filters by free text taxon rank.
exclude	(character) An array of usage keys to exclude from the match.
strict	(logical) If set to true, fuzzy matches only the given name, but never a taxon in the upper classification.
verbose	(logical) If set to true, it shows alternative matches which were considered but then rejected.
checklistKey	(character) The key of a checklist to use. The default is the GBIF Backbone taxanomy.
start	(integer) Currently ignored.
limit	(integer) Currently ignored.
curlopts	A list of curl options passed on to `httr::GET()`.

Details

If you don't get a match, GBIF gives back a data.frame with columns `synonym`, `confidence`, and `matchType='NONE'`.

`name_backbone_verbose()` is a legacy wrapper function that returns returns alternatives in a separate `tibble`.

Value

A single row `tibble` of the best matched name. If `verbose=TRUE`, a longer `tibble` with all potential alternatives is returned.

References

https://techdocs.gbif.org/en/openapi/v1/species#/Searching%20names/matchNames

Examples

```
## Not run:
# Returns COL (Catalogue of Life) Extended Release alpha-numeric keys
name_backbone("Calopteryx splendens") # Returns usageKey "Q2M4"
name_backbone("Calopteryx splendens", kingdom = "Animalia")
name_backbone("Calopteryx splendens", kingdom = "Animalia", verbose = TRUE)
name_backbone_verbose("Calopteryx splendens", kingdom = "Animalia")
name_backbone("Calopteryx splendens", kingdom = "Plantae")

# Use GBIF Backbone Taxonomy by explicitly setting checklistKey
name_backbone("Calopteryx splendens",
  checklistKey = "d7dddbf4-2cf0-4f39-9b2a-bb099caae36c")


## End(Not run)
```

---

name_backbone_checklist

Match names in the GBIF backbone taxonomy in a checklist.

Description

Match names in the GBIF backbone taxonomy in a checklist.

Usage

```
name_backbone_checklist(
  name_data,
  rank = NULL,
  kingdom = NULL,
  phylum = NULL,
  class = NULL,
  order = NULL,
  superfamily = NULL,
  family = NULL,
  subfamily = NULL,
  tribe = NULL,
  subtribe = NULL,
  genus = NULL,
```

```
  subgenus = NULL,
  species = NULL,
  usageKey = NULL,
  taxonID = NULL,
  taxonConceptID = NULL,
  scientificNameID = NULL,
  scientificNameAuthorship = NULL,
  genericName = NULL,
  specificEpithet = NULL,
  infraspecificEpithet = NULL,
  verbatimTaxonRank = NULL,
  exclude = NULL,
  strict = NULL,
  verbose = NULL,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  bucket_size = 300,
  sleep = 1,
  curlopts = list(http_version = 2)
)
```

Arguments

name_data	name_data (data.frame or vector) see details. (required)
rank	(character) Filter by taxonomic rank. See API reference for available values.
kingdom	(character) Kingdom to match.
phylum	(character) Phylum to match.
class	(character) Class to match.
order	(character) Order to match.
superfamily	(character) Superfamily to match.
family	(character) Family to match.
subfamily	(character) Subfamily to match.
tribe	(character) Tribe to match.
subtribe	(character) Subtribe to match.
genus	(character) Genus to match.
subgenus	(character) Subgenus to match.
species	(character) Species to match.
usageKey	(character) The usage key to look up. When provided, all other fields are ignored.
taxonID	(character) The taxon ID to look up. Matches to a taxonID will take precedence over scientificName values supplied. A comparison of the matched scientific and taxonID is performed tocheck for inconsistencies.
taxonConceptID	(character) The taxonConceptID to match. Matches to a taxonConceptID will take precedence over scientificName values supplied. A comparison of the matched scientific and taxonConceptID is performed to check for inconsistencies.

`scientificNameID`
: (character) Matches to a scientificNameID will take precedence over scientificName values supplied. A comparison of the matched scientific and scientificNameID is performed to check for inconsistencies.

`scientificNameAuthorship`
: (character) The scientific name authorship to match against.

`genericName`
: (character) Generic part of the name to match when given as atomised parts instead of the full name parameter.

`specificEpithet`
: (character) Specific epithet to match.

`infraspecificEpithet`
: (character) Infraspecific epithet to match.

`verbatimTaxonRank`
: (character) Filters by free text taxon rank.

`exclude`
: (character) An array of usage keys to exclude from the match.

`strict`
: (logical) If set to true, fuzzy matches only the given name, but never a taxon in the upper classification.

`verbose`
: (logical) If true it shows alternative matches which were considered but then rejected.

`checklistKey`
: (character) The key of a checklist to use. The default is COL (Catalogue of Life) Extended Release with UUID "7ddf754f-d193-4cc9-b351-99906754a03b".

`bucket_size`
: (integer) Number of requests to make in parallel. Default: 300. Lower this number if you get HTTP 0 errors.

`sleep`
: (integer) Number of seconds to wait between batches of requests. Default: 1 second.

`curlopts`
: A list of curl options passed on to `httr::GET()`.#'

Details

This function is an alternative for `name_backbone()`, which will work with a list of names (a vector or a data.frame). The `data.frame` can have any of the arguments as column names. The arguments can also be used as default values, and then don't need to be repeated as values in the input `name_data`. If only one column is present, then that column is assumed to be the scientificName column.

The input columns will be returned as "verbatim_scientificName","verbatim_rank", "verbatim_phylum" ect.

If `verbose=TRUE`, a column called `is_alternative` will be returned, which species if a name was originally a first choice or not. `is_alternative=TRUE` means the name was not is not considered to be the best match by GBIF.

Default values for any of the other arguments can can be supplied. If a default value is supplied, the values for these fields are ignored in `name_data`, and the default value is used instead. This is most useful if you have a list of names and you know they are all plants, insects, birds, ect. You can also input multiple values, if they are the same length as list of names you are trying to match.

This function can also be used with a character vector of names. In that case no column names are needed of course.

This function is very similar to the GBIF species-lookup tool. https://www.gbif.org/tools/species-lookup.

If you have 1000s of names to match, it can take some minutes to get back all of the matches. I have tested it with 60K names. Scientific names with author details usually get better matches.

See also article Working With Taxonomic Names.

Value

A `data.frame` of matched names.

Examples

```
## Not run:
name_data <- data.frame(
 scientificName = c(
   "Cirsium arvense (L.) Scop.", # a plant
   "Calopteryx splendens (Harris, 1780)", # an insect
   "Puma concolor (Linnaeus, 1771)", # a big cat
   "Ceylonosticta alwisi (Priyadarshana & Wijewardhane, 2016)", # newly discovered insect
   "Puma concuolor (Linnaeus, 1771)", # a mis-spelled big cat
   "Fake species (John Waller 2021)", # a fake species
   "Calopteryx" # Just a Genus
 ), description = c(
   "a plant",
   "an insect",
   "a big cat",
   "newly discovered insect",
   "a mis-spelled big cat",
   "a fake species",
   "just a GENUS"
 ),
 kingdom = c(
   "Plantae",
   "Animalia",
   "Animalia",
   "Animalia",
   "Animalia",
   "Johnlia",
   "Animalia"
 ))

name_backbone_checklist(name_data)

# return more than 1 result per name
name_backbone_checklist(name_data,verbose=TRUE)

# works with just vectors too
name_list <- c(
"Cirsium arvense (L.) Scop.",
"Calopteryx splendens (Harris, 1780)",
"Puma concolor (Linnaeus, 1771)",
"Ceylonosticta alwisi (Priyadarshana & Wijewardhane, 2016)",
```

```
"Puma concuolor",
"Fake species (John Waller 2021)",
"Calopteryx")

name_backbone_checklist(name_list)
name_backbone_checklist(name_list,verbose=TRUE)
name_backbone_checklist(name_list,strict=TRUE)

# default values
name_backbone_checklist(c("Aloe arborecens Mill.",
"Cirsium arvense (L.) Scop."),kingdom="Plantae")
name_backbone_checklist(c("Aloe arborecens Mill.",
"Calopteryx splendens (Harris, 1780)"),kingdom=c("Plantae","Animalia"))


## End(Not run)
```

`name_issues` *Parse and examine further GBIF name issues on a dataset.*

Description

Parse and examine further GBIF name issues on a dataset.

Usage

```
name_issues(.data, ..., mutate = NULL)
```

Arguments

`.data`	Output from a call to `name_usage()`
`...`	Named parameters to only get back (e.g. bbmn), or to remove (e.g. -bbmn).
`mutate`	(character) One of: • `split` Split issues into new columns. • `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. • `split_expand` Split into new columns, and expand issue names. For split and split_expand, values in cells become y ("yes") or n ("no")

Deprecation Notice

This function is deprecated. It depends on `name_usage()` which only works with the GBIF Backbone Taxonomy. Use `rcol::col_usage()` from the rcol package to parse and examine name issues with COL XR support.

References

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

Examples

```
## Not run:
# what do issues mean, can print whole table
head(gbif_issues())
# or just name related issues
gbif_issues()[which(gbif_issues()$type %in% c("name")),]
# or search for matches
gbif_issues()[gbif_issues()$code %in% c('bbmn','clasna','scina'),]
# compare out data to after name_issues use
(aa <- name_usage(name = "Lupus"))
aa %>% name_issues("clasna")

## or parse issues in various ways
### remove data rows with certain issue classes
aa %>% name_issues(-clasna, -scina)

### expand issues to more descriptive names
aa %>% name_issues(mutate = "expand")

### split and expand
aa %>% name_issues(mutate = "split_expand")

### split, expand, and remove an issue class
aa %>% name_issues(-bbmn, mutate = "split_expand")

## Or you can use name_issues without %>%
name_issues(aa, -bbmn, mutate = "split_expand")

## End(Not run)
```

---

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

```
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,
  issue = NULL,
  constituentKey = NULL,
  verbose = FALSE,
  return = NULL,
  curlopts = list(http_version = 2)
)
```

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. • HETEROTYPIC_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 x, e.g. http://bit.ly/2osAUQB only shows the type values 'CHECKLIST' and 'OCCURRENCE' because the other types have counts less than 10000
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/2JAymaC still shows all type values even though type is being filtered by type=CHECKLIST.
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.
issue	Filters by issue. Issue has to be related to names. Type gbif_issues() to get complete list of issues.
constituentKey	Filters by the dataset's constituent key (a uuid).
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	Defunct. All components are returned; index to the one(s) you want
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options

Value

An object of class gbif, which is a S3 class list, with slots for metadata (meta), the data itself (data), the taxonomic hierarchy data (hierarchies), and vernacular names (names). In addition, the object has attributes listing the user supplied arguments and type of search, which is, differently from occurrence data, always equals to 'single' even if multiple values for some parameters are given. meta is a list of length four with offset, limit, endOfRecords and count fields. data is a tibble (aka data.frame) containing all information about the found taxa. hierarchies is a list of data.frame's, one per GBIF key (taxon), containing its taxonomic classification. Each data.frame contains two columns: rankkey and name. names returns a list of data.frame's, one per GBIF key (taxon), containing all vernacular names. Each data.frame contains two columns: vernacularName and language.

A list of length five:

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

Deprecation Notice

This function is deprecated. It only works with the GBIF Backbone Taxonomy and does not support COL (Catalogue of Life) Extended Release. Use `rcol::col_search()` from the rcol package instead for COL XR support.

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**

References

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

Examples

```
## 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) %in% c("descriptions","descriptionsSerialized")]
})

# Search for a genus
name_lookup(query="Cnaemidophorus", rank="genus")
# 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)
## and 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", "204"))
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-bbc5-522bfb90d847",
  "d7c60346-44b6-400d-ba27-8d3fbeffc8a5"))
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(verbose = TRUE))

## End(Not run)
```

`name_parse` *Parse taxon names using the GBIF name parser.*

Description

Parse taxon names using the GBIF name parser.

Usage

```
name_parse(scientificname, curlopts = list(http_version = 2))
```

Arguments

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

https://www.gbif.org/developer/species#parser

Examples

```
## Not run:
name_parse(scientificname='x Agropogon littoralis')
name_parse(c('Arrhenatherum elatius var. elatius',
             'Secale cereale subsp. cereale', 'Secale cereale ssp. cereale',
             'Vanessa atalanta (Linnaeus, 1758)'))
name_parse("Ajuga pyramidata")
name_parse("Ajuga pyramidata x reptans")

# Pass on curl options
# res <- name_parse(c('Arrhenatherum elatius var. elatius',
#          'Secale cereale subsp. cereale', 'Secale cereale ssp. cereale',
#          'Vanessa atalanta (Linnaeus, 1758)'), curlopts=list(verbose=TRUE))

## End(Not run)
```

---

name_suggest *Suggest up to 20 name usages.*

Description

Suggest up to 20 name usages.

Usage

```
name_suggest(
  q = NULL,
  datasetKey = NULL,
  rank = NULL,
  fields = NULL,
  start = NULL,
  limit = 100,
  curlopts = list(http_version = 2)
)
```

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, superphylum, 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::curl_options` for curl options

Value

A list, with two elements `data` (tibble) and `hierarchy` (list of data.frame's). If 'higherClassificationMap' is one of the `fields` requested, then `hierarchy` is a list of data.frame's; if not included, `hierarchy` is an empty list.

Deprecation Notice

This function is deprecated. It only works with the GBIF Backbone Taxonomy and does not support COL (Catalogue of Life) Extended Release. Use `rcol::col_suggest()` from the rcol package instead for COL XR support.

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.

Repeat parmeter 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**

References

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

Examples

```
## 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-ba27-8d3fbeffc8a5"))

# If 'higherClassificationMap' in fields, a list is returned
name_suggest(q='Puma', fields=c('key','higherClassificationMap'))

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

## End(Not run)
```

---

name_usage *Lookup details for specific names in all taxonomies in GBIF.*

Description

Lookup details for specific names in all taxonomies in GBIF.

Usage

```
name_usage(
  key = NULL,
  name = NULL,
  data = "all",
  language = NULL,
  datasetKey = NULL,
  uuid = NULL,
  rank = NULL,
  shortname = NULL,
  start = 0,
  limit = 100,
  return = NULL,
  curlopts = list(http_version = 2)
)
```

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
start	Record number to start at. Default: 0.
limit	Number of records to return. Default: 100.
return	Defunct. All components are returned; index to the one(s) you want
curlopts	list of named curl options passed on to HttpClient. see curl::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).

Important: When key is provided, the datasetKey parameter is ignored by the GBIF API. The API returns data based solely on the key, regardless of what datasetKey is set to. A warning will be issued if both parameters are provided.

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', 'iucnRedListCategory'

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 more information about issues in issues column.

Value

An object of class gbif, which is a S3 class list, with slots for metadata (meta) and the data itself (data). In addition, the object has attributes listing the user supplied arguments and type of search, which is, differently from occurrence data, always equals to 'single' even if multiple values for some parameters are given. meta is a list of length four with offset, limit, endOfRecords and count fields. data is a tibble (aka data.frame) containing all information about the found taxa.

Deprecation Notice

This function is deprecated. It only works with the GBIF Backbone Taxonomy and does not support COL (Catalogue of Life) Extended Release. Use rcol::col_usage() from the rcol package instead for COL XR support.

Repeat parameter inputs

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

- **rank**
- **name**
- **langugae**
- **datasetKey**

References

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

Examples

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

# Name usage for a taxonomic name
name_usage(name='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=5231190, data='speciesProfiles')
name_usage(key=5231190, data='descriptions')
name_usage(key=2435099, data='children')

# Vernacular names for a name usage
name_usage(key=5231190, data='vernacularNames')

# Limit number of results returned
name_usage(key=5231190, data='vernacularNames', limit=3)

# Search for names by dataset with datasetKey parameter
name_usage(datasetKey="d7dddbf4-2cf0-4f39-9b2a-bb099caae36c")

# Search for a particular language
name_usage(key=5231190, 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(verbose=TRUE))

# look up iucn red list category
name_usage(key = 7707728, data = 'iucnRedListCategory')

## End(Not run)
```

`network` *Get data about GBIF networks*

Description

Get data about GBIF networks

Usage

```
network(
  data = "all",
  uuid = NULL,
  query = NULL,
  identifier = NULL,
  identifierType = NULL,
  limit = 100,
  start = NULL,
  curlopts = list(http_version = 2)
)

network_constituents(uuid = NULL, limit = 100, start = 0)
```

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 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::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.
- URI No description.
- URL No description.
- UUID No description.

Get various information about GBIF networks. `network_constituents()` is a convenience function that allows you to get all the datasets in a network.

Value

- `network()` returns a list
- `network_constituents()` returns a data.frame of datasets in the network

References

https://www.gbif.org/developer/registry#networks

Examples

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

network_constituents('2b7c7b4f-4d4f-40d3-94de-c28b6fa054a6')

# curl options
network(curlopts = list(verbose=TRUE))

## 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(http_version = 2)
)
```

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 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::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.
- URI No description.
- URL No description.
- UUID No description.

References

https://www.gbif.org/developer/registry#networks

Examples

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

# curl options
networks(curlopts = list(verbose=TRUE))

## End(Not run)
```

---

nodes *Nodes metadata.*

Description

Nodes metadata.

Usage

```
nodes(
  data = "all",
  uuid = NULL,
  query = NULL,
  identifier = NULL,
  identifierType = NULL,
  limit = 100,
  start = NULL,
  isocode = NULL,
  curlopts = list(http_version = 2)
)
```

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::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.
- URI No description.
- URL No description.
- UUID No description.

References

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

Examples

```
## Not run:
nodes(limit=5)
nodes(uuid="1193638d-32d1-43f0-a855-8727c94299d8")
nodes(data='identifier', uuid="03e816b3-8f58-49ae-bc12-4e18b358d6d9")
nodes(data=c('identifier','organization','comment'),
  uuid="03e816b3-8f58-49ae-bc12-4e18b358d6d9")

uuids = c("8cb55387-7802-40e8-86d6-d357a583c596",
  "02c40d2a-1cba-4633-90b7-e36e5e97aba8",
  "7a17efec-0a6a-424c-b743-f715852c3c1f",
  "b797ce0f-47e6-4231-b048-6b62ca3b0f55",
  "1193638d-32d1-43f0-a855-8727c94299d8",
  "d3499f89-5bc0-4454-8cdb-60bead228a6d",
  "cdc9736d-5ff7-4ece-9959-3c744360cdb3",
  "a8b16421-d80b-4ef3-8f22-098b01a89255",
```

```
  "8df8d012-8e64-4c8a-886e-521a3bdfa623",
  "b35cf8f1-748d-467a-adca-4f9170f20a4e",
  "03e816b3-8f58-49ae-bc12-4e18b358d6d9",
  "073d1223-70b1-4433-bb21-dd70afe3053b",
  "07dfe2f9-5116-4922-9a8a-3e0912276a72",
  "086f5148-c0a8-469b-84cc-cce5342f9242",
  "0909d601-bda2-42df-9e63-a6d51847ebce",
  "0e0181bf-9c78-4676-bdc3-54765e661bb8",
  "109aea14-c252-4a85-96e2-f5f4d5d088f4",
  "169eb292-376b-4cc6-8e31-9c2c432de0ad",
  "1e789bc9-79fc-4e60-a49e-89dfc45a7188",
  "1f94b3ca-9345-4d65-afe2-4bace93aa0fe")

res <- lapply(uuids, function(x) nodes(x, data='identifier')$data)
res <- res[!sapply(res, NROW)==0]
res[1]

# Pass on curl options
nodes(limit=20, curlopts=list(verbose=TRUE))

## End(Not run)
```

`occ_count` *Get number of occurrence records.*

Description

Get number of occurrence records.

Usage

```
occ_count(..., occurrenceStatus = "PRESENT", curlopts = list(http_version = 2))
```

Arguments

`...`	parameters passed to `occ_search()`.
`occurrenceStatus`	(character) Default is "PRESENT". Specify whether search should return "PRESENT" or "ABSENT" data.
`curlopts`	(list) curl options.

Details

`occ_count()` is a short convenience wrapper for `occ_search(limit=0)$meta$count`.

The current version (since rgbif 3.7.6) of `occ_count()` uses a different GBIF API endpoint from previous versions. This change greatly improves the usability of `occ_count()`. Legacy parameters `georeferenced`, `type`, `date`, `to`, `from` are no longer supported and not guaranteed to work correctly.

Multiple values of the type `c("a","b")` will give an error, but `"a;b"` will work.

Value

The occurrence count of the `occ_search()` query.

See Also

`occ_count_year()`, `occ_count_country()`, `occ_count_pub_country()`, `occ_count_basis_of_record()`

Examples

```
## Not run:
# total occurrences mediated by GBIF
occ_count() # should be > 2 billion!

# number of plant occurrences
occ_count(kingdomKey=name_backbone("Plantea")$usageKey)
occ_count(scientificName = 'Ursus americanus')

occ_count(country="DK") # found in Denmark
occ_count(country="DK;US") # found in Denmark and United States
occ_count(publishingCountry="US") # published by the United States
# number of repatriated eBird records in India
occ_count(repatriated = TRUE,country="IN")

# Use COL XR alpha-numeric taxonKey
occ_count(taxonKey="Q2M4") # Calopteryx splendens occurrences
# or use numeric keys with GBIF Backbone
occ_count(taxonKey=212,
  checklistKey = "d7dddbf4-2cf0-4f39-9b2a-bb099caae36c") # bird occurrences
# between years 1800-1900
occ_count(basisOfRecord="PRESERVED_SPECIMEN", year="1800,1900")
occ_count(recordedBy="John Waller") # recorded by John Waller
occ_count(decimalLatitude=0, decimalLongitude=0) # exactly on 0,0

# close to a known iso2 centroid
occ_count(distanceFromCentroidInMeters="0,2000")
# close to a known iso2 centroid in Sweden
occ_count(distanceFromCentroidInMeters="0,2000",country="SE")

occ_count(hasCoordinate=TRUE) # with coordinates
occ_count(protocol = "DIGIR") # published using DIGIR format
occ_count(mediaType = 'StillImage') # with images

# number of occurrences iucn status "critically endangered"
occ_count(iucnRedListCategory="CR")
occ_count(verbatimScientificName="Calopteryx splendens;Calopteryx virgo")
occ_count(
geometry="POLYGON((24.70938 48.9221,24.71056 48.92175,24.71107
 48.92296,24.71002 48.92318,24.70938 48.9221))")

# getting a table of counts using the facets interface
# occurrence counts by year
occ_count(facet="year")
```

```
occ_count(facet="year",facetLimit=400)

# top scientificNames from Japan
occ_count(facet="scientificName",country="JP")
# top countries publishing specimen bird records between 1850 and 1880
occ_count(facet="scientificName",taxonKey=212,basisOfRecord="PRESERVED_SPECIMEN"
,year="1850,1880")

# Number of present or absence records of Elephants
occ_count(facet="occurrenceStatus",scientificName="Elephantidae")

# top 100 datasets publshing occurrences to GBIF
occ_count(facet="datasetKey",facetLimit=100)
# top datasets publishing country centroids on GBIF
occ_count(facet="datasetKey",distanceFromCentroidInMeters="0")

# common values for coordinateUncertaintyInMeters for museum specimens
occ_count(facet="coordinateUncertaintyInMeters",basisOfRecord="PRESERVED_SPECIMEN")

# number of iucn listed bird and insect occurrences in Mexico
occ_count(facet="iucnRedListCategory",taxonKey="212;216",country="MX")

# most common latitude values mediated by GBIF
occ_count(facet="decimalLatitude")

# top iNaturalist users publishing research-grade obs to GBIF
occ_count(facet="recordedBy",datasetKey="50c9509d-22c7-4a22-a47d-8c48425ef4a7")
# top 100 iNaturalist users from Ukraine
occ_count(facet="recordedBy",datasetKey="50c9509d-22c7-4a22-a47d-8c48425ef4a7"
,country="UA",facetLimit=100)

# top institutions publishing specimen occurrences to GBIF
occ_count(facet="institutionCode",basisOfRecord="PRESERVED_SPECIMEN")


## End(Not run)
```

`occ_count_` *Get quick pre-computed occurrence counts of a limited number of dimensions.*

Description

Get quick pre-computed occurrence counts of a limited number of dimensions.

Usage

```
occ_count_country(publishingCountry = NULL)

occ_count_pub_country(country = NULL)
```

```
occ_count_year(year = NULL)

occ_count_basis_of_record(curlopts = list(http_version = 2))
```

Arguments

publishingCountry	The 2-letter country code (as per ISO-3166-1) the country from which the occurrence was published.
country	(character) The 2-letter country code (ISO-3166-1) in which the occurrence was recorded.
year	The 4 digit year. Supports range queries, 'smaller,larger' (e.g., '1990,1991', whereas 1991, 1990' wouldn't work).
curlopts	(list) curl options.

Details

Get quick pre-computed counts of a limited number of dimensions.

`occ_count_country()` will return a data.frame with occurrence counts by country. By using `occ_count_country(publishingCountry="DK")` will return the occurrence contributions Denmark has made to each country.

`occ_count_pub_country()` will return a data.frame with occurrence counts by publishing country. Using `occ_count_pub_country(country="DK")`, will return the occurrence contributions each country has made to that focal `country=DK`.

`occ_count_year()` will return a data.frame with the total occurrences mediated by GBIF for each year. By using `occ_counts_year(year="1800,1900")` will only return counts for that range.

`occ_count_basis_of_record()` will return a data.frame with total occurrences mediated by GBIF for each basis of record.

Value

A `data.frame` of counts.

See Also

`occ_count()`

Examples

```
## Not run:
# total occurrence counts for all countries and iso2 places
occ_count_country()
# the occurrences Mexico has published in other countries
occ_count_country("MX")
# the occurrences Denmark has published in other countries
occ_count_country("DK")
```

```
# the occurrences other countries have published in Denmark
occ_count_pub_country("DK")
# the occurrences other countries have published in Mexico
occ_count_pub_country("MX")

# total occurrence counts for each year that an occurrence was
# recorded or collected.
occ_count_year()
# supports ranges
occ_count_year("1800,1900")

# table of occurrence counts by basis of record
occ_count_basis_of_record()


## End(Not run)
```

`occ_data` *Legacy alternative to occ_search*

Description

Legacy alternative to occ_search

Usage

```
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,
  recordedByID = NULL,
  identifiedByID = 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,
  speciesKey = NULL,
  establishmentMeans = NULL,
  degreeOfEstablishment = NULL,
  protocol = NULL,
  license = NULL,
  organismId = NULL,
  publishingOrg = NULL,
  stateProvince = NULL,
  waterBody = NULL,
  locality = NULL,
  occurrenceStatus = "PRESENT",
  gadmGid = NULL,
  coordinateUncertaintyInMeters = NULL,
  verbatimScientificName = NULL,
  eventId = NULL,
  identifiedBy = NULL,
  networkKey = NULL,
  verbatimTaxonId = NULL,
  occurrenceId = NULL,
  organismQuantity = NULL,
  organismQuantityType = NULL,
  relativeOrganismQuantity = NULL,
  iucnRedListCategory = NULL,
  lifeStage = NULL,
  isInCluster = NULL,
  distanceFromCentroidInMeters = NULL,
  skip_validate = TRUE,
  limit = 500,
  start = 0,
```

```
  curlopts = list(http_version = 2)
)
```

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 will match all birds, no matter which species. You can pass many keys to `occ_search(taxonKey=c(1,212))`.
`scientificName`	A scientific name from the GBIF backbone. All included and synonym taxa are included in the search.
`country`	(character) The 2-letter country code (ISO-3166-1) in which the occurrence was recorded. `enumeration_country()`.
`publishingCountry`	The 2-letter country code (as per ISO-3166-1) of the country in which the occurrence was recorded. See `enumeration_country()`.
`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.
`recordNumber`	Number recorded by collector of the data, different from GBIF record number.
`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`	The source supplied continent. • "africa" • "antarctica" • "asia" • "europe" • "north_america" • "oceania" • "south_america" Continent is not inferred but only populated if provided by the dataset publisher. Applying this filter may exclude many relevant records.
`geometry`	(character) Searches for occurrences inside a polygon in Well Known Text (WKT) format. A WKT shape written as either • "POINT" • "LINESTRING" • "LINEARRING" • "POLYGON" • "MULTIPOLYGON" For Example, "POLYGON((37.08 46.86,38.06 46.86,38.06 47.28,37.08 47.28, 37.0 46.8))". See also the section **WKT** below.

`geom_big` (character) One"bbox" or "asis" (default).

`geom_size` (integer) An integer indicating size of the cell. Default: 40.

`geom_n` (integer) An integer indicating number of cells in each dimension. Default: 10.

`recordedBy` (character) The person who recorded the occurrence.

`recordedByID` (character) Identifier (e.g. ORCID) for the person who recorded the occurrence

`identifiedByID` (character) Identifier (e.g. ORCID) for the person who provided the taxonomic identification of the occurrence.

`basisOfRecord` (character) The specific nature of the data record. See here.

- "FOSSIL_SPECIMEN"
- "HUMAN_OBSERVATION"
- "MATERIAL_CITATION"
- "MATERIAL_SAMPLE"
- "LIVING_SPECIMEN"
- "MACHINE_OBSERVATION"
- "OBSERVATION"
- "PRESERVED_SPECIMEN"
- "OCCURRENCE"

`datasetKey` (character) The occurrence dataset uuid key. That can be found in the dataset page url. For example, "7e380070-f762-11e1-a439-00145 eb45e9a" is the key for Natural History Museum (London) Collection Specimens.

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

`catalogNumber` (character) 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 WGS84. 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 WGS84. 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.

`collectionCode`
: (character) 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. Issues passed to this parameter filter results by the issue. One of many options. See here for definitions.

`search`
: (character) Query terms. The value for this parameter can be a simple word or a phrase. For example, search="puma"

`mediaType`
: (character) Media type of "MovingImage", "Sound", or "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.

`speciesKey`
: (numeric) Species classification key.

`establishmentMeans`
: (character) provides information about whether an organism or organisms have been introduced to a given place and time through the direct or indirect activity of modern humans.

  - "Introduced"
  - "Native"
  - "NativeReintroduced"
  - "Vagrant"
  - "Uncertain"
  - "IntroducedAssistedColonisation"

`degreeOfEstablishment`
: (character) Provides information about degree to which an Organism survives, reproduces, and expands its range at the given place and time. One of many options.

`protocol`
: (character) Protocol or mechanism used to provide the occurrence record. One of many options.

`license` (character) The type license applied to the dataset or record.

- "CC0_1_0"
- "CC_BY_4_0"
- "CC_BY_NC_4_0"

`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.

`occurrenceStatus`
(character) Default is "PRESENT". Specify whether search should return "PRESENT" or "ABSENT" data.

`gadmGid` (character) The gadm id of the area occurrences are desired from. https://gadm.org/.

`coordinateUncertaintyInMeters`
A number or range between 0-1,000,000 which specifies the desired coordinate uncertainty. A coordinateUncertainty InMeters=1000 will be interpreted all records with exactly 1000m. Supports range queries, 'smaller,larger' (e.g., '1000,10000', whereas '10000,1000' wouldn't work).

`verbatimScientificName`
(character) Scientific name as provided by the source.

`eventId` (character) identifier(s) for a sampling event.

`identifiedBy` (character) names of people, groups, or organizations.

`networkKey` (character) The occurrence network key (a uuid) who assigned the Taxon to the subject.

`verbatimTaxonId`
(character) The taxon identifier provided to GBIF by the data publisher.

`occurrenceId` (character) occurrence id from source.

`organismQuantity`
A number or range which specifies the desired organism quantity. An organismQuantity=5 will be interpreted all records with exactly 5. Supports range queries, smaller,larger (e.g., '5,20', whereas '20,5' wouldn't work).

`organismQuantityType`
(character) The type of quantification system used for the quantity of organisms. For example, "individuals" or "biomass".

`relativeOrganismQuantity`
(numeric) A relativeOrganismQuantity=0.1 will be interpreted all records with exactly 0.1 The relative measurement of the quantity of the organism (a number between 0-1). Supports range queries, "smaller,larger" (e.g., '0.1,0.5', whereas '0.5,0.1' wouldn't work).

`iucnRedListCategory`
(character) The IUCN threat status category.

- "NE" (Not Evaluated)
- "DD" (Data Deficient)
- "LC" (Least Concern)
- "NT" (Near Threatened)
- "VU" (Vulnerable)
- "EN" (Endangered)
- "CR" (Critically Endangered)
- "EX" (Extinct)
- "EW" (Extinct in the Wild)

`lifeStage` (character) the life stage of the occurrence. One of many options.

`isInCluster` (logical) identify potentially related records on GBIF.

`distanceFromCentroidInMeters`
A number or range. A value of "2000,*" means at least 2km from known centroids. A value of "0" would mean occurrences exactly on known centroids. A value of "0,2000" would mean within 2km of centroids. Max value is 5000.

`skip_validate` (logical) whether to skip wellknown::validate_wkt call or not. passed down to check_wkt(). Default: TRUE

`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 100,000, which is calculated as the `limit+start`, so `start=99,000` 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

`curlopts` (list)

Details

This function is a legacy alternative to `occ_search()`. It is not recommended to use `occ_data()` as it is not as flexible as `occ_search()`. New search terms will not be added to this function and it is only supported for legacy reasons.

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)

occ_download *Spin up a download request for GBIF occurrence data.*

Description

Spin up a download request for GBIF occurrence data.

Usage

```
occ_download(
  ...,
  body = NULL,
  type = "and",
  format = "DWCA",
  verbatim_extensions = NULL,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  user = NULL,
  pwd = NULL,
  email = NULL,
  curlopts = list(http_version = 2)
)

occ_download_prep(
  ...,
  body = NULL,
  type = "and",
  format = "DWCA",
  verbatim_extensions = NULL,
  checklistKey = NULL,
  user = NULL,
  pwd = NULL,
  email = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

...	For `occ_download()` and `occ_download_prep()`, one or more objects of class `occ_predicate` or `occ_predicate_list`, created by `pred*` functions (see download_predicate_dsl). If you use this, don't use body parameter.
body	if you prefer to pass in the payload yourself, use this parameter. If you 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, isNotNull

`format` (character) The download format. One of 'DWCA' (default), 'SIMPLE_CSV', or 'SPECIES_LIST'

`verbatim_extensions` (character vector) A character vector of verbatim extensions to include in the download. This parameter is only applied when `format = "DWCA"` and will be ignored for other formats.

`checklistKey` (character) The UUID key for a checklist dataset to use for taxonomy in the download. The default is COL (Catalogue of Life) Extended Release (7ddf754f-d193-4cc9-b351-99906754a03b). Optional

`user` (character) User name within GBIF's website. Required. See "Authentication" below

`pwd` (character) User password within GBIF's website. Required. See "Authentication" below

`email` (character) Email address to receive download notice done email. Required. See "Authentication" below

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

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 `POLYGON((-19.5 34.1, -25.3 68.1, 35.9 68.1, 27.8 34.1, -19.5 34.1))`, whereas they expect the other order: `POLYGON((-19.5 34.1, 27.8 34.1, 35.9 68.1, -25.3 68.1, -19.5 34.1))`

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 clockwise WKT to those functions but they treat it as an exclusion, so get all data not inside the WKT area.

checklistKey

You can specify the taxonomy to be included in occurrence downloads by adding the `checklistKey` parameter to the download request. The value should be a UUID for a checklist dataset in GBIF. By default, the GBIF Backbone Taxonomy will be used if no `checklistKey` is supplied.

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

When numeric taxonomic keys (taxonKey, speciesKey, kingdomKey, etc.) are detected in predicates and checklistKey is set to COL XR (the default) or NULL, the function automatically switches to the GBIF Backbone taxonomy checklistKey and issues a warning. These numeric keys are legacy identifiers. If you explicitly set checklistKey to Backbone or another taxonomy, no warning is issued. Consider migrating to COL XR identifiers using `gbif_to_col()`.

References

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

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dataset()`, `occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`

Examples

```
## Not run:
# Uses COL (Catalogue of Life) Extended Release with alpha-numeric keys by default
# occ_download(pred("basisOfRecord", "LITERATURE"))
# occ_download(pred("taxonKey", "Q2M4"), pred_gt("elevation", 5000)) # Calopteryx splendens
# occ_download(pred_gt("decimalLatitude", 50))
# occ_download(pred_gte("elevation", 9000))
# occ_download(pred_gte('decimalLatitude", 65))
```

```
# occ_download(pred("country", "US"))
# occ_download(pred("institutionCode", "TLMF"))
# occ_download(pred("catalogNumber", 217880))
# occ_download(pred("gbifId", 142317604))

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

# res <- occ_download(pred("taxonKey", "9WLSS"), pred("hasCoordinate", TRUE))

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

# Multiple queries
# occ_download(pred_gte("decimalLatitude", 65),
#  pred_lte("decimalLatitude", -65), type="or")
# gg <- occ_download(pred("depth", 80), pred("taxonKey", "Q2M4"),
#  type="or")
# x <- occ_download(pred_and(pred_within("POLYGON((-14 42, 9 38, -7 26, -14 42))"),
#  pred_gte("elevation", 5000)))

# complex example with many predicates
# shows example of how to do date ranges for both year and month
# res <- occ_download(
#  pred_gt("elevation", 5000),
#  pred_in("basisOfRecord", c('HUMAN_OBSERVATION','OBSERVATION','MACHINE_OBSERVATION')),
#  pred("country", "US"),
#  pred("hasCoordinate", TRUE),
#  pred("hasGeospatialIssue", FALSE),
#  pred_gte("year", 1999),
#  pred_lte("year", 2011),
#  pred_gte("month", 3),
#  pred_lte("month", 8)
# )

# Using body parameter - pass in your own complete query
## as JSON (using COL XR alpha-numeric key)
query1 <- '{"creator":"sckott",
  "notification_address":["stuff1@gmail.com"],
  "predicate":{"type":"and","predicates":[
    {"type":"equals","key":"TAXON_KEY","value":"Q2M4"},
    {"type":"equals","key":"HAS_COORDINATE","value":"TRUE"}]}
 }'
# res <- occ_download(body = query1, curlopts=list(verbose=TRUE))

## as a list
library(jsonlite)
query <- list(
  creator = unbox("sckott"),
  notification_address = "stuff1@gmail.com",
  predicate = list(
    type = unbox("and"),
```

```
    predicates = list(
      list(type = unbox("equals"), key = unbox("TAXON_KEY"),
        value = unbox("Q2M4")),
      list(type = unbox("equals"), key = unbox("HAS_COORDINATE"),
        value = unbox("TRUE"))
    )
  )
)
# res <- occ_download(body = query, curlopts = list(verbose = TRUE))

# Prepared query (uses COL XR by default)
occ_download_prep(pred("basisOfRecord", "LITERATURE"))
occ_download_prep(pred("basisOfRecord", "LITERATURE"), format = "SIMPLE_CSV")
occ_download_prep(pred("basisOfRecord", "LITERATURE"), format = "SPECIES_LIST")
occ_download_prep(pred_in("taxonKey", c("Q2M4", "9WLSS", "Q2N2", "Q2KZ")))
occ_download_prep(pred_within("POLYGON((-14 42, 9 38, -7 26, -14 42))"))

## a complicated example (using COL XR alpha-numeric keys)
occ_download_prep(
  pred_in("basisOfRecord", c("MACHINE_OBSERVATION", "HUMAN_OBSERVATION")),
  pred_in("taxonKey", c("Q2M4", "9WLSS", "Q2N2")),
  pred_in("country", c("GB", "IE")),
  pred_or(pred_lte("year", 1989), pred("year", 2000))
)

## COL XR is now the default checklist
# To use GBIF Backbone Taxonomy, explicitly set checklistKey to the backbone UUID
# occ_download_prep(
#   pred("basisOfRecord", "PRESERVED_SPECIMEN"),
#   pred_in("country", c("VC", "GD")),
#   checklistKey = "d7dddbf4-2cf0-4f39-9b2a-bb099caae36c"
# )

# x = occ_download(
  pred_in("basisOfRecord", c("MACHINE_OBSERVATION", "HUMAN_OBSERVATION")),
  pred_in("taxonKey", c("Q2M4", "9WLSS")),
  pred_in("country", c("US", "MX")),
  pred_and(pred_gte("year", 1989), pred_lte("year", 1991))
# )
# occ_download_meta(x)
# z <- occ_download_get(x)
# df <- occ_download_import(z)
# str(df)
# library(dplyr)
# unique(df$basisOfRecord)
# unique(df$taxonKey)
# unique(df$countryCode)
# sort(unique(df$year))

## End(Not run)
```

`occ_download_cached` *Check for downloads already in your GBIF account*

Description

Check for downloads already in your GBIF account

Usage

```
occ_download_cached(
  ...,
  body = NULL,
  type = "and",
  format = "DWCA",
  user = NULL,
  pwd = NULL,
  email = NULL,
  refresh = FALSE,
  age = 30,
  curlopts = list(http_version = 2)
)
```

Arguments

`...`	For `occ_download()` and `occ_download_prep()`, one or more objects of class `occ_predicate` or `occ_predicate_list`, created by `pred*` functions (see download_predicate_dsl). If you use this, don't use body parameter.
`body`	if you prefer to pass in the payload yourself, use this parameter. If you 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, isNotNull
`format`	(character) The download format. One of 'DWCA' (default), 'SIMPLE_CSV', or 'SPECIES_LIST'
`user`	(character) User name within GBIF's website. Required. See "Authentication" below
`pwd`	(character) User password within GBIF's website. Required. See "Authentication" below
`email`	(character) Email address to receive download notice done email. Required. See "Authentication" below

refresh	(logical) refresh your list of downloads. on the first request of each R session we'll cache your stored GBIF occurrence downloads locally. you can refresh this list by setting refresh=TRUE; if you're in the same R session, and you've done many download requests, then refreshing may be a good idea if you're using this function
age	(integer) number of days after which you want a new download. default: 30
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dat occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

```
## Not run:
# these are examples from the package maintainer's account;
# outcomes will vary by user
occ_download_cached(pred_gte("elevation", 12000L))
occ_download_cached(pred("catalogNumber", 217880))
occ_download_cached(pred_gte("decimalLatitude", 65),
  pred_lte("decimalLatitude", -65), type="or")
occ_download_cached(pred_gte("elevation", 12000L))
occ_download_cached(pred_gte("elevation", 12000L), refresh = TRUE)

## End(Not run)
```

---

occ_download_cancel *Cancel a download creation process.*

Description

Cancel a download creation process.

Usage

```
occ_download_cancel(
  key,
  user = NULL,
  pwd = NULL,
```

```
  curlopts = list(http_version = 2)
)

occ_download_cancel_staged(
  user = NULL,
  pwd = NULL,
  limit = 20,
  start = 0,
  curlopts = list(http_version = 2)
)
```

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

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dat occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

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

## End(Not run)
```

occ_download_countries *List countries for a download*

Description

List countries for a download

Usage

```
occ_download_countries(
  key,
  sortBy = NULL,
  sortOrder = NULL,
  limit = 20,
  start = 0,
  curlopts = list(http_version = 2)
)
```

Arguments

key	A key generated from a request, like that from occ_download()
sortBy	(character) Sort field. One of COUNTRY_CODE or RECORD_COUNT. Optional.
sortOrder	(character) Sort order. One of ASC or DESC. Optional.
limit	(integer/numeric) Number of records to return. Default: 20, Max: 1000
start	(integer/numeric) Record number to start at. Default: 0
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options

Value

a list with two slots:

- meta: a single row data.frame with columns: offset, limit, endofrecords, count
- results: a tibble with the results, with columns: downloadKey, publishingCountryCode, numberRecords

Examples

```
## Not run:
occ_download_countries(key="0003983-140910143529206")
occ_download_countries(key="0003983-140910143529206", limit = 3)
occ_download_countries(key="0003983-140910143529206", limit = 3, start = 10)
occ_download_countries(key="0003983-140910143529206", sortBy = "RECORD_COUNT",
  sortOrder = "DESC")

## End(Not run)
```

`occ_download_datasets` *List datasets for a download*

Description

List datasets for a download

Usage

```
occ_download_datasets(
  key,
  limit = 20,
  start = 0,
  curlopts = list(http_version = 2)
)
```

Arguments

`key`	A key generated from a request, like that from `occ_download()`
`limit`	(integer/numeric) Number of records to return. Default: 20, Max: 1000
`start`	(integer/numeric) Record number to start at. Default: 0
`curlopts`	list of named curl options passed on to `HttpClient`. see `curl::curl_options` for curl options

Value

a list with two slots:

- meta: a single row data.frame with columns: `offset`, `limit`, `endofrecords`, `count`
- results: a tibble with the results, of three columns: `downloadKey`, `datasetKey`, `numberRecords`

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dat`
`occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
occ_download_datasets(key="0003983-140910143529206")
occ_download_datasets(key="0003983-140910143529206", limit = 3)
occ_download_datasets(key="0003983-140910143529206", limit = 3, start = 10)

## End(Not run)
```

`occ_download_dataset_activity`

Lists the downloads activity of a dataset

Description

Lists the downloads activity of a dataset

Usage

```
occ_download_dataset_activity(
  dataset,
  limit = 20,
  start = 0,
  curlopts = list(http_version = 2)
)
```

Arguments

`dataset`	(character) A dataset key
`limit`	(integer/numeric) Number of records to return. Default: 20, Max: 1000
`start`	(integer/numeric) Record number to start at. Default: 0
`curlopts`	list of named curl options passed on to `HttpClient`. see `curl::curl_options` for curl options

Value

a list with two slots:

- meta: a single row data.frame with columns: `offset`, `limit`, `endofrecords`, `count`
- results: a tibble with the nested data flattened, with many columns with the same `download.` or `download.request.` prefixes

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dat occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

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

# pagination
occ_download_dataset_activity("7f2edc10-f762-11e1-a439-00145eb45e9a",
limit = 3000)
occ_download_dataset_activity("7f2edc10-f762-11e1-a439-00145eb45e9a",
limit = 3, start = 10)

## End(Not run)
```

---

occ_download_describe *Describes the fields available in GBIF downloads*

Description

Describes the fields available in GBIF downloads

Usage

```
occ_download_describe(x = "dwca", curlopts = list(http_version = 2))
```

Arguments

x	a character string (default: "dwca"). Accepted values: "simpleCsv", "simpleAvro", "simpleParquet","speciesList", "sql".
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options.

Details

The function returns a list with the fields available in GBIF downloads. It is considered experimental by GBIF, so the output might change in the future.

Value

a list.

Examples

```
## Not run:
occ_download_describe("dwca")$verbatimFields
occ_download_describe("dwca")$verbatimExtensions
occ_download_describe("simpleCsv")$fields
occ_download_describe("sql")$fields

## End(Not run)
```

`occ_download_doi` *Get download meta data from a doi*

Description

Get download meta data from a doi

Usage

```
occ_download_doi(doi = NULL, curlopts = list(http_version = 2))
```

Arguments

`doi`	(character) the doi of the download you want to get metadata for.
`curlopts`	(list) named list of curl options passed on to crul::HttpClient.

Value

a list.

Examples

```
## Not run:
occ_download_doi("10.15468/dl.zdfkkf")

occ_download_doi("10.15468/dl.zdfkkf")$key %>%
occ_download_get() %>%
occ_download_import()


## End(Not run)
```

`occ_download_get` *Get a download from GBIF.*

Description

Get a download from GBIF.

Usage

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

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

Details

Downloads the zip file to a directory you specify on your machine. `crul::HttpClient()` is used internally to write the zip file to disk. See crul::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

This function used to check for HTTP response content type, but it has changed enough that we no longer check it. If you run into issues with this function, open an issue in the GitHub repository.

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dat`
`occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
occ_download_get("0000066-140928181241064")
occ_download_get("0003983-140910143529206", overwrite = TRUE)

## End(Not run)
```

occ_download_import *Import a downloaded file from GBIF.*

Description

Import a downloaded file from GBIF.

Usage

```
occ_download_import(
  x = NULL,
  key = NULL,
  path = ".",
  fill = FALSE,
  encoding = "UTF-8",
  ...
)

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.
encoding	(character) encoding to read in data; passed to data.table::fread(). default: "UTF-8". other allowed options: "Latin-1" and "unknown". see ?data.table::fread docs
...	parameters passed on to data.table::fread(). See fread docs for details. Some fread parameters that may be particular useful here are: select (select which columns to read in; others are dropped), nrows (only read in a certain number of rows)

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)

Problems reading data

You may run into errors when using `occ_download_import()`; most often these are due to `data.table::fread()` not being able to parse the `occurrence.txt` file correctly. The `fill` parameter passes down to `data.table::fread()` and the `...` allows you to pass on any other parameters that `data.table::fread()` accepts. Read the docs for `fread` for help.

countryCode result column and Namibia

The country code for Namibia is `"NA"`. Unfortunately in R an `"NA"` string will be read in to R as an NA/missing. To avoid this, in this function we read in the data, then convert an NA/missing values to the character string `"NA"`. When a country code is truly missing it will be an empty string.

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dat`
`occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
# First, kick off at least 1 download, then wait for the job to be complete
# Then use your download keys
res <- occ_download_get(key="0000066-140928181241064", overwrite=TRUE)
occ_download_import(res)

occ_download_get(key="0000066-140928181241064", overwrite = TRUE) %>%
  occ_download_import

# coerce a file path to the right class to feed to occ_download_import
# as.download("0000066-140928181241064.zip")
# as.download(key = "0000066-140928181241064")
# occ_download_import(as.download("0000066-140928181241064.zip"))

# download a dump that has a CSV file
# res <- occ_download_get(key = "0001369-160509122628363", overwrite=TRUE)
# occ_download_import(res)
# occ_download_import(key = "0001369-160509122628363")

# download and import a species list (in csv format)
# x <- occ_download_get("0000172-190415153152247")
```

```
# occ_download_import(x)

## End(Not run)
```

`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(http_version = 2)
)
```

Arguments

`user`	(character) User name within GBIF's website. Required. See Details.
`pwd`	(character) User password within GBIF's website. Required. See Details.
`limit`	(integer/numeric) Number of records to return. Default: 20, Max: 1000
`start`	(integer/numeric) Record number to start at. Default: 0
`curlopts`	list of named curl options passed on to `HttpClient`. see `curl::curl_options` for curl options

Value

a list with two slots:

- meta: a single row data.frame with columns: `offset`, `limit`, `endofrecords`, `count`
- results: a tibble with the nested data flattened, with many columns with the same `request.` prefix

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dat`
`occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## 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(http_version = 2))
```

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::curl_options` for curl options

Value

an object of class `occ_download_meta`, a list with slots for the download key, the DOI assigned to the download, license link, the request details you sent in the `occ_download()` request, and metadata about the size and date/time of the request

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dat`
`occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

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

## End(Not run)
```

`occ_download_organizations` *List organizations for a download*

Description

List organizations for a download

Usage

```
occ_download_organizations(
  key,
  organizationTitle = NULL,
  sortBy = NULL,
  sortOrder = NULL,
  limit = 20,
  start = 0,
  curlopts = list(http_version = 2)
)
```

Arguments

`key`	A key generated from a request, like that from `occ_download()`
`organizationTitle`	(character) Organization title filter. Optional.
`sortBy`	(character) Sort field. One of `ORGANIZATION_TITLE`, `COUNTRY_CODE` or `RECORD_COUNT`. Optional.
`sortOrder`	(character) Sort order. One of `ASC` or `DESC`. Optional.
`limit`	(integer/numeric) Number of records to return. Default: 20, Max: 1000
`start`	(integer/numeric) Record number to start at. Default: 0
`curlopts`	list of named curl options passed on to `HttpClient`. see `curl::curl_options` for curl options

Value

a list with two slots:

- meta: a single row data.frame with columns: `offset`, `limit`, `endofrecords`, `count`
- results: a tibble with the results, with columns: `downloadKey`, `organizationKey`, `organizationTitle`, `numberRecords`, `publishingCountryCode`

Examples

```
## Not run:
occ_download_organizations(key="0024953-260519110011954")
occ_download_organizations(key="0024953-260519110011954", limit = 3)
occ_download_organizations(
  key="0024953-260519110011954",
  organizationTitle = "University of Alaska Museum of the North"
)
occ_download_organizations(key="0024953-260519110011954", sortBy = "RECORD_COUNT",
  sortOrder = "DESC")

## 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 (but does not use lazy evaluation if use the `.list` parameter). Then it kicks of the first 3 requests. Then in a while loop, we check status of those requests, and when any request finishes (see `When is a job done?` below), 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.

When is a job done?

We mark a job as done by checking the `/occurrence/download/` API route with our `occ_download_meta()` function. If the status of the job is any of "succeeded", "killed", or "cancelled", then we mark the job as done and move on to other jobs in the queue.

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

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_stats_dataset_records()`, `occ_download_stats_data` `occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
if (interactive()) { # dont run in automated example runs, too costly
# passing occ_download() requests via ...
out <- occ_download_queue(
  occ_download(pred('taxonKey', 5231190), pred("year", 1976)),
  occ_download(pred('taxonKey', 5231190), pred("year", 2001)),
  occ_download(pred('taxonKey', 5231190), pred("year", 2001),
    pred_lte("month", 8)),
  occ_download(pred('taxonKey', 5229208), pred("year", 2011)),
  occ_download(pred('taxonKey', 2480946), pred("year", 2015)),
  occ_download(pred("country", "NZ"), pred("year", 1999),
    pred("month", 3)),
  occ_download(pred("catalogNumber", "Bird.27847588"),
    pred("year", 1998), pred("month", 2))
)

# supports <= 3 requests too
out <- occ_download_queue(
  occ_download(pred("country", "NZ"), pred("year", 1999), pred("month", 3)),
  occ_download(pred("catalogNumber", "Bird.27847588"), pred("year", 1998),
    pred("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(
    pred("taxonKey", keys[i]),
    pred_in("basisOfRecord", c("HUMAN_OBSERVATION","OBSERVATION")),
    pred("hasCoordinate", TRUE),
    pred("hasGeospatialIssue", FALSE),
    pred("year", 1993)
  )
}
out <- occ_download_queue(.list = queries)
out

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

`occ_download_sql` *Download occurrence data using a SQL query*

Description

Download occurrence data using a SQL query

Usage

```
occ_download_sql(
  q = NULL,
  format = "SQL_TSV_ZIP",
  user = NULL,
  pwd = NULL,
  email = NULL,
  validate = TRUE,
  curlopts = list(http_version = 2)
)

occ_download_sql_validate(
```

```
  q = NULL,
  user = NULL,
  pwd = NULL,
  curlopts = list(http_version = 2)
)

occ_download_sql_prep(
  q = NULL,
  format = "SQL_TSV_ZIP",
  user = NULL,
  pwd = NULL,
  email = NULL,
  validate = TRUE,
  curlopts = list(http_version = 2)
)
```

Arguments

q	sql query
format	only "SQL_TSV_ZIP" is supported right now
user	your GBIF user name
pwd	your GBIF password
email	your email address
validate	should the query be validated before submission. Default is TRUE.
curlopts	list of curl options

Details

This is an experimental feature, and the implementation may change throughout 2024. The feature is currently only available for preview by invited users. Contact helpdesk@gbif.org to request access.

Please see the article here for more information: https://docs.ropensci.org/rgbif/articles/gbif_sql_downloads.html

Value

an object of class 'occ_download_sql'

References

https://techdocs.gbif.org/en/data-use/api-sql-downloads

Examples

```
## Not run:
occ_download_sql("SELECT gbifid,countryCode FROM occurrence
                  WHERE genusKey = 2435098")
```

```
## End(Not run)
```

`occ_download_stats` *Occurrence download statistics*

Description

Retrieve statistics about GBIF occurrence downloads. Filters for downloads matching the provided criteria, then provides counts by year, month and dataset of the total number of downloads, and the total number of records included in those downloads.

Usage

```
occ_download_stats(
  from = NULL,
  to = NULL,
  publishingCountry = NULL,
  datasetKey = NULL,
  publishingOrgKey = NULL,
  limit = NULL,
  offset = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

`from`	(character) Start date in format `YYYY-MM`. Optional.
`to`	(character) End date in format `YYYY-MM`. Optional.
`publishingCountry`	(character) ISO 2-letter country code. Optional.
`datasetKey`	(character) Dataset UUID. Optional.
`publishingOrgKey`	(character) Publishing organization UUID. Optional.
`limit`	(integer) Number of results to return. Optional.
`offset`	(integer) Offset for pagination. Optional.
`curlopts`	list of named curl options passed on to crul::HttpClient. See curl::curl_options for curl options

Value

A list with two slots:

- meta: a single row data.frame with columns: `offset`, `limit`, `endofrecords`, `count`
- results: a tibble with the results containing columns: `datasetKey`, `totalRecords`, `numberDownloads`, `year`, `month`

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dataset(), occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_wait(), occ_download()

Examples

```
## Not run:
# Get summarized download statistics
occ_download_stats()

# Filter by date range and country
occ_download_stats(from = "2023-01", to = "2023-12", publishingCountry = "US")

# Filter by publishing organization iNaturalist
occ_download_stats(publishingOrgKey = "28eb1a3f-1c15-4a95-931a-4af90ecb574d")

## End(Not run)
```

---

occ_download_stats_dataset

Downloads by dataset

Description

Summarize downloads by dataset.

Usage

```
occ_download_stats_dataset(
  from = NULL,
  to = NULL,
  publishingCountry = NULL,
  datasetKey = NULL,
  publishingOrgKey = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

from	(character) Start date in format YYYY-MM. Optional.
to	(character) End date in format YYYY-MM. Optional.
publishingCountry	(character) ISO 2-letter country code. Optional.
datasetKey	(character) Dataset UUID. Optional.
publishingOrgKey	(character) Publishing organization UUID. Optional.
curlopts	list of named curl options passed on to crul::HttpClient. See curl::curl_options for curl options

Value

A tibble with columns: year, month, number_downloads. Each row represents the total number of downloads for a given year and month.

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

```
## Not run:
# Get downloads by dataset
occ_download_stats_dataset()

# Filter by date range and publishing country
occ_download_stats_dataset(from = "2023-01", publishingCountry = "US")

# Filter by publishing organization (e.g., iNaturalist)
occ_download_stats_dataset(publishingOrgKey = "28eb1a3f-1c15-4a95-931a-4af90ecb574d")

## End(Not run)
```

`occ_download_stats_dataset_records` *Downloaded records by dataset*

Description

Summarize downloaded records by dataset.

Usage

```
occ_download_stats_dataset_records(
  from = NULL,
  to = NULL,
  publishingCountry = NULL,
  datasetKey = NULL,
  publishingOrgKey = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

`from`	(character) Start date in format `YYYY-MM`. Optional.
`to`	(character) End date in format `YYYY-MM`. Optional.
`publishingCountry`	(character) ISO 2-letter country code. Optional.
`datasetKey`	(character) Dataset UUID. Optional.
`publishingOrgKey`	(character) Publishing organization UUID. Optional.
`curlopts`	list of named curl options passed on to crul::HttpClient. See curl::curl_options for curl options

Value

A tibble with columns: `year`, `month`, `number_records`. Each row represents the total number of records downloaded for a given year and month.

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset()`, `occ_download_stats_export()`, `occ_download_stats_source()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
# Get downloaded records by dataset
occ_download_stats_dataset_records()

# Filter by date range
occ_download_stats_dataset_records(from = "2023-01", to = "2023-12")

# Filter by specific dataset
occ_download_stats_dataset_records(
  datasetKey = "50c9509d-22c7-4a22-a47d-8c48425ef4a7"
)

## End(Not run)
```

---

occ_download_stats_export

Export summary of occurrence downloads

Description

Export a summary of occurrence downloads. Note that `from`, `to`, and `publishingCountry` are required parameters for this endpoint.

Usage

```
occ_download_stats_export(
  from,
  to,
  publishingCountry,
  datasetKey = NULL,
  publishingOrgKey = NULL,
  limit = NULL,
  offset = NULL
)
```

Arguments

`from`	(character) Start date in format `YYYY-MM`. Required.
`to`	(character) End date in format `YYYY-MM`. Required.
`publishingCountry`	(character) ISO 2-letter country code. Required.
`datasetKey`	(character) Dataset UUID. Optional.
`publishingOrgKey`	(character) Publishing organization UUID. Optional.
`limit`	(integer) Number of results to return. Optional.
`offset`	(integer) Offset for pagination. Optional.

Value

A tibble with download summary data

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dataset(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

```
## Not run:
# Export download summary (from, to, and publishingCountry are required)
occ_download_stats_export(from = "2023-01", to = "2023-12", publishingCountry = "US")

## End(Not run)
```

---

occ_download_stats_source

Downloads by source

Description

Summarize downloads by source.

Usage

```
occ_download_stats_source(
  from = NULL,
  to = NULL,
  source = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

from	(character) Start date in format YYYY-MM. Optional.
to	(character) End date in format YYYY-MM. Optional.
source	(character) Restrict to a particular source (e.g., "rgbif", "pygbif"). Optional.
curlopts	list of named curl options passed on to crul::HttpClient. See curl::curl_options for curl options

Value

A tibble with columns: `year`, `month`, `number_downloads`. Each row represents the total number of downloads for a given year and month.

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: `download_predicate_dsl`, `occ_download_cached()`, `occ_download_cancel()`, `occ_download_dataset_activity()`, `occ_download_datasets()`, `occ_download_get()`, `occ_download_import()`, `occ_download_list()`, `occ_download_meta()`, `occ_download_queue()`, `occ_download_stats_dataset_records()`, `occ_download_stats_dataset()`, `occ_download_stats_export()`, `occ_download_stats_user_country()`, `occ_download_stats()`, `occ_download_wait()`, `occ_download()`

Examples

```
## Not run:
# Get downloads by source
occ_download_stats_source()

# Filter by date range
occ_download_stats_source(from = "2023-01", to = "2023-12")

# Filter by source
occ_download_stats_source(source = "pygbif")

## End(Not run)
```

---

occ_download_stats_user_country

Downloads by user country

Description

Summarizes downloads by month, grouped by the user's country code.

Usage

```
occ_download_stats_user_country(
  from = NULL,
  to = NULL,
  userCountry = NULL,
  publishingCountry = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

from	(character) Start date in format YYYY-MM. Optional.
to	(character) End date in format YYYY-MM. Optional.
userCountry	(character) ISO 2-letter country code. Optional.
publishingCountry	(character) ISO 2-letter country code. Optional.
curlopts	list of named curl options passed on to crul::HttpClient. See curl::curl_options for curl options

Value

A tibble with download counts by user country and month

Note

see downloads for an overview of GBIF downloads methods

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dataset(), occ_download_stats_export(), occ_download_stats_source(), occ_download_stats(), occ_download_wait(), occ_download()

Examples

```
## Not run:
# Run with no args to get monthly download counts for all of GBIF
occ_download_stats_user_country()

# Filter by date range
occ_download_stats_user_country(from = "2023-01", to = "2023-12")

# Filter by user country
occ_download_stats_user_country(userCountry = "US")

## End(Not run)
```

---

occ_download_user_count

Count downloads for a user.

Description

Count downloads for a user.

Usage

```
occ_download_user_count(
  user = NULL,
  pwd = NULL,
  from = NULL,
  status = NULL,
  curlopts = list(http_version = 2)
)
```

Arguments

user	(character) User name within GBIF's website. Required. See Details.
pwd	(character) User password within GBIF's website. Required. See Details.
from	(character) Optional. Start date in format YYYY-MM-DD. Only downloads created on or after this date will be counted.
status	(character) Optional. Filter by download status. One of "PREPARING", "RUNNING", "SUCCEEDED", "CANCELLED", "KILLED", "FAILED", "SUSPENDED", or "FILE_ERASED".
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options

Details

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

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

See ?Startup for help.

Value

a single integer with the total number of downloads for the user.

Examples

```
## Not run:
occ_download_user_count(user="jwaller", pwd="your_password")
occ_download_user_count(user="jwaller", pwd="your_password", from="2023-01-01")
occ_download_user_count(user="jwaller", pwd="your_password", status="SUCCEEDED")

## End(Not run)
```

occ_download_wait *Wait for an occurrence download to be done*

Description

Wait for an occurrence download to be done

Usage

```
occ_download_wait(
  x,
  status_ping = 5,
  curlopts = list(http_version = 2),
  quiet = FALSE
)
```

Arguments

x	and object of class occ_download or downloadkey
status_ping	(integer) seconds between each occ_download_meta() request. default is 5, and cannot be < 3
curlopts	(list) curl options, as named list, passed on to occ_download_meta()
quiet	(logical) suppress messages. default: FALSE

Value

an object of class occ_download_meta, see occ_download_meta() for details

Note

occ_download_queue() is similar, but handles many requests at once; occ_download_wait handles one request at a time

See Also

Other downloads: download_predicate_dsl, occ_download_cached(), occ_download_cancel(), occ_download_dataset_activity(), occ_download_datasets(), occ_download_get(), occ_download_import(), occ_download_list(), occ_download_meta(), occ_download_queue(), occ_download_stats_dataset_records(), occ_download_stats_dataset(), occ_download_stats_export(), occ_download_stats_source(), occ_download_stats_user_country(), occ_download_stats(), occ_download()

Examples

```
## Not run:
x <- occ_download(
  pred("taxonKey", 9206251),
  pred_in("country", c("US", "MX")),
  pred_gte("year", 1971)
)
res <- occ_download_wait(x)
occ_download_meta(x)

# works also with a downloadkey
occ_download_wait("0000066-140928181241064")


## End(Not run)
```

`occ_facet` *Facet GBIF occurrences*

Description

Facet GBIF occurrences

Usage

```
occ_facet(facet, facetMincount = NULL, curlopts = list(http_version = 2), ...)
```

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::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

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

# facetMincount - minimum number of records to be included
#   in the faceting results
occ_facet(facet = "country", facetMincount = 30000000L)
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_get *Get data for GBIF occurrences by occurrence key*

Description

Get data for GBIF occurrences by occurrence key

Usage

```
occ_get(
  key,
  fields = "minimal",
  curlopts = list(http_version = 2),
  return = NULL,
  verbatim = NULL
)

occ_get_verbatim(key, fields = "minimal", curlopts = list(http_version = 2))
```

Arguments

key	(numeric/integer) one or more occurrence keys. required
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::curl_options for curl options
return	Defunct. All components are returned now; index to the one(s) you want
verbatim	Defunct. verbatim records can now be retrieved using occ_get_verbatim()

Value

For occ_get a list of lists. For occ_get_verbatim a data.frame

References

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

Examples

```
## Not run:
occ_get(key=855998194)

# many occurrences
occ_get(key=c(101010, 240713150, 855998194))

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

# curl options, pass in a named list
occ_get(key=855998194, curlopts = list(verbose=TRUE))

## End(Not run)
```

---

occ_issues *Parse and examine further GBIF occurrence issues on a dataset.*

Description

Parse and examine further GBIF occurrence 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(). 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. • 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. • split_expand Split into new columns, and expand issue names. 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 removed 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

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

Examples

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

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

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

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

## or parse issues in various ways
### include only rows with cdround issue
gg <- res %>% occ_issues(cdround)
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(-cdround, -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_expand")

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

## Or you can use occ_issues without %>%
occ_issues(res, -cdround, mutate = "split_expand")

# from GBIF downloaded data via occ_download_* functions
res <- occ_download_get(key="0000066-140928181241064", overwrite=TRUE)
x <- occ_download_import(res)
occ_issues(x, -txmathi)
occ_issues(x, txmathi)
occ_issues(x, gass84)
occ_issues(x, zerocd)
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_expand")
```

```
# 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
length(xyz) # length 3
names(xyz) # matches taxonKey values passed in
occ_issues(xyz, -gass84)
occ_issues(xyz, -cdround)
occ_issues(xyz, -cdround, -gass84)

## End(Not run)
```

`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(http_version = 2)
)
```

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::curl_options` for curl options

References

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

Examples

```
## 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(verbose = TRUE))

## End(Not run)
```

---

occ_search *Search for GBIF occurrences*

Description

Search for GBIF occurrences

Usage

```
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,
  recordedByID = NULL,
  identifiedByID = 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,
  speciesKey = NULL,
  establishmentMeans = NULL,
  degreeOfEstablishment = NULL,
  protocol = NULL,
  license = NULL,
  organismId = NULL,
  publishingOrg = NULL,
  stateProvince = NULL,
  waterBody = NULL,
  locality = NULL,
  occurrenceStatus = "PRESENT",
  gadmGid = NULL,
  coordinateUncertaintyInMeters = NULL,
  verbatimScientificName = NULL,
  eventId = NULL,
  identifiedBy = NULL,
  networkKey = NULL,
  verbatimTaxonId = NULL,
  occurrenceId = NULL,
```

```
organismQuantity = NULL,
organismQuantityType = NULL,
relativeOrganismQuantity = NULL,
iucnRedListCategory = NULL,
lifeStage = NULL,
isInCluster = NULL,
distanceFromCentroidInMeters = NULL,
geoDistance = NULL,
sex = NULL,
dwcaExtension = NULL,
gbifId = NULL,
gbifRegion = NULL,
projectId = NULL,
programme = NULL,
preparations = NULL,
datasetId = NULL,
datasetName = NULL,
publishedByGbifRegion = NULL,
island = NULL,
islandGroup = NULL,
taxonId = NULL,
taxonConceptId = NULL,
taxonomicStatus = NULL,
acceptedTaxonKey = NULL,
collectionKey = NULL,
institutionKey = NULL,
otherCatalogNumbers = NULL,
georeferencedBy = NULL,
installationKey = NULL,
hostingOrganizationKey = NULL,
crawlId = NULL,
modified = NULL,
higherGeography = NULL,
fieldNumber = NULL,
parentEventId = NULL,
samplingProtocol = NULL,
sampleSizeUnit = NULL,
pathway = NULL,
gadmLevel0Gid = NULL,
gadmLevel1Gid = NULL,
gadmLevel2Gid = NULL,
gadmLevel3Gid = NULL,
earliestEonOrLowestEonothem = NULL,
latestEonOrHighestEonothem = NULL,
earliestEraOrLowestErathem = NULL,
latestEraOrHighestErathem = NULL,
earliestPeriodOrLowestSystem = NULL,
latestPeriodOrHighestSystem = NULL,
```

```
  earliestEpochOrLowestSeries = NULL,
  latestEpochOrHighestSeries = NULL,
  earliestAgeOrLowestStage = NULL,
  latestAgeOrHighestStage = NULL,
  lowestBiostratigraphicZone = NULL,
  highestBiostratigraphicZone = NULL,
  group = NULL,
  formation = NULL,
  member = NULL,
  bed = NULL,
  associatedSequences = NULL,
  nucleotideSequence.nucleotideSequenceID = NULL,
  nucleotideSequence.targetGene = NULL,
  nucleotideSequence.sequence = NULL,
  nucleotideSequence.sequenceLength = NULL,
  nucleotideSequence.gcContent = NULL,
  nucleotideSequence.nonIupacFraction = NULL,
  nucleotideSequence.nonACGTNFraction = NULL,
  nucleotideSequence.nFraction = NULL,
  nucleotideSequence.nRunsCapped = NULL,
  nucleotideSequence.naturalLanguageDetected = NULL,
  nucleotideSequence.endsTrimmed = NULL,
  nucleotideSequence.gapsOrWhitespaceRemoved = NULL,
  nucleotideSequence.invalid = NULL,
  isSequenced = NULL,
  startDayOfYear = NULL,
  endDayOfYear = NULL,
  checklistKey = "7ddf754f-d193-4cc9-b351-99906754a03b",
  limit = 500,
  start = 0,
  fields = "all",
  return = NULL,
  facet = NULL,
  facetMincount = NULL,
  facetMultiselect = NULL,
  skip_validate = TRUE,
  curlopts = list(http_version = 2),
  ...
)
```

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 will match all birds, no matter which species. You can pass many keys to occ_search(taxonKey=c("N","V2")).
scientificName	A scientific name from the GBIF backbone. All included and synonym taxa are included in the search.

`country` (character) The 2-letter country code (ISO-3166-1) in which the occurrence was recorded. `enumeration_country()`.

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

`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.

`recordNumber` Number recorded by collector of the data, different from GBIF record number.

`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` The source supplied continent.

- "africa"
- "antarctica"
- "asia"
- "europe"
- "north_america"
- "oceania"
- "south_america"

Continent is not inferred but only populated if provided by the dataset publisher. Applying this filter may exclude many relevant records.

`geometry` (character) Searches for occurrences inside a polygon in Well Known Text (WKT) format. A WKT shape written as either

- "POINT"
- "LINESTRING"
- "LINEARRING"
- "POLYGON"
- "MULTIPOLYGON"

For Example, "POLYGON((37.08 46.86,38.06 46.86,38.06 47.28,37.08 47.28, 37.0 46.8))". See also the section **WKT** below.

`geom_big` (character) One"bbox" or "asis" (default).

`geom_size` (integer) An integer indicating size of the cell. Default: 40.

`geom_n` (integer) An integer indicating number of cells in each dimension. Default: 10.

`recordedBy` (character) The person who recorded the occurrence.

`recordedByID` (character) Identifier (e.g. ORCID) for the person who recorded the occurrence

`identifiedByID` (character) Identifier (e.g. ORCID) for the person who provided the taxonomic identification of the occurrence.

`basisOfRecord` (character) The specific nature of the data record. See here.

- "FOSSIL_SPECIMEN"

- "HUMAN_OBSERVATION"
- "MATERIAL_CITATION"
- "MATERIAL_SAMPLE"
- "LIVING_SPECIMEN"
- "MACHINE_OBSERVATION"
- "OBSERVATION"
- "PRESERVED_SPECIMEN"
- "OCCURRENCE"

`datasetKey` (character) The occurrence dataset uuid key. That can be found in the dataset page url. For example, "7e380070-f762-11e1-a439-00145 eb45e9a" is the key for Natural History Museum (London) Collection Specimens.

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

`catalogNumber` (character) 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 WGS84. 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 WGS84. 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.

`collectionCode` (character) 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. Issues passed to this parameter filter results by the issue. One of many options. See here for definitions.

`search` (character) Query terms. The value for this parameter can be a simple word or a phrase. For example, search="puma"

`mediaType` (character) Media type of "MovingImage", "Sound", or "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.

`speciesKey` (numeric) Species classification key.

`establishmentMeans` (character) provides information about whether an organism or organisms have been introduced to a given place and time through the direct or indirect activity of modern humans.

- "Introduced"
- "Native"
- "NativeReintroduced"
- "Vagrant"
- "Uncertain"
- "IntroducedAssistedColonisation"

`degreeOfEstablishment` (character) Provides information about degree to which an Organism survives, reproduces, and expands its range at the given place and time. One of many options.

`protocol` (character) Protocol or mechanism used to provide the occurrence record. One of many options.

`license` (character) The type license applied to the dataset or record.

- "CC0_1_0"
- "CC_BY_4_0"
- "CC_BY_NC_4_0"

`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.

`occurrenceStatus`
(character) Default is "PRESENT". Specify whether search should return "PRESENT" or "ABSENT" data.

`gadmGid` (character) The gadm id of the area occurrences are desired from. https://gadm.org/.

`coordinateUncertaintyInMeters`
A number or range between 0-1,000,000 which specifies the desired coordinate uncertainty. A coordinateUncertainty InMeters=1000 will be interpreted all records with exactly 1000m. Supports range queries, 'smaller,larger' (e.g., '1000,10000', whereas '10000,1000' wouldn't work).

`verbatimScientificName`
(character) Scientific name as provided by the source.

`eventId` (character) identifier(s) for a sampling event.

`identifiedBy` (character) names of people, groups, or organizations.

`networkKey` (character) The occurrence network key (a uuid) who assigned the Taxon to the subject.

`verbatimTaxonId`
(character) The taxon identifier provided to GBIF by the data publisher.

`occurrenceId` (character) occurrence id from source.

`organismQuantity`
A number or range which specifies the desired organism quantity. An organismQuantity=5 will be interpreted all records with exactly 5. Supports range queries, smaller,larger (e.g., '5,20', whereas '20,5' wouldn't work).

`organismQuantityType`
(character) The type of quantification system used for the quantity of organisms. For example, "individuals" or "biomass".

`relativeOrganismQuantity`
(numeric) A relativeOrganismQuantity=0.1 will be interpreted all records with exactly 0.1 The relative measurement of the quantity of the organism (a number between 0-1). Supports range queries, "smaller,larger" (e.g., '0.1,0.5', whereas '0.5,0.1' wouldn't work).

`iucnRedListCategory`
(character) The IUCN threat status category.

- "NE" (Not Evaluated)
- "DD" (Data Deficient)
- "LC" (Least Concern)
- "NT" (Near Threatened)
- "VU" (Vulnerable)
- "EN" (Endangered)
- "CR" (Critically Endangered)
- "EX" (Extinct)
- "EW" (Extinct in the Wild)

`lifeStage` (character) the life stage of the occurrence. One of many options.

`isInCluster` (logical) identify potentially related records on GBIF.

`distanceFromCentroidInMeters`
A number or range. A value of "2000,*" means at least 2km from known centroids. A value of "0" would mean occurrences exactly on known centroids. A value of "0,2000" would mean within 2km of centroids. Max value is 5000.

`geoDistance` (character) Filters to match occurrence records with coordinate values within a specified distance of a coordinate. Distance may be specified in kilometres (km) or metres (m). Example : "90,100,5km"

`sex` (character) The sex of the biological individual(s) represented in the occurrence.

`dwcaExtension` (character) A known Darwin Core Archive extension RowType. Limits the search to occurrences which have this extension, although they will not necessarily have any useful data recorded using the extension.

`gbifId` (numeric) The unique GBIF key for a single occurrence.

`gbifRegion` (character) Gbif region based on country code.

`projectId` (character) The identifier for a project, which is often assigned by a funded programme.

`programme` (character) A group of activities, often associated with a specific funding stream, such as the GBIF BID programme.

`preparations` (character) Preparation or preservation method for a specimen.

`datasetId` (character) The ID of the dataset. Parameter may be repeated. Example : https://doi.org/10.1594/PANGAEA.315492

`datasetName` (character) The exact name of the dataset. Not the same as dataset title.

`publishedByGbifRegion`
(character) GBIF region based on the owning organization's country.

`island` (character) The name of the island on or near which the location occurs.

`islandGroup` (character) The name of the island group in which the location occurs.

`taxonId` (character) The taxon identifier provided to GBIF by the data publisher. Example : urn:lsid:dyntaxa.se:Taxon:103026

`taxonConceptId` (character) An identifier for the taxonomic concept to which the record refers - not for the nomenclatural details of a taxon. Example : 8fa58e08-08de-4ac1-b69c-1235340b7001

`taxonomicStatus`
(character) A taxonomic status. Example : SYNONYM

`acceptedTaxonKey`
(numeric) A taxon key from the GBIF backbone. Only synonym taxa are included in the search, so a search for Aves with acceptedTaxonKey="V2" will match occurrences identified as birds, but not any known family, genus or species of bird.

`collectionKey` (character) A key (UUID) for a collection registered in the Global Registry of Scientific Collections. Example : dceb8d52-094c-4c2c-8960-75e0097c6861

`institutionKey` (character) A key (UUID) for an institution registered in the Global Registry of Scientific Collections.

otherCatalogNumbers
: (character) Previous or alternate fully qualified catalog numbers.

georeferencedBy
: (character) Name of a person, group, or organization who determined the georeference (spatial representation) for the location. Example : Brad Millen

installationKey
: (character) The occurrence installation key (a UUID). Example : 17a83780-3060-4851-9d6f-029d5fcb81c9

hostingOrganizationKey
: (character) The key (UUID) of the publishing organization whose installation (server) hosts the original dataset. Example : fbca90e3-8aed-48b1-84e3-369afbd000ce

crawlId
: (numeric) Crawl attempt that harvested this record.

modified
: (character) The most recent date-time on which the occurrence was changed, according to the publisher. Can be a range. Example : 2023-02-20

higherGeography
: (character) Geographic name less specific than the information captured in the locality term.

fieldNumber
: (character) An identifier given to the event in the field. Often serves as a link between field notes and the event.

parentEventId
: (character) An identifier for the information associated with a sampling event.

samplingProtocol
: (character) The name of, reference to, or description of the method or protocol used during a sampling event. Example : malaise trap

sampleSizeUnit
: (character) The unit of measurement of the size (time duration, length, area, or volume) of a sample in a sampling event. Example : hectares

pathway
: (character) The process by which an organism came to be in a given place at a given time, as defined in the GBIF Pathway vocabulary. Example : Agriculture

gadmLevel0Gid
: (character) A GADM geographic identifier at the zero level, for example AGO.

gadmLevel1Gid
: (character) A GADM geographic identifier at the first level, for example AGO.1_1.

gadmLevel2Gid
: (character) A GADM geographic identifier at the second level, for example AFG.1.1_1.

gadmLevel3Gid
: (character) A GADM geographic identifier at the third level, for example AFG.1.1.1_1.

earliestEonOrLowestEonothem
: (character) geochronologic era term.

latestEonOrHighestEonothem
: (character) geochronologic era term.

earliestEraOrLowestErathem
: (character) geochronologic era term.

latestEraOrHighestErathem
: (character) geochronologic era term.

earliestPeriodOrLowestSystem
: (character) geochronologic era term.

latestPeriodOrHighestSystem
: (character) geochronologic era term.

`earliestEpochOrLowestSeries`
: (character) geochronologic era term.

`latestEpochOrHighestSeries`
: (character) geochronologic era term.

`earliestAgeOrLowestStage`
: (character) geochronologic era term.

`latestAgeOrHighestStage`
: (character) geochronologic era term.

`lowestBiostratigraphicZone`
: (character) geochronologic era term.

`highestBiostratigraphicZone`
: (character) geochronologic era term.

`group`
: (character) The full name of the lithostratigraphic group from which the material entity was collected.

`formation`
: (character) The full name of the lithostratigraphic formation from which the material entity was collected.

`member`
: (character) The full name of the lithostratigraphic member from which the material entity was collected.

`bed`
: (character) The full name of the lithostratigraphic bed from which the material entity was collected.

`associatedSequences`
: (character) Identifier (publication, global unique identifier, URI) of genetic sequence information associated with the material entity. Example : http://www.ncbi.nlm.nih.gov/nuccore/U

`nucleotideSequence.nucleotideSequenceID`
: (character) Identifier for the nucleotide sequence associated with the occurrence.

`nucleotideSequence.targetGene`
: (character) Gene targeted by the nucleotide sequence. See possible values at https://registry.gbif.org/vocabulary/target_gene/concepts

`nucleotideSequence.sequence`
: (character) Nucleotide sequence string.

`nucleotideSequence.sequenceLength`
: (numeric) Length of the nucleotide sequence.

`nucleotideSequence.gcContent`
: (numeric) GC content fraction or range.

`nucleotideSequence.nonIupacFraction`
: (numeric) Fraction or range of non-IUPAC characters in the sequence.

`nucleotideSequence.nonACGTNFraction`
: (numeric) Fraction or range of characters outside A, C, G, T, and N.

`nucleotideSequence.nFraction`
: (numeric) Fraction or range of N characters in the sequence.

`nucleotideSequence.nRunsCapped`
: (numeric) Count or range of capped N runs in the sequence.

`nucleotideSequence.naturalLanguageDetected`
: (logical) Whether natural language was detected in the sequence.

`nucleotideSequence.endsTrimmed`
: (logical) Whether sequence ends were trimmed.

`nucleotideSequence.gapsOrWhitespaceRemoved`
: (logical) Whether gaps or whitespace were removed from the sequence.

`nucleotideSequence.invalid`
: (logical) Whether the sequence is marked as invalid.

`isSequenced`
: (logical) Indicates whether `associatedSequences` genetic sequence information exists.

`startDayOfYear`
: (numeric) The earliest integer day of the year on which the event occurred.

`endDayOfYear`
: (numeric) The latest integer day of the year on which the event occurred.

`checklistKey`
: (character) The checklist uuid. This determines which taxonomy will be used for the search in conjunction with other taxon keys or scientificName. If this is not specified, the GBIF backbone taxonomy will be used.

`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 100,000, which is calculated as the `limit+start`, so `start=99,000` 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, datasetKey, latitude, and longitute. Or specify each field you want returned by name, e.g. fields = c('name','latitude','elevation').

`return`
: Defunct. All components (meta, hierarchy, data, media, facets) are returned now; index to the one(s) you want. See `occ_data()` if you just want the data component

`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 `wellknown::validate_wkt` call or not. passed down to `check_wkt()`. Default: `TRUE`

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

`...`
: additional facet parameters

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`), media metadata (`media`), taxonomic classifications (`classifications`), and facets (`facets`). 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.frames 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. `classifications` is a named list of tibbles, with one tibble per checklistKey. Each tibble contains one row per occurrence with the full taxonomic classification path pivoted into camelCase columns: checklistKey, kingdomName, kingdomKey, phylumName, phylumKey, className, classKey, orderName, orderKey, familyName, familyKey, genusName, genusKey, subgenusName, subgenusKey, speciesName, speciesKey. The function dynamically discovers all taxonomic ranks from the API. Known checklists (COL, backbone) are shown with friendly names, while unknown checklists use their UUID.

Multiple values passed to a parameter

There are some parameters you can pass multiple values to in a vector, each value of which produces a different request (multiple different requests = c("a","b")). Some parameters allow multiple values to be passed in the same request (multiple same request = "a;b") in a semicolon separated string (e.g., 'a;b'); if given we'll do a single request with that parameter repeated for each value given (e.g., `foo=a&foo=b` if the parameter is `foo`).

See article Multiple Values.

Hierarchies

Hierarchies are returned with each occurrence object. There is no option 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.

curl debugging

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

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)'

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 is deprecated since rgbif v3.8.0. Might return error, since the GBIF's polygon interpretation has changed.

  This method uses sf::st_make_grid and sf::st_intersection, which has two parameters cellsize and n. 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.

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

Note

Maximum number of records you can get with this function is 100,000. See https://www.gbif.org/developer/occurrence

When numeric taxonomic keys (taxonKey, speciesKey, kingdomKey, etc.) are detected and checklistKey is set to COL XR (the default), the function automatically switches to the GBIF Backbone taxonomy checklistKey and issues a warning. These numeric keys are legacy identifiers. If you explicitly set checklistKey to Backbone or another taxonomy, no warning is issued. Consider migrating to COL XR identifiers using gbif_to_col().

References

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

See Also

downloads(), occ_data()

Examples

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

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

# Get just metadata
occ_search(taxonKey=key, limit=0)$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{scientifcName} 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', limit=20)$data

# 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)$data
occ_search(datasetKey='7b5d6a48-f762-11e1-a439-00145eb45e9a',start=20,limit=5)$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
## The `data` slot has a data.frame of all data together
## for easy manipulation
occ_search(taxonKey=key, limit=20)$data

# Taxonomic hierarchy data
## In the `hier` slot
occ_search(taxonKey=key, limit=10)$hier

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

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

# recordedByID
occ_search(recordedByID="https://orcid.org/0000-0003-1691-239X", limit=20)

# identifiedByID
occ_search(identifiedByID="https://orcid.org/0000-0003-4710-2648", limit=20)

# Pass in curl options for extra fun
occ_search(taxonKey="Q2M4", limit=20, curlopts=list(verbose=TRUE))$hier
occ_search(taxonKey="Q2M4", limit=20,
  curlopts = list(
    noprogress = FALSE,
    progressfunction = function(down, up) {
      cat(sprintf("up: %d | down %d\n", up, down))
      return(TRUE)
    }
  )
)$hier
# occ_search(taxonKey="Q2M4", 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)$data$key[1], 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(scientificName = 'Pulsatilla patens', fields = c('name','scientificName'), limit=5)

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

```
# Search on a bounding box
## in well known text format
### polygon
occ_search(geometry='POLYGON((30.1 10.1,40 40,20 40,10 20,30.1 10.1))', limit=20)
### multipolygon
wkt <- 'MULTIPOLYGON(((-123 38,-116 38,-116 43,-123 43,-123 38)),
   ((-97 41,-93 41,-93 45,-97 45,-97 41)))'
occ_search(geometry = gsub("\n\\s+", "", wkt), limit = 20)

## taxonKey + WKT
key <- name_suggest(q='Aesculus hippocastanum')$data$key[1]
occ_search(taxonKey=key, geometry='POLYGON((30.1 10.1,40 40,20 40,10 20,30.1 10.1))',
   limit=20)
## or using bounding box, converted to WKT internally
occ_search(geometry=c(-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
##  then clip the results down to just those in the original polygon
##  - Alternatively, you can set the parameter `geom_big="bbox"`
##  - An additional alternative is to use the GBIF download API, see ?downloads
wkt <- "POLYGON((-9.178796777343678 53.22769021556159,
-12.167078027343678 51.56540789297837,
-12.958093652343678 49.78333685689162,-11.024499902343678 49.21251756301334,
-12.079187402343678 46.68179685941719,-15.067468652343678 45.83103608186854,
-15.770593652343678 43.58271629699817,-15.067468652343678 41.57676278827219,
-11.815515527343678 40.44938999172728,-12.958093652343678 37.72112962230871,
-11.639734277343678 36.52987439429357,-8.299890527343678 34.96062625095747,
-8.739343652343678 32.62357394385735,-5.223718652343678 30.90497915232165,
1.1044063476563224 31.80562077746643,1.1044063476563224 30.754036557416256,
6.905187597656322 32.02942785462211,5.147375097656322 32.99292810780193,
9.629796972656322 34.164474406524725,10.860265722656322 32.91918014319603,
14.551671972656322 33.72700959356651,13.409093847656322 34.888564192275204,
16.748937597656322 35.104560368110114,19.561437597656322 34.81643887792552,
18.594640722656322 36.38849705969625,22.989171972656322 37.162874858929854,
19.825109472656322 39.50651757842751,13.760656347656322 38.89353140585116,
14.112218847656322 42.36091601976124,10.596593847656322 41.11488736647705,
9.366125097656322 43.70991402658437,5.059484472656322 42.62015372417812,
2.3348750976563224 45.21526500321446,-0.7412967773436776 46.80225692528942,
6.114171972656322 47.102229890207894,8.047765722656322 45.52399303437107,
12.881750097656322 48.22681126957933,9.190343847656322 48.693079457106684,
8.750890722656322 50.68283120621287,5.059484472656322 50.40356146487845,
4.268468847656322 52.377558897655156,1.4559688476563224 53.28027243658647,
0.8407344726563224 51.62000971578333,0.5770625976563224 49.32721423860726,
-2.5869999023436776 49.49875947592088,-2.4991092773436776 51.18135535408638,
-2.0596561523436776 52.53822562473851,-4.696374902343678 51.67454591918756,
-5.311609277343678 50.009802108095776,-6.629968652343678 48.75106196817059,
-7.684656152343678 50.12263634382465,-6.190515527343678 51.83776110910459,
-5.047937402343678 54.267098895684235,-6.893640527343678 53.69860705549198,
-8.915124902343678 54.77719740243195,-12.079187402343678 54.52294465763567,
-13.573328027343678 53.437631551347174,
```

```
-11.288171777343678 53.48995552517918,
-9.178796777343678 53.22769021556159))"
wkt <- gsub("\n", " ", 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(geometry = wkt, geom_big = "bbox")$data

# Search on country
occ_search(country='US', fields=c('name','country'), limit=20)
occ_search(country='FR', fields=c('name','country'), limit=20)
occ_search(country='DE', fields=c('name','country'), limit=20)
### separate requests: use a vector of strings
occ_search(country=c('US','DE'), limit=20)
### one request, many instances of same parameter: use semi-colon sep. string
occ_search(country = 'US;DE', limit=20)

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

# Get only occurrences that were recorded as living specimens
occ_search(taxonKey=key, basisOfRecord="LIVING_SPECIMEN", hasCoordinate=TRUE, limit=20)
## multiple values in a vector = a separate request for each value
occ_search(taxonKey=key,
  basisOfRecord=c("LIVING_SPECIMEN", "HUMAN_OBSERVATION"), limit=20)
## mutiple values in a single string, ";" separated = one request including all values
occ_search(taxonKey=key,
  basisOfRecord="LIVING_SPECIMEN;HUMAN_OBSERVATION", limit=20)

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

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

# 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 = "N", limit = 5)

# search on classKey
occ_search(classKey = "H6", limit = 5)

# search on orderKey
occ_search(orderKey = "X3", limit = 5)

# search on familyKey
occ_search(familyKey = "C7ZVG", limit = 5)

# search on genusKey
occ_search(genusKey = "9WLSS", 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
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')

## Range search with distanceFromCentroidInMeters
occ_search(distanceFromCentroidInMeters = "2000,*") # at least 2km from centroids
occ_search(distanceFromCentroidInMeters = "0,2000") # close to centroids within 2km
occ_search(distanceFromCentroidInMeters = 0) # exactly on centroids

# 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')$meta
occ_search(continent = 'africa')$meta
occ_search(continent = 'oceania')$meta
occ_search(continent = 'antarctica')$meta

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

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

```
occ_search(taxonKey="N", issue=c('DEPTH_UNLIKELY','COORDINATE_ROUNDED'))
# Show all records in the Arizona State Lichen Collection that cant be matched to the GBIF
# backbone properly:
occ_search(datasetKey='84c0e1a0-f762-11e1-a439-00145eb45e9a',
   issue=c('TAXON_MATCH_NONE','TAXON_MATCH_HIGHERRANK'))

# Parsing output by issue
(res <- occ_search(geometry='POLYGON((30.1 10.1,40 40,20 40,10 20,30.1 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','gass84','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
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("N","Q2M4"), recordedBy=c("smith","BJ Stacey"))

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

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

### the WKT string is fine, but GBIF says bad polygon
wkt <- 'POLYGON((-178.59375 64.83258989321493,-165.9375 59.24622380205539,
-147.3046875 59.065977905449806,-130.78125 51.04484764446178,-125.859375 36.70806354647625,
-112.1484375 23.367471303759686,-105.1171875 16.093320185359257,-86.8359375 9.23767076398516,
-82.96875 2.9485268155066175,-82.6171875 -14.812060061226388,-74.8828125 -18.849111862023985,
-77.34375 -47.661687803329166,-84.375 -49.975955187343295,174.7265625 -50.649460483096114,
179.296875 -42.19189902447192,-176.8359375 -35.634976650677295,176.8359375 -31.835565983656227,
163.4765625 -6.528187613695323,152.578125 1.894796132058301,135.703125 4.702353722559447,
127.96875 15.077427674847987,127.96875 23.689804541429606,139.921875 32.06861069132688,
149.4140625 42.65416193033991,159.2578125 48.3160811030533,168.3984375 57.019804336633165,
178.2421875 59.95776046458139,-179.6484375 61.16708631440347,-178.59375 64.83258989321493))'

# occ_search(geometry = 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(geometry = 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(geometry = 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(geometry = wkt)

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

### Apparently a point is allowed, but errors
# wkt <- 'POINT(45 -122)'
# occ_search(geometry = 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 = 30000000L, 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
))
x$facets


# You can set limit=0 to get number of results found
occ_search(datasetKey = '7b5d6a48-f762-11e1-a439-00145eb45e9a', limit = 0)$meta
occ_search(scientificName = 'Ursus americanus', limit = 0)$meta
occ_search(scientificName = 'Ursus americanus', limit = 0)$meta

## End(Not run)
```

`occ_term` *Get occurrence terms.*

Description

Get occurrence terms.

Usage

```
occ_term(curlopts = list(http_version = 2))
```

Arguments

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

Value

A data.frame with occurrence term definitions.

References

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

Examples

```
## Not run:
occ_term()

# Pass on curl options
occ_term(curlopts = list(verbose = TRUE))

## End(Not run)
```

---

organizations *Organizations metadata.*

Description

Organizations metadata.

Usage

```
organizations(
  data = "all",
  country = NULL,
  uuid = NULL,
  query = NULL,
  limit = 100,
  start = NULL,
  isEndorsed = NULL,
  networkKey = NULL,
  numPublishedDatasets = NULL,
  canModify = NULL,
  identifierType = NULL,
  identifier = NULL,
```

```
  machineTagNamespace = NULL,
  machineTagName = NULL,
  machineTagValue = NULL,
  modified = NULL,
  created = NULL,
  curlopts = list(http_version = 2)
)
```

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', 'installation' or the special 'all'. Default: 'all'
country	(character) Filters by country.
uuid	(character) UUID of the data node provider. This must be specified if data is anything other than 'all', 'deleted', 'pending', or 'nonPublishing'.
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.
isEndorsed	(logical) Whether the organization is endorsed by a GBIF node. Optional.
networkKey	(character) The UUID key of the network to filter organizations by. Optional.
numPublishedDatasets	(integer) Filters by the number of published datasets. Optional.
canModify	(logical) Whether the organization can be modified. Optional.
identifierType	(character) Used in combination with the identifier parameter to filter identifiers by identifier type. One of: DOI, FTP, GBIF_NODE, GBIF_PARTICIPANT, GBIF_PORTAL, HANDLER, LSID, SOURCE_ID, UNKNOWN, URI, URL, UUID. Optional.
identifier	(character) The value for this parameter can be a simple string or integer, e.g. identifier=120. Optional.
machineTagNamespace	(character) Filters by machine tag namespace. Optional.
machineTagName	(character) Filters by machine tag name. Optional.
machineTagValue	(character) Filters by machine tag value. Optional.
modified	(character) Filters by the date the organization was last modified. Optional.
created	(character) Filters by the date the organization was created. Optional.
curlopts	list of named curl options passed on to HttpClient. see curl::curl_options for curl options

Value

A list of length of two, consisting of a data.frame meta when uuid is NULL, and data which can either be a list or a data.frame depending on the requested type of data.

References

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

Examples

```
## Not run:
organizations(limit=5)
organizations(query="france", limit=5)
organizations(country = "SPAIN")
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")
organizations(data="installation", uuid="96710dc8-fecb-440d-ae3e-c34ae8a9616f")
organizations(isEndorsed=TRUE, limit=5)
organizations(networkKey="99d66b6c-9087-452f-a9d4-f15f2c2d0e7e", limit=5)

# Pass on curl options
organizations(query="spain", curlopts = list(verbose=TRUE))

## End(Not run)
```

---

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::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

https://www.gbif.org/developer/species#parser

Examples

```
## Not run:
parsenames(scientificname='x Agropogon littoralis')
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(verbose=TRUE))

## End(Not run)
```

---

rgbif-defunct *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
- occurrencedensity(): 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
- stylegeojson(): 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
- occ_spellcheck(): GBIF has removed the spellCheck parameter from their API

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

rgb_country_codes *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

```
## Not run:
rgb_country_codes(country_name="United")

## End(Not run)
```

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

```
taxrank()
```

Examples

```
## Not run:
taxrank()

## End(Not run)
```

`wkt_parse` *parse wkt into smaller bits*

Description

parse wkt into smaller bits

Usage

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

Arguments

`wkt`	(character) A WKT string. Required.
`geom_big`	(character) Only "bbox" works since rgbif 3.8.0.
`geom_size`	(integer) An integer indicating size of the cell. Default: 40.
`geom_n`	(integer) An integer indicating number of cells in each dimension. Default: 10.

Examples

```
wkt <- "POLYGON((13.26349675655365 52.53991761181831,18.36115300655365 54.11445544219924,
21.87677800655365 53.80418956368524,24.68927800655365 54.217364774722455,28.20490300655365
54.320018299365124,30.49005925655365 52.85948216284084,34.70880925655365 52.753220564427814,
35.93927800655365 50.46131871049754,39.63068425655365 49.55761261299145,40.86115300655365
46.381388009130845,34.00568425655365 45.279102926537,33.30255925655365 48.636868465271846,
30.13849675655365 49.78513301801265,28.38068425655365 47.2236377039631,29.78693425655365
44.6572866068524,27.67755925655365 42.62220075124676,23.10724675655365 43.77542058000212,
24.51349675655365 47.10412345120368,26.79865300655365 49.55761261299145,23.98615300655365
52.00209943876426,23.63459050655365 49.44345313705238,19.41584050655365 47.580567827212114,
19.59162175655365 44.90682206053508,20.11896550655365 42.36297154876359,22.93146550655365
40.651849782081555,25.56818425655365 39.98171166226459,29.61115300655365 40.78507856230178,
32.95099675655365 40.38459278067577,32.95099675655365 37.37491910393631,26.27130925655365
33.65619609886799,22.05255925655365 36.814081996401605,18.71271550655365 36.1072176729021,
18.53693425655365 39.16878677351903,15.37287175655365 38.346355762190846,15.19709050655365
41.578843777436326,12.56037175655365 41.050735748143424,12.56037175655365 44.02872991212046,
15.19709050655365 45.52594200494078,16.42755925655365 48.05271546733352,17.48224675655365
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-9.41228449344635 38.346355762190846,-12.40056574344635 35.10683619158607,-15.74040949344635
38.07010978950028,-14.68572199344635 41.31532459432774,-11.69744074344635 43.64836179231387,
-8.88494074344635 42.88035509418534,-4.31462824344635 43.52103366008421,-8.35759699344635
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-2.73259699344635 46.25998980446569,-1.67790949344635 44.154980365192,-1.32634699344635
39.30493590580802,2.18927800655365 41.44721797271696,4.47443425655365 43.26556960420879,
2.18927800655365 46.7439668697322,1.83771550655365 50.3492841273576,6.93537175655365
49.671505849335254,5.00177800655365 52.32557322466785,7.81427800655365 51.67627099802223,
7.81427800655365 54.5245591562317,10.97834050655365 51.89375191441792,10.97834050655365
55.43241335888528,13.26349675655365 52.53991761181831))"
```

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

if (requireNamespace("sf", quietly=TRUE)) {
# to a bounding box in wkt format
wkt_parse(wkt, geom_big = "bbox")

}
```

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