

# Package: suwo (via r-universe)

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**Type** Package

**Title** Access Nature Media Repositories

**Version** 0.2.0

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**Description** Streamline searching/downloading of nature media files (e.g. audios, photos) from online repositories. The package offers functions for obtaining media metadata from online repositories, downloading associated media files and updating data sets with new records.

**URL** <https://docs.ropensci.org/suwo>, <https://github.com/ropensci/suwo>

**BugReports** <https://github.com/maRce10/suwo/issues/>

**License** GPL (>= 2)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

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download_media	<i>Download media files from repositories</i>
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## Description

download\_media downloads media files from online repositories.

## Usage

```
download_media(
  metadata,
  path = ".",
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  overwrite = FALSE,
  folder_by = NULL
)
```

## Arguments

metadata	data frame previously obtained from any suwo query function (i.e. query_reponame()).
path	Directory path where the output media files will be saved. By default files are saved into the current working directory (".").
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. options(mc.cores = 2)). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.

pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( <code>options(suwo_pb = TRUE)</code> ). Not shown if only a few observations are found.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( <code>options(suwo_verbose = TRUE)</code> ).
overwrite	Logical. If TRUE, existing files (in "path") with the same name will be overwritten. Default is FALSE.
folder_by	Character string with the name of a character or factor column in the metadata data frame. If supplied the function will use the unique values in that column to create subfolders within "path" and the files will be downloaded into the corresponding folder. It can be used for instance to save files in subfolders by country or recordist. By default no subfolders are created and all files are saved in the path provided. Missing values (NAs) are saved in a folder called <code>paste0("unknown_", folder_by)</code> . Special characters that are not allowed in folder names will be modified or removed. If any of the folder names already exist in "path", they will be used as is.

### Details

This function will take the output data frame of any of the "query\_reponame()" functions and download the associated media files. The function will download all files into a single directory (argument "path"). File downloading process can be interrupted and resume later as long as the working directory is the same. Users only need to rerun the same function call. By default only the missing files will be downloaded when resuming. Can also be used on a updated query output (see [update\\_metadata\(\)](#)) to add the new media files to the existing media pool.

### Value

Downloads media files into the supplied directory path ("path") and returns (invisibly) the input data frame with two additional columns: `downloaded_file_name` with the name of the downloaded file (if downloaded or already in the directory), and `download_status` with the result of the download process for each file (either "saved", "overwritten", "already there (not downloaded)", or "failed").

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### See Also

[query\\_gbif\(\)](#), [query\\_macaulay\(\)](#)

### Examples

```
a_zambiana <- query_inaturalist(species = "Amanita zambiana",
format = "image")

# run if query didnt fail
```

```

if (!is.null(a_zambiana)) {
  # download the first to files
  phae_anth_downl <- download_media(metadata = a_zambiana[1:2, ],
  path = tempdir())
}

```

---

find\_duplicates

*Find duplicated entries in metadata*


---

### Description

find\_duplicates detect possible duplicated entries from merged metadata from several repositories.

### Usage

```

find_duplicates(
  metadata,
  sort = TRUE,
  criteria = paste("country > 0.8", "locality > 0.5", "user_name > 0.8", "time == 1",
  "date == 1", sep = " & "),
  verbose = getOption("suwo_verbose", TRUE)
)

```

### Arguments

metadata	data frame obtained from combining the output metadata of two or more suwo query function using the merge_metadata() function. Data frames obtained from a single suwo query function can also be used but duplicates are not really expected within the same repository. The data frame must have the following columns: user_name, locality, repository, country, format, time, and date.
sort	Logical argument indicating if the output data frame should be sorted by the duplicate_group column added by this function. This will group all potential duplicates together in the output data frame. Default is TRUE.
criteria	A character string indicating the criteria to use to determine duplicates. By default, the criteria is set to country > 0.8 & locality > 0.5 & user_name > 0.8 & time == 1 & date == 1 which means that two entries will be considered duplicates if they have a country similarity greater than 0.8, locality similarity greater than 0.5, user_name similarity greater than 0.8, and exact matches for time and date (similarities range from 0 to 1). These values have been found to work well in most cases. Users can modify this string to adjust the sensitivity of the duplicate detection based on their specific needs.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option (options(suwo_verbose = TRUE)).

## Details

This function compares the information in the entries of a combined metadata data frame (typically the output of `merge_metadata()`) and labels those possible duplicates with a common index in a new column named `duplicate_group`. The comparison is based on the similarity of the following fields: `user_name`, `locality`, `time` and `country`. Only rows with no missing data for those fields will be considered. The function uses the `RecordLinkage` package to perform the a fuzzy matching comparison and identify potential duplicates based on predefined similarity thresholds (see argument `'criteria'`). The function only spots duplicates from different repositories and assumes those duplicates should have the same format and date. This function is useful for curating the data obtained by merging data from multiple sources, as the same observation might be recorded in different repositories. This is a common issue in citizen science repositories, where users might upload the same observation to different platforms. This can also occur as some repositories automatically share data with other repositories, particularly with GBIF.

## Value

A data frame with the input data frame and an additional column named `duplicate_group` indicating potential duplicates with a common index. Entries without potential duplicates are labeled as NA in this new column.

## Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

## Examples

```
# get metadata from 2 repos
gb <- query_gbif(species = "Turdus rufiventris", format = "sound")
inat <- query_inaturalist(species = "Turdus rufiventris",
  format = "sound")

# run if queries didnt fail
if (!is.null(gb) && !is.null(inat)) {
# combine metadata
merged_metadata <- merge_metadata(inat, gb)

# find duplicates
label_dup_metadata <- find_duplicates(metadata = merged_metadata)
}
```

## Description

`map_locations` creates maps to visualize the geographic spread of media records.

**Usage**

```
map_locations(  
  metadata,  
  cluster = FALSE,  
  palette = grDevices::hcl.colors,  
  by = "species"  
)
```

**Arguments**

metadata	data frame previously obtained from any suwo query function (i.e. query_reponame()).
cluster	Logical to control if icons are clustered by locality. Default is FALSE.
palette	Color palette function used for location markers. By default it uses the viridis palette (grDevices::hcl.colors).
by	Name of column to be used for coloring markers. Default is "species".

**Details**

This function creates maps for visualizing the geographic spread of observations. Note that only observations with geographic coordinates are displayed.

**Value**

An interactive map with the locations of the observations.

**Author(s)**

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>) and Grace Smith Vidaurre

**Examples**

```
# search in xeno-canto  
e_hochs <- query_gbif(species = "Entoloma hochstetteri", format = "image")  
  
# run if query didnt fail  
if (!is.null(e_hochs)) {  
  
  # create map  
  map_locations(e_hochs)  
}
```

---

merge_metadata	<i>Merge metadata data frames</i>
----------------	-----------------------------------

---

## Description

merge\_metadata merges metadata data frames from suwo queries.

## Usage

```
merge_metadata(..., check_columns = TRUE)
```

## Arguments

... two or more data frames (each one as a separate entry) referring to the metadata obtained from suwo query functions (query\_x()). Alternatively, a single list of data frames can be provided. The name provided for each data frame (either as individual data frames or in a list) will be used as label in the source column in the output data frame.

check\_columns Logical argument indicating if the function should check that all input data frames have the required basic columns. Default is TRUE.

## Details

This function combines metadata from multiple sources (e.g. WikiAves and xeno-canto) into a single data frame for easier analysis and comparison. Each input data frame must be obtained from one of the suwo query functions (e.g., query\_wikiaves(), query\_xenocanto(), etc.) with raw\_data = FALSE.

## Value

A single data frame with the data from all input data frames combined and with an additional column named source indicating the original data frame from which each row originated. The column source will contain the name provided for each data frame (either as individual data frames or in a list). If no names were provided, the object names will be used instead.

## Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

## Examples

```
# get metadata from 2 repos
wa <- query_wikiaves(species = "Glaucis dohrnii", format = "sound")
gb <- query_gbif(species = "Glaucis dohrnii", format = "sound")

# run if queries didnt fail
if (!is.null(wa) && !is.null(gb)) {
  # combine metadata using single data frames
```

```
merged_mt <- merge_metadata(wa, gb)

# combine metadata using named single data frames
merged_mt <- merge_metadata(wikiaves = wa, gbif = gb)

# combine metadata using a list of data frames
mt_list <- list(wikiaves = wa, gbif = gb)
merged_mt <- merge_metadata(mt_list)
}
```

---

query\_gbif

*Access 'gbif' media file metadata*


---

## Description

query\_gbif searches for metadata from **GBIF**.

## Usage

```
query_gbif(
  species = getOption("suwo_species"),
  format = getOption("suwo_format", c("image", "sound", "video", "interactive resource")),
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  dataset = NULL,
  all_data = getOption("suwo_all_data", FALSE),
  raw_data = getOption("suwo_raw_data", FALSE)
)
```

## Arguments

- |         |   |
|---------|---|
| species | Character string with the scientific name of a species in the format: "Genus epithet". Required. Can be set globally for the current R session via the "suwo_species" option (e.g. options(suwo_species = "Hypsiboas rufitelus").   |
| format  | Character vector with the media format to query for. Options are 'sound', 'image', 'video' and 'interactive resource'. Can be set globally for the current R session via the "suwo_format" option (e.g. options(suwo_format = "image")). Required.  |
| cores   | Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. options(mc.cores = 2)). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack. |

pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( options(suwo_pb = TRUE)). Not shown if only a few observations are found.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( options(suwo_verbose = TRUE)).
dataset	The name of a specific dataset in which to focus the query (by default it searches across all available datasets). Users can check available dataset names by downloading this csv file <a href="https://api.gbif.org/v1/dataset/search/export?format=CSV&amp;">https://api.gbif.org/v1/dataset/search/export?format=CSV&amp;</a> . See <a href="https://www.gbif.org/dataset/search?q=">https://www.gbif.org/dataset/search?q=</a> for more details.
all_data	Logical argument that determines if all data available from database is shown in the results of search. Default is FALSE. Can be set globally for the current R session via the "suwo_all_data" option ( options(suwo_all_data = TRUE)).
raw_data	Logical argument that determines if the raw data from the repository is returned (e.g. without any manipulation). Default is FALSE. Can be set globally for the current R session via the "suwo_raw_data" option ( options(suwo_raw_data = TRUE)). If TRUE all_data is set to TRUE internally. Useful for developers, or if users suspect that some data is mishandled during processing (i.e. date information is lost). Note that the metadata obtained when raw_data = TRUE is not standardized, so most suwo functions for downstream steps will not work on them.

### Details

This function queries for species observation info in the open-access online repository **GBIF**. GBIF (the Global Biodiversity Information Facility) is an international network and data infrastructure funded by the world's governments and aimed at providing open access to data about all types of life on Earth. Note that some of the records returned by this function could be duplicates of records returned by other suwo functions (e.g., [query\\_inaturalist\(\)](#)).

### Value

The function returns a data frame with the metadata of the media files matching the search criteria. If all\_data = TRUE, all metadata fields (columns) are returned. If raw\_data = TRUE, the raw data as obtained from the repository is returned (without any formatting).

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### References

GBIF.org (2024), GBIF Home Page. Available from: <https://www.gbif.org/>

### See Also

[query\\_inaturalist\(\)](#)

**Examples**

```
# search dink frog sound files
```

---

```
query_inaturalist      Access 'iNaturalist' media file metadata
```

---

**Description**

query\_inaturalist searches for metadata from [iNaturalist](#).

**Usage**

```
query_inaturalist(
  species = getOption("suwo_species"),
  format = getOption("suwo_format", c("image", "sound")),
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  all_data = getOption("suwo_all_data", FALSE),
  raw_data = getOption("suwo_raw_data", FALSE),
  identified = FALSE,
  verifiable = FALSE
)
```

**Arguments**

species	Character string with the scientific name of a species in the format: "Genus epithet". Required. Can be set globally for the current R session via the "suwo_species" option (e.g. <code>options(suwo_species = "Hypsiboas rufitelus")</code> ).
format	Character vector with the media format to query for. Currently 'image' and 'sound' are available. Can be set globally for the current R session via the "suwo_format" option (e.g. <code>options(suwo_format = "image")</code> ). Required.
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. <code>options(mc.cores = 2)</code> ). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.
pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( <code>options(suwo_pb = TRUE)</code> ). Not shown if only a few observations are found.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( <code>options(suwo_verbose = TRUE)</code> ).

all_data	Logical argument that determines if all data available from database is shown in the results of search. Default is TRUE.
raw_data	Logical argument that determines if the raw data from the repository is returned (e.g. without any manipulation). Default is FALSE. Can be set globally for the current R session via the "suwo_raw_data" option ( options(suwo_raw_data = TRUE)). If TRUE all_data is set to TRUE internally. Useful for developers, or if users suspect that some data is mishandled during processing (i.e. date information is lost). Note that the metadata obtained when raw_data = TRUE is not standardized, so most suwo functions for downstream steps will not work on them.
identified	Logical argument to define if search results are categorized as identified by inaturalist.
verifiable	Logical argument to define if search results are categorized as verifiable by inaturalist.

### Details

This function queries for species observation info in the open-access online repository [iNaturalist](https://www.inaturalist.org). iNaturalist is a free, crowdsourced online platform for nature enthusiasts to document and identify plants, animals, fungi, and other organisms in the wild. Note that Inaturalist observations do not include a 'country' field.

### Value

The function returns a data frame with the metadata of the media files matching the search criteria. If all\_data = TRUE, all metadata fields (columns) are returned. If raw\_data = TRUE, the raw data as obtained from the repository is returned (without any formatting).

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### References

iNaturalist. Available from <https://www.inaturalist.org>. (Accessed on 10-02-2026)

### Examples

```
# search Bleeding Tooth mushroom images
```

---

query\_macaulay                      *Searches for media files in the Macaulay Library*

---

## Description

query\_macaulay searches for metadata from [Macaulay library](#).

## Usage

```
query_macaulay(
  species = getOption("suwo_species"),
  taxon_code = NULL,
  format = getOption("suwo_format", c("image", "sound", "video")),
  verbose = getOption("suwo_verbose", TRUE),
  all_data = getOption("suwo_all_data", FALSE),
  raw_data = getOption("suwo_raw_data", FALSE),
  path = ".",
  files = NULL,
  dates = NULL,
  taxon_code_info = ml_taxon_code
)
```

## Arguments

species	Character string with the scientific name of a species in the format: "Genus epithet". Required. Can be set globally for the current R session via the "suwo_species" option (e.g. <code>options(suwo_species = "Hypsiboas rufitelus")</code> ).
taxon_code	Optional character string with the Macaulay Library taxon code (see vignette for more details). If provided, 'species' is ignored.
format	Character vector with the media format to query for. Options are 'sound', 'image' or 'video'. Can be set globally for the current R session via the "suwo_format" option (e.g. <code>options(suwo_format = "image")</code> ). Required.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( <code>options(suwo_verbose = TRUE)</code> ).
all_data	Logical argument that determines if all data available from database is shown in the results of search. Default is FALSE. Can be set globally for the current R session via the "suwo_all_data" option ( <code>options(suwo_all_data = TRUE)</code> ).
raw_data	Logical argument that determines if the raw data from the repository is returned (e.g. without any manipulation). Default is FALSE. Can be set globally for the current R session via the "suwo_raw_data" option ( <code>options(suwo_raw_data = TRUE)</code> ). If TRUE all_data is set to TRUE internally. Useful for developers, or if users suspect that some data is mishandled during processing (i.e. date information is lost). Note that the metadata obtained when raw_data = TRUE is not standardized, so most suwo functions for downstream steps will not work on them.

path	Directory path where the .csv file will be saved. By default it is saved into the current working directory (".").
files	Optional character vector with the name(s) of the .csv file(s) to read. If provided, the function will import the data from the .csv files instead of opening the Macaulay Library search page in a browser ('species' is ignored if supplied).
dates	Optional numeric vector with years to split the search. If provided, the function will perform separate queries for each date range (between consecutive date values) and combine the results. Useful for queries that return large number of results (i.e. > 10000 results limit). For example, to search for the species between 2010 to 2020 and between 2021 to 2025 use dates = c(2010, 2020, 2025). If years contain decimals searches will be split by months within years as well.
taxon_code_info	Data frame containing the taxon code information. By default the function will use the internal data frame "ml_taxon_code" included as example data in the package. This object contains the data from the October-2025 eBird taxonomy (downloaded from <a href="https://www.birds.cornell.edu/clementschecklist">https://www.birds.cornell.edu/clementschecklist</a> ). If new versions of the list become available it will be updated in new package versions. However, if users need to update it they can download the new list version, read it in R as a data frame and provide it to the function through this argument.

## Details

This function queries for species observation info in the [Macaulay library](#) online repository and returns the metadata of media files matching the query. The Macaulay Library is the world's largest repository of digital media (audio, photo, and video) of wildlife (mostly birds but also other vertebrates and invertebrates), and their habitats. The archive hosts more than 77 million images, 3 million sound recordings, and 350k videos, from more than 80k contributors, and is integrated with eBird, the world's largest biodiversity dataset. For bird species the species name must be valid according to the Macaulay Library taxonomy (which follows the Clements checklist). For non-bird species users must use the argument taxon\_code. The species taxon code can be found by running a search at the [Macaulay Library's search page](#) and checking the URL of the species page. For instance, the URL when searching for jaguar (*Panthera onca*) is 'https://search.macaulaylibrary.org/catalog?taxonCode=t-11032765' so the taxon code is "t-11032765". If all\_data = TRUE, all metadata fields (columns) are returned. If raw\_data = TRUE, the raw data as obtained from the repository is returned (without any formatting). Here are some instructions for using this function properly:

- Valid bird species names can be checked at `suwo::ml_taxon_code$SCI_NAME`.
- Users must save the .csv file manually
- If the file is saved overwriting a pre-existing file (i.e. same file name) the function will not detect it
- A maximum of 10000 records per query can be returned, but this can be bypassed by using the dates argument to split the search into smaller date ranges
- Users must log in to the Macaulay Library/eBird account in order to access large batches of observations

**Value**

This is an interactive function which opens a browser window to the Macaulay Library's search page, where the user must download a .csv file with the metadata. The function then reads the .csv file and returns a data frame with the metadata. The function can also import previously downloaded metadata (in csv format) with the argument files.

**Author(s)**

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

**References**

Scholes III, Ph.D. E (2015). Macaulay Library Audio and Video Collection. Cornell Lab of Ornithology. Occurrence dataset <https://doi.org/10.15468/ckcdpy> accessed via GBIF.org on 2024-05-09.

Clements, J. F., P. C. Rasmussen, T. S. Schulenberg, M. J. Iliff, J. A. Gerbracht, D. Lepage, A. Spencer, S. M. Billerman, B. L. Sullivan, M. Smith, and C. L. Wood. 2025. The eBird/Clements checklist of Birds of the World: v2025. Downloaded from <https://www.birds.cornell.edu/clementschecklist/download/>

**Examples**

```
if (interactive()){
# query sounds
tur_ili <- query_macaulay(species = "Turdus iliacus", format = "sound",
path = tempdir())

# test a query with more than 10000 results paging by date
# this example splits by entire year intervals
cal_cos <- query_macaulay(species = "Calypte costae", format = "image",
path = tempdir(), dates = c(1976, 2019, 2022, 2024, 2025, 2026))

# this example splits by year-month intervals (as dates have decimals)
cal_cos <- query_macaulay(species = "Calypte costae", format = "image",
path = tempdir(), dates = seq(2020, 2026, length.out = 10))

## update clement list (note that this is actually the same list used in the
# current 'suwo' version, just for the sake of the example)

# url to the clements list version october 2024
# (split so it is not truncated by CRAN)
clements_url <- paste0(
"https://www.birds.cornell.edu/clementschecklist/wp-content/uploads/2024/10",
"/Clements-v2024-October-2024-rev.csv"
)

# read list from url
new_clements <- utils::read.csv(clements_url)

# provide "updated" clements list to query_macaulay()
tur_ili2 <- query_macaulay(species = "Turdus iliacus", format = "sound",
```

```

taxon_code_info = new_clements, path = tempdir())

# query using taxon code
# this is the URL when querying jaguars:
# https://search.macaulaylibrary.org/catalog?taxonCode=t-11032765
p_onca <- query_macaulay(taxon_code = "t-11032765", format = "image")
}

```

---

query\_wikiaves      *Access 'WikiAves' media file metadata*

---

## Description

query\_wikiaves searches for metadata from [WikiAves](#).

## Usage

```

query_wikiaves(
  species = getOption("suwo_species"),
  format = getOption("suwo_format", c("image", "sound")),
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  all_data = getOption("suwo_all_data", FALSE),
  raw_data = getOption("suwo_raw_data", FALSE)
)

```

## Arguments

species	Character string with the scientific name of a species in the format: "Genus epithet". Required. Can be set globally for the current R session via the "suwo_species" option (e.g. options(suwo_species = "Hypsiboas rufitelus").
format	Character vector with the media format to query for. Options are 'image' or 'sound'. Can be set globally for the current R session via the "suwo_format" option (e.g. options(suwo_format = "image")). Required.
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. options(mc.cores = 2)). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.
pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( options(suwo_pb = TRUE)). Not shown if only a few observations are found.

verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( options(suwo_verbose = TRUE)).
all_data	Logical argument that determines if all data available from database is shown in the results of search. Default is FALSE. Can be set globally for the current R session via the "suwo_all_data" option ( options(suwo_all_data = TRUE)).
raw_data	Logical argument that determines if the raw data from the repository is returned (e.g. without any manipulation). Default is FALSE. Can be set globally for the current R session via the "suwo_raw_data" option ( options(suwo_raw_data = TRUE)). If TRUE all_data is set to TRUE internally. Useful for developers, or if users suspect that some data is mishandled during processing (i.e. date information is lost). Note that the metadata obtained when raw_data = TRUE is not standardized, so most suwo functions for downstream steps will not work on them.

### Details

This function queries for avian digital media in the open-access online repository [WikiAves](#) and returns its metadata. WikiAves is a Brazilian online platform and citizen science project that serves as the largest community for birdwatchers in Brazil. It functions as a collaborative, interactive encyclopedia of Brazilian birds, where users contribute georeferenced photographs and sound recordings, which are then used to build a vast database for research and conservation.

### Value

The function returns a data frame with the metadata of the media files matching the search criteria. If all\_data = TRUE, all metadata fields (columns) are returned. If raw\_data = TRUE, the raw data as obtained from the repository is returned (without any formatting).

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### References

Schubert, Stephanie Caroline, Lilian Tonelli Manica, and André De Camargo Guaraldo. 2019. Revealing the potential of a huge citizen-science platform to study bird migration. *Emu-Austral Ornithology* 119.4: 364-373.

### Examples

```
# search
p_nattereri <- query_wikiaves(species = "Phaethornis nattereri",
                             format = "image")
```

---

query_xenocanto	<i>Access 'Xeno-Canto' recording metadata</i>
-----------------	---

---

## Description

query\_xenocanto searches for metadata from [Xeno-Canto](#).

## Usage

```
query_xenocanto(
  species = getOption("suwo_species"),
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  all_data = getOption("suwo_all_data", FALSE),
  raw_data = getOption("suwo_raw_data", FALSE),
  api_key = Sys.getenv("xc_api_key")
)
```

## Arguments

species	Character string with the scientific name of a species in the format: "Genus epithet". Required. Can be set globally for the current R session via the "suwo_species" option (e.g. <code>options(suwo_species = "Hypsiboas rufitelus")</code> ). Alternatively, a character string containing additional tags that follows the Xeno-Canto advanced query syntax can be provided. Tags are of the form 'tag:searchterm'. For instance, 'type:"song"' will search for recordings where the sound type contains 'song'. Multiple tags can be provided (e.g., '"cnt:"belize" type:"song"'). See examples down below and check <a href="#">Xeno-Canto's search help</a> for a full description.
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. <code>options(mc.cores = 2)</code> ). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.
pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( <code>options(suwo_pb = TRUE)</code> ). Not shown if only a few observations are found.
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( <code>options(suwo_verbose = TRUE)</code> ).
all_data	Logical argument that determines if all data available from database is shown in the results of search. Default is FALSE. Can be set globally for the current R session via the "suwo_all_data" option ( <code>options(suwo_all_data = TRUE)</code> ).

raw_data	Logical argument that determines if the raw data from the repository is returned (e.g. without any manipulation). Default is FALSE. Can be set globally for the current R session via the "suwo_raw_data" option ( options(suwo_raw_data = TRUE)). If TRUE all_data is set to TRUE internally. Useful for developers, or if users suspect that some data is mishandled during processing (i.e. date information is lost). Note that the metadata obtained when raw_data = TRUE is not standardized, so most suwo functions for downstream steps will not work on them.
api_key	Character string referring to the key assigned by Xeno-Canto as authorization for searches. Get yours at <a href="https://xeno-canto.org/account">https://xeno-canto.org/account</a> . Required. Avoid setting your API key directly in the function call to prevent exposing it in your code. Instead, set it as an environment variable (e.g., in your .Renviro file using Sys.setenv(xc_api_key = "your_key_here")) named 'xc_api_key', so it can be accessed securely using Sys.getenv("xc_api_key").

### Details

This function queries metadata for animal sound recordings in the open-access online repository [Xeno-Canto](https://xeno-canto.org). [Xeno-Canto](https://xeno-canto.org) hosts sound recordings of birds, frogs, non-marine mammals and grasshoppers. Complex queries can be constructed using the [Xeno-Canto](https://xeno-canto.org) advanced query syntax (see examples).

### Value

The function returns a data frame with the metadata of the media files matching the search criteria. If all\_data = TRUE, all metadata fields (columns) are returned. If raw\_data = TRUE, the raw data as obtained from the repository is returned (without any formatting).

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### References

Planqué, Bob, & Willem-Pier Vellinga. 2008. Xeno-canto: a 21st-century way to appreciate Neotropical bird song. *Neotrop. Birding* 3: 17-23.

### See Also

[query\\_gbif\(\)](#), [query\\_wikiaves\(\)](#), [query\\_inaturalist\(\)](#)

### Examples

```
if (interactive()){
# An API key is required. Get yours at https://xeno-canto.org/account.
# run this in the console but dont save it in script
Sys.setenv(xc_api_key = "YOUR_API_KEY_HERE")

# Simple search for a species
p_anth <- query_xenocanto(species = "Phaethornis anthophilus")
```

```
# Search for same species and add specify country
p_anth_cr <- query_xenocanto(
  species = 'sp:"Phaethornis anthophilus" cnt:"Panama"',
  raw_data = TRUE)

# Search for female songs of a species
femsong <- query_xenocanto(
  species = 'sp:"Thryothorus ludovicianus" type:"song" type:"female"'
)
```

---

remove_duplicates	<i>Remove duplicated media records</i>
-------------------	--

---

## Description

remove\_duplicates removes duplicated media records.

## Usage

```
remove_duplicates(
  metadata,
  same_repo = FALSE,
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  repo_priority = c("Xeno-Canto", "GBIF", "iNaturalist", "Macaulay Library", "WikiAves",
    "Observation"),
  verbose = getOption("suwo_verbose", TRUE)
)
```

## Arguments

metadata	data frame obtained from possible duplicates with the function <a href="#">find_duplicates()</a> . The data frame must have the column 'duplicate_group' returned by <a href="#">find_duplicates()</a> .
same_repo	Logical argument indicating if observations labeled as duplicates that belong to the same repository should be removed. Default is FALSE. If TRUE, only one of the duplicated observations from the same repository will be retained in the output data frame. This is useful as it can be expected that observations from the same repository are not true duplicates (e.g. different recordings uploaded to Xeno-Canto with the same date, time and location by the same user), but rather have not been documented with enough precision to be told apart.
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. <code>options(mc.cores = 2)</code> ). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.

pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( options(suwo_pb = TRUE)). Not shown if only a few observations are found.
repo_priority	Character vector indicating the priority of repositories when selecting which observation to retain when duplicates are found. Default is c("Xeno-Canto", "GBIF", "iNaturalist", "Macaulay Library", "Wikiaves", "Observation"), which gives priority to repositories in which media downloading is more straightforward (Xeno-Canto and GBIF).
verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option ( options(suwo_verbose = TRUE)).

### Details

When compiling data from multiple repositories, duplicated media records are a common issue, particularly for sound recordings. These duplicates occur both through data sharing between repositories like Xeno-Canto and GBIF, and when users upload the same file to multiple platforms. In such cases those multiple observations seem to refer to the same media file and therefore, only one copy is needed. This function removes duplicate observations identified with the function `find_duplicates()`. When duplicates are found, one observation from each group of duplicates is retained in the output data frame. However, if multiple observations from the same repository are labeled as duplicates, by default (`same_repo = FALSE`) all of them are retained in the output data frame. This is useful as it can be expected that observations from the same repository are not true duplicates (e.g. different recordings uploaded to Xeno-Canto with the same date, time and location by the same user), but rather have not been documented with enough precision to be told apart. This behavior can be modified. If `same_repo = TRUE`, only one of the duplicated observations from the same repository will be retained in the output data frame. The function will give priority to repositories in which media downloading is more straightforward (Xeno-Canto and GBIF), but this can be modified with the argument `'repo_priority'`.

### Value

A single data frame with a subset of the `'metadata'` with those observations that were determined not to be duplicates.

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### See Also

`find_duplicates()`, `merge_metadata()`

### Examples

```
# get metadata from 2 repos
gb <- query_gbif(species = "Turdus rufiventris", format = "sound")

if(interactive()){
```

```

key <- "YOUR XENO CANTO API KEY"
xc <- query_xenocanto(species = "Turdus rufiventris", api_key = key)

# combine metadata
merged_metadata <- merge_metadata(xc, gb)

# find duplicates
label_dup_metadata <- find_duplicates(metadata = merged_metadata)

# remove duplicates
dedup_metadata <- remove_duplicates(label_dup_metadata)
}

```

---

update_metadata	<i>Update metadata</i>
-----------------	------------------------

---

## Description

update\_metadata update metadata from previous queries.

## Usage

```

update_metadata(
  metadata,
  path = ".",
  cores = getOption("suwo_cores", 1),
  pb = getOption("suwo_pb", TRUE),
  verbose = getOption("suwo_verbose", TRUE),
  api_key = NULL,
  dates = NULL
)

```

## Arguments

metadata	data frame previously obtained from any suwo query function (i.e. query_reponame()).
path	Directory path where the .csv file will be saved. Only applicable for <code>query_macaulay()</code> query results. By default it is saved into the current working directory (".").
cores	Numeric vector of length 1. Controls whether parallel computing is applied by specifying the number of cores to be used. Default is 1 (i.e. no parallel computing). Can be set globally for the current R session via the "mc.cores" option (e.g. <code>options(mc.cores = 2)</code> ). Note that some repositories might not support parallel queries from the same IP address as it might be identified as denial-of-service cyberattack.
pb	Logical argument to control if progress bar is shown. Default is TRUE. Can be set globally for the current R session via the "suwo_pb" option ( <code>options(suwo_pb = TRUE)</code> ). Not shown if only a few observations are found.

verbose	Logical argument that determines if text is shown in console. Default is TRUE. Can be set globally for the current R session via the "suwo_verbose" option (options(suwo_verbose = TRUE)).
api_key	Character string referring to the key assigned by Xeno-Canto as authorization for searches. Get yours at <a href="https://xeno-canto.org/account">https://xeno-canto.org/account</a> . Only needed if the input metadata comes from <code>query_xenocanto()</code> .
dates	Optional numeric vector with years to split the search. If provided, the function will perform separate queries for each date range (between consecutive date values) and combine the results. Useful for queries that return large number of results (i.e. > 10000 results limit). For example, to search for the species between 2010 to 2020 and between 2021 to 2025 use <code>dates = c(2010, 2020, 2025)</code> . If years contain decimals searches will be split by months within years as well. Only needed if the input metadata comes from <code>query_macaulay()</code> .

### Details

This function updates the metadata from a previous query to add entries found in the source repository. All observations must belong to the same repository. The function adds the column `new_entry` which labels those entries that are new (i.e., not present in the input metadata). The input data frame must have been obtained from any of the query functions with the argument `raw_data = FALSE`. The function uses the same query species and format as in the original query. If no new entries are found, the function returns the original metadata and prints a message. If some old entries are not returned in the new query they are still retained. The function assumes that no new files are added to existing repository entries.

### Value

returns a data frame similar to the input 'metadata' with new data appended.

### Author(s)

Marcelo Araya-Salas (<marcelo.araya@ucr.ac.cr>)

### Examples

```
# query metadata
a_gioiosa <- query_gbif(species = "Amanita gioiosa", format = "image")

# run if query didnt fail
if (!is.null(a_gioiosa)) {
  # remove last 3 rows to test update_metadata
  sub_a_gioiosa <- a_gioiosa[1:(nrow(a_gioiosa)- 3), ]

  # update
  up_a_gioiosa <- update_metadata(metadata = sub_a_gioiosa)

  # check number of rows is the same
  # nrow(up_a_gioiosa) == nrow(a_gioiosa)
}
```

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