

# Package: f2g (via r-universe)

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**Title** FinBIF to GBIF

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---

archive\_occurrences    *Archive occurrences*

---

## Description

Archive occurrence records in a Darwin Core archive.

## Usage

```
archive_occurrences(
  archive,
  file_name,
  media_file_name,
  filter,
  select = sub("^.*:", "", config::get("fields")),
  facts = config::get("facts"),
  combine = config::get("combine"),
  n = config::get("nmax"),
  quiet = TRUE
)
```

## Arguments

archive	Character. Path to the archive.
file_name	Character. The name of the file to write to the archive.
media_file_name	Character. The name of the media extension file to write to the archive.
filter	List of named character vectors. Filters to apply to records.

select	Character vector. Variables to return. If not specified, a default set of commonly used variables will be used. Use "default_vars" as a shortcut for this set. Variables can be deselected by prepending a - to the variable name. If only deselections are specified the default set of variables without the deselection will be returned.
facts	List of extra variables to be extracted from record, event and document "facts".
combine	List of fields to combine.
n	Integer. How many records to download/import.
quiet	Logical. Suppress the progress indicator for multipage downloads.

**Value**

The status value returned by the zip command, invisibly.

**Examples**

```
## Not run:

archive_occurrences(
  "dwca.zip", "occurrence.txt", list(collection = "HR.139"),
  c("occurrenceID", "basisOfRecord")
)

## End(Not run)
```

---

clean_occurrences	<i>Clean occurrences</i>
-------------------	--------------------------

---

**Description**

Clean occurrence files in an archive.

**Usage**

```
clean_occurrences(archive, filters)
```

**Arguments**

archive	Character. Path to the archive.
filters	List.

**Value**

The status value returned by the zip command, invisibly.

**Examples**

```
## Not run:  
  
clean_occurrences("dwca.zip", list())  
  
## End(Not run)
```

---

count_occurrences	<i>Count occurrences</i>
-------------------	--------------------------

---

**Description**

Count the number of occurrences.

**Usage**

```
count_occurrences(x, ...)
```

**Arguments**

x	Object to count occurrences for.
...	Arguments passed to methods.

**Value**

Integer.

**Examples**

```
## Not run:  
  
count_occurrences(list(collection = "HR.3991"))  
  
## End(Not run)
```

---

get\_archive\_path      *Get archive file path*

---

**Description**

Get the file path of an archive for a collection.

**Usage**

```
get_archive_path(collection_id, dir = "archives/split")
```

**Arguments**

collection\_id    Character. Collection id.  
dir              Character. Path to the archive directory.

**Value**

Character. The file path of the archive.

**Examples**

```
## Not run:  
  
get_archive_path("HR.3991")  
  
## End(Not run)
```

---

get\_collection\_ids      *Get collection IDs*

---

**Description**

Get collection IDs of FinBIF collections that are published to GBIF.

**Usage**

```
get_collection_ids(datasets, collection_ids = config::get("collections"))
```

**Arguments**

datasets            List. GBIF dataset metadata retrieved using gbif\_datasets.  
collection\_ids    Character. Collection ids to include regardless of sharing status.

**Value**

A character vector.

**Examples**

```
## Not run:  
  
get_collection_ids()  
  
## End(Not run)
```

---

get_endpoint	<i>Get endpoint</i>
--------------	---------------------

---

**Description**

Get FinBIF collection data endpoint needed for GBIF registration.

**Usage**

```
get_endpoint(collection_id, url_base = Sys.getenv("ENDPOINTS"))
```

**Arguments**

`collection_id` Character. ID string of FinBIF collection.  
`url_base` Character. The base URL for the collection's data endpoint. Defaults to system environment variable, "ENDPOINTS".

**Value**

A list.

**Examples**

```
## Not run:  
  
get_endpoint("HR.3991")  
  
## End(Not run)
```

---

get_file_name	<i>Get occurrence file name.</i>
---------------	----------------------------------

---

**Description**

Get the file name of occurrences in an archive

**Usage**

```
get_file_name(filter, select = config::get("fields"), prefix = "occurrence")
```

**Arguments**

filter	List.
select	Character.
prefix	Character.

**Value**

Character. The file name holding occurrence records.

**Examples**

```
## Not run:  
  
get_file_name(list())  
  
## End(Not run)
```

---

get_gbif_datasets	<i>GBIF datasets</i>
-------------------	----------------------

---

**Description**

Get metadata for GBIF registered datasets of a given installation.

**Usage**

```
get_gbif_datasets(  
  url = Sys.getenv("GBIF_API"),  
  installation = Sys.getenv("GBIF_INSTALLATION")  
)
```

**Arguments**

url Character. URL of GBIF API. Defaults to system environment variable, "GBIF\_API".

installation Character. ID key of GBIF installation. Defaults to system environment variable, "GBIF\_INSTALLATION".

**Value**

A list.

**Examples**

```
## Not run:

get_gbif_datasets()

## End(Not run)
```

---

get_metadata	<i>Get metadata</i>
--------------	---------------------

---

**Description**

Get FinBIF collection metadata needed for GBIF registration.

**Usage**

```
get_metadata(
  collection_id,
  metadata_fields = config::get("metadata"),
  org = Sys.getenv("GBIF_ORG"),
  installation = Sys.getenv("GBIF_INSTALLATION")
)
```

**Arguments**

collection\_id Character. ID string of FinBIF collection.

metadata\_fields List. Map of GBIF to FinBIF metadata fields to use.

org Character. GBIF organization key. Defaults to system environment variable, "GBIF\_ORG".

installation Character. ID key of GBIF installation. Defaults to system environment variable, "GBIF\_INSTALLATION".

**Value**

A list.



**Examples**

```
## Not run:

get_metadata("HR.3991")

## End(Not run)
```

---

get_occurrences	<i>Get occurrences</i>
-----------------	------------------------

---

**Description**

Get occurrence records from FinBIF.

**Usage**

```
get_occurrences(filter, select, facts, combine, n, quiet = TRUE)
```

**Arguments**

filter	List of named character vectors. Filters to apply to records.
select	Character vector. Variables to return. If not specified, a default set of commonly used variables will be used. Use "default_vars" as a shortcut for this set. Variables can be deselected by prepending a - to the variable name. If only deselections are specified the default set of variables without the deselection will be returned.
facts	List of extra variables to be extracted from record, event and document "facts".
combine	List of fields to combine.
n	Integer. How many records to download/import.
quiet	Logical. Suppress the progress indicator for multipage downloads.

**Value**

A finbif\_occ object.

**Examples**

```
## Not run:

get_occurrences(
  c(collection = "HR.3991"), c("occurrenceID", "basisOfRecord"), 100
)

## End(Not run)
```

---

get_registration	<i>Check registration</i>
------------------	---------------------------

---

**Description**

Check if a FinBIF collection is registered with GBIF.

**Usage**

```
get_registration(datasets, collection_id, quiet = FALSE)
```

**Arguments**

datasets	List. GBIF dataset metadata retrieved using gbif_datasets.
collection_id	Character. ID string of FinBIF collection.
quiet	Logical. Suppress messages.

**Value**

Integer.

**Examples**

```
## Not run:  
  
get_registration(gbif_datasets(), "HR.3991")  
  
## End(Not run)
```

---

get_subsets	<i>Get subsets</i>
-------------	--------------------

---

**Description**

Get subset filters for a collection.

**Usage**

```
get_subsets(  
  collection_id,  
  filters = config::get("filters"),  
  nmax = config::get("nmax")  
)
```

**Arguments**

collection\_id   Character. ID string of FinBIF collection.  
filters           List.  
nmax             Integer. Maximum allowed size of subset.

**Value**

A list.

**Examples**

```
## Not run:  
  
get_subsets("HR.3991")  
  
## End(Not run)
```

---

get_uuid	<i>Get UUID</i>
----------	-----------------

---

**Description**

Get the UUID of a registered dataset.

**Usage**

```
get_uuid(registration)
```

**Arguments**

registration   Integer.

**Value**

Character.

**Examples**

```
## Not run:  
  
registration <- get_registration(gbif_datasets(), "HR.3991")  
get_uuid(registration)  
  
## End(Not run)
```

---

```
initiate_gbif_ingestion
```

*Initiate ingestion*

---

### Description

Initiate GBIF ingestion of FinBIF data.

### Usage

```
initiate_gbif_ingestion(  
  uuid,  
  url = Sys.getenv("GBIF_API"),  
  user = Sys.getenv("GBIF_USER"),  
  pass = Sys.getenv("GBIF_PASS")  
)
```

### Arguments

uuid	Integer. GBIF registration id.
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

### Value

NULL.

### Examples

```
## Not run:  
  
collection <- get_collection_ids()[[1L]]  
registration <- get_registration(get_gbif_datasets(), collection)  
initiate_gbif_ingestion(registration)  
  
## End(Not run)
```

---

last_mod	<i>Get last modified date</i>
----------	-------------------------------

---

**Description**

Get the last modified data for FinBIF records

**Usage**

```
last_mod(x, ...)
```

**Arguments**

x	Object to get last modified time for.
...	Arguments passed to methods.

**Value**

A Date object.

**Examples**

```
## Not run:

last_mod(list(collection = "HR.3991"))

## End(Not run)
```

---

n_archived_subsets	<i>Number of archived subsets</i>
--------------------	-----------------------------------

---

**Description**

Count the number of occurrence data subsets that have been archived.

**Usage**

```
n_archived_subsets(archive)
```

**Arguments**

archive	Darwin Core archive file.
---------	---------------------------

**Value**

Integer.

**Examples**

```
## Not run:  
  
n_archived_subsets("archive.zip")  
  
## End(Not run)
```

---

publish_archive	<i>Publish archive</i>
-----------------	------------------------

---

**Description**

Publish a Darwin Core archive.

**Usage**

```
publish_archive(staged_archive, dir = "archives")
```

**Arguments**

staged\_archive Character. Path to the staged archive.  
dir Character. Path to the archive directory.

**Value**

Character. The file path of the staged archive.

**Examples**

```
## Not run:  
  
publish_archive("stage/archive.zip")  
  
## End(Not run)
```

---

```
send_gbif_dataset_endpoint  
    GBIF dataset endpoint
```

---

## Description

Send FinBIF dataset endpoint to GBIF.

## Usage

```
send_gbif_dataset_endpoint(  
  endpoint,  
  uuid,  
  url = Sys.getenv("GBIF_API"),  
  user = Sys.getenv("GBIF_USER"),  
  pass = Sys.getenv("GBIF_PASS")  
)
```

## Arguments

endpoint	Character. URL of dataset endpoint generated by <code>get_endpoint</code> .
uuid	Character. GBIF dataset identifier. Returned by <code>send_gbif_dataset_metadata</code> .
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

## Value

If successful returns NULL invisibly.

## Examples

```
## Not run:  
  
m <- get_metadata("HR.3991")  
ep <- get_endpoint("HR.3991")  
uuid <- send_gbif_dataset_metadata(m)  
send_gbif_dataset_endpoint(ep, uuid)  
  
## End(Not run)
```

---

send\_gbif\_dataset\_id *GBIF dataset identifier*

---

### Description

Send FinBIF dataset identifier to GBIF.

### Usage

```
send_gbif_dataset_id(  
  id,  
  uuid,  
  url = Sys.getenv("GBIF_API"),  
  user = Sys.getenv("GBIF_USER"),  
  pass = Sys.getenv("GBIF_PASS")  
)
```

### Arguments

id	Character. FinBIF collection ID for dataset.
uuid	Character. GBIF dataset identifier. Returned by send_gbif_dataset_metadata.
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

### Value

If successful returns NULL invisibly.

### Examples

```
## Not run:  
  
m <- get_metadata("HR.3991")  
uuid <- send_gbif_dataset_metadata(m)  
send_gbif_dataset_id("HR.3991", uuid)  
  
## End(Not run)
```



---

```
send_gbif_dataset_metadata  
    Send metadata
```

---

## Description

Send FinBIF dataset metadata to GBIF.

## Usage

```
send_gbif_dataset_metadata(  
  metadata,  
  url = Sys.getenv("GBIF_API"),  
  user = Sys.getenv("GBIF_USER"),  
  pass = Sys.getenv("GBIF_PASS")  
)
```

## Arguments

metadata	List. FinBIF dataset metadata generated by <code>get_metadata</code> .
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

## Value

A list.

## Examples

```
## Not run:  
  
m <- get_metadata("HR.3991")  
send_gbif_dataset_metadata(m)  
  
## End(Not run)
```

---

skip_collection	<i>Skip collection</i>
-----------------	------------------------

---

**Description**

Should the collection be skipped?

**Usage**

```
skip_collection(  
  collection_id,  
  enabled = config::get("enabled"),  
  whitelist = "whitelist.txt"  
)
```

**Arguments**

collection_id	Character. Collection id.
enabled	Logical.
whitelist	Character. Path to white-list file.

**Value**

Logical.

**Examples**

```
## Not run:  
  
skip_collection("HR.139")  
  
## End(Not run)
```

---

skip_gbif	<i>Skip GBIF update</i>
-----------	-------------------------

---

**Description**

Should updating the collection for GBIF be skipped?

**Usage**

```
skip_gbif(collection_id, enabled = config::get("gbif"))
```

**Arguments**

collection\_id    Character. Collection id.  
enabled           Logical.

**Value**

Logical.

**Examples**

```
## Not run:  
  
skip_gbif("HR.139")  
  
## End(Not run)
```

---

stage_archive	<i>Get archive file path</i>
---------------	------------------------------

---

**Description**

Get the file path of an archive for a collection.

**Usage**

```
stage_archive(archive, stage = "stage")
```

**Arguments**

archive            Character. Path to the archive.  
stage              Character. Path to the staging directory.

**Value**

Character. The file path of the staged archive.

**Examples**

```
## Not run:  
  
stage_archive("archive.zip")  
  
## End(Not run)
```

unstage\_archive      *Unstage archive*

---

**Description**

Unstage an updated archive file.

**Usage**

```
unstage_archive(staged_archive, dir = "archives")
```

**Arguments**

staged\_archive    Character. Path to the staged archive.  
dir                Character. Path to the archive directory.

**Value**

Character. The file path of the staged archive.

**Examples**

```
## Not run:  
  
publish_archive("stage/archive.zip")  
  
## End(Not run)
```

---

update\_gbif\_dataset\_endpoint  
                          *Update GBIF endpoint*

---

**Description**

Update FinBIF dataset endpoint for GBIF.

**Usage**

```
update_gbif_dataset_endpoint(  
  endpoint,  
  uuid,  
  url = Sys.getenv("GBIF_API"),  
  user = Sys.getenv("GBIF_USER"),  
  pass = Sys.getenv("GBIF_PASS")  
)
```

**Arguments**

endpoint	Character. URL of dataset endpoint generated by get_endpoint.
uuid	Character. GBIF dataset identifier.
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

**Value**

If successful returns NULL invisibly.

**Examples**

```
## Not run:

m <- get_metadata("HR.3991")
ep <- get_endpoint("HR.3991")
uuid <- send_gbif_dataset_metadata(m)
update_gbif_dataset_endpoint(ep, uuid)

## End(Not run)
```

---

```
update_gbif_dataset_metadata
      Update metadata
```

---

**Description**

Update FinBIF dataset metadata at GBIF.

**Usage**

```
update_gbif_dataset_metadata(
  metadata,
  registration,
  url = Sys.getenv("GBIF_API"),
  user = Sys.getenv("GBIF_USER"),
  pass = Sys.getenv("GBIF_PASS")
)
```

**Arguments**

metadata	List. FinBIF dataset metadata generated by get_metadata.
registration	Integer. GBIF registration.
url	Character. URL of GBIF API. Defaults to system environment variable, "GBIF_API".
user	Character. GBIF username. Defaults to system environment variable, "GBIF_USER".
pass	Character. GBIF password. Defaults to system environment variable, "GBIF_PASS".

**Value**

NULL.

**Examples**

```
## Not run:

collection <- get_collection_ids()[[1L]]
registration <- get_registration(get_gbif_datasets(), collection)
update_gbif_dataset_metadata(get_metadata(collection), registration)

## End(Not run)
```

---

write\_eml

*Write EML*

---

**Description**

Write an EML metadata file.

**Usage**

```
write_eml(archive, collection_id, uuid, metadata, eml = config::get("eml"))
```

**Arguments**

archive	Character. Path to a DarwinCore archive.
collection_id	Character. Collection ID.
uuid	Character. GBIF ID.
metadata	List.
eml	List.

**Value**

The status value returned by the zip command, invisibly.

**Examples**

```
## Not run:

registration <- get_registration(gbif_datasets(), "HR.3991")
uuid <- get_uuid(registration)
write_eml("dwca.zip", "HR.447", uuid, list())

## End(Not run)
```

---

`write_meta`*Write metafile*

---

**Description**

Write a Darwin Core archive metadata file.

**Usage**

```
write_meta(  
  archive,  
  filters,  
  fields = config::get("fields"),  
  facts = config::get("facts"),  
  id = 1  
)
```

**Arguments**

<code>archive</code>	Character. Path to the archive.
<code>filters</code>	List.
<code>fields</code>	Character vector. The field names of the data files. Field names can optionally be prepended with a namespace (one of "dwc", "dwciri", "dc" or "dcterms") separated from the field by a ":". If no namespace is specified, "dwc" will be assumed.
<code>facts</code>	List of extra variables to be extracted from record, event and document "facts".
<code>id</code>	Integer. Indicates which field can be considered the record identifier. No ID field will be specified if <code>id</code> is not an integer between 1 and the number of fields specified.

**Value**

The status value returned by the zip command, invisibly.

**Examples**

```
## Not run:  
  
write_meta(  
  "dwca.zip", list(collection = "HR.447"), c("occurrenceID", "basisOfRecord")  
)  
  
## End(Not run)
```

---

write_occurrences	<i>Write occurrences</i>
-------------------	--------------------------

---

**Description**

Write occurrence records to a Darwin Core archive.

**Usage**

```
write_occurrences(  
  data,  
  archive,  
  file_name = "occurrence.txt",  
  media_file_name = "media.txt"  
)
```

**Arguments**

data	A data.frame. Occurrence records.
archive	Character. Path to the archive.
file_name	Character. The name of the file to write to the archive.
media_file_name	Character. The name of the media extension file to write to the archive.

**Value**

The status value returned by the zip command, invisibly.

**Examples**

```
## Not run:  
  
data <- get_occurrences(  
  c(collection = "HR.3991"), c("occurrenceID", "basisOfRecord"), 100  
)  
write_occurrences(data, "dwca.zip")  
  
## End(Not run)
```



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