

# Package ‘galah’

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**Type** Package

**Title** Biodiversity Data from the Living Atlas Community

**Version** 1.5.1

**Description** The living atlas community provides tools to enable users to find, access, combine and visualise data on biodiversity. 'galah' enables the R community to directly access data and resources hosted by the living atlases.

**Depends** R (>= 4.1.0)

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**Suggests** vcr (>= 0.6.0), covr, gt, kableExtra, knitr, magrittr, pkgdown, rmarkdown, testthat

**License** MPL-2.0

**URL** <https://galah.ala.org.au>

**BugReports** <https://github.com/AtlasOfLivingAustralia/galah-R/issues>

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## R topics documented:

atlas_citation	2
atlas_counts	3
atlas_media	4
atlas_occurrences	6
atlas_species	8
atlas_taxonomy	9
clear_cached_files	11
collect_media	11
collect_occurrences	12
count.data_request	13
filter.data_request	14
galah_apply_profile	14
galah_call	15
galah_config	17
galah_down_to	19
galah_filter	19
galah_geolocate	21
galah_group_by	23
galah_identify	24
galah_select	25
group_by.data_request	27
identify.data_request	28
search_all	29
search_identifiers	31
search_media	32
search_taxa	32
select.data_request	34
show_all	35
show_values	37
slice_head.data_request	39
st_crop.data_request	39
<b>Index</b>	<b>41</b>

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atlas_citation	<i>Generate a citation for occurrence data</i>
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### Description

If a `data.frame` was generated using `atlas_occurrences()`, and the `mint_doi` argument was set to `TRUE`, the DOI associated with that dataset is appended to the resulting `data.frame` as an attribute. This function simply formats that DOI as a citation that can be included in a scientific publication. Please also consider citing this package, using the information in `citation("galah")`.

**Usage**

```
atlas_citation(data)
```

**Arguments**

data                    data.frame: occurrence data generated by [atlas\\_occurrences\(\)](#)

**Value**

A string containing the citation for that dataset.

**Examples**

```
## Not run:  
atlas_citation(doi)  
  
## End(Not run)
```

---

atlas_counts	<i>Return a count of records</i>
--------------	----------------------------------

---

**Description**

Prior to downloading data it is often valuable to have some estimate of how many records are available, both for deciding if the query is feasible, and for estimating how long it will take to download. Alternatively, for some kinds of reporting, the count of observations may be all that is required, for example for understanding how observations are growing or shrinking in particular locations, or for particular taxa. To this end, `atlas_counts()` takes arguments in the same format as [atlas\\_occurrences\(\)](#), and provides either a total count of records matching the criteria, or a `data.frame` of counts matching the criteria supplied to the `group_by` argument.

**Usage**

```
atlas_counts(  
  request = NULL,  
  identify = NULL,  
  filter = NULL,  
  geolocate = NULL,  
  data_profile = NULL,  
  group_by = NULL,  
  limit = NULL,  
  type = c("record", "species"),  
  refresh_cache = FALSE  
)
```

**Arguments**

request	optional data_request object: generated by a call to <code>galah_call()</code> .
identify	data.frame: generated by a call to <code>galah_identify()</code> .
filter	data.frame: generated by a call to <code>galah_filter()</code>
geolocate	string: generated by a call to <code>galah_geolocate()</code>
data_profile	string: generated by a call to <code>galah_apply_profile()</code>
group_by	data.frame: An object of class <code>galah_group_by</code> , as returned by <code>galah_group_by()</code> . Alternatively a vector of field names (see <code>search_all(fields)</code> and <code>show_all(fields)</code> ).
limit	numeric: maximum number of categories to return, defaulting to 100. If limit is NULL, all results are returned. For some categories this will take a while.
type	string: one of <code>c("record", "species")</code> . Defaults to "record". If "species", the number of species matching the criteria will be returned, if "record", the number of records matching the criteria will be returned.
refresh_cache	logical: if set to TRUE and <code>galah_config(caching = TRUE)</code> then files cached from a previous query will be replaced by the current query

**Value**

An object of class `tbl_df` and `data.frame` (aka a tibble) returning:

- A single number, if `group_by` is not specified or,
- A summary of counts grouped by field(s), if `group_by` is specified

**Examples**

```
galah_call() |>
  galah_filter(year == 2015) |>
  atlas_counts()
```

---

atlas\_media

*Get metadata on images, sounds and videos*


---

**Description**

In addition to text data describing individual occurrences and their attributes, ALA stores images, sounds and videos associated with a given record. `atlas_media` displays metadata for any and all of the media types.

**Usage**

```
atlas_media(
  request = NULL,
  identify = NULL,
  filter = NULL,
  geolocate = NULL,
  data_profile = NULL,
  download_dir = NULL,
  refresh_cache = FALSE
)
```

**Arguments**

request	optional data_request object: generated by a call to <a href="#">galah_call()</a> .
identify	data.frame: generated by a call to <a href="#">galah_identify()</a> .
filter	data.frame: generated by a call to <a href="#">galah_filter()</a>
geolocate	string: generated by a call to <a href="#">galah_geolocate()</a>
data_profile	string: generated by a call to <a href="#">galah_apply_profile()</a>
download_dir	string: path to directory where downloaded media will be stored. DEPRECATED; use <a href="#">collect_media()</a> instead.
refresh_cache	logical: if set to TRUE and <a href="#">galah_config(caching = TRUE)</a> then files cached from a previous query will be replaced by the current query. DEPRECATED; use <a href="#">collect_media()</a> instead.

**Details**

[atlas\\_media\(\)](#) works by first finding all occurrence records matching the filter which contain media, then downloading the metadata for the media. To actually download the files themselves, use [collect\\_media\(\)](#). It may be beneficial when requesting a large number of records to show a progress bar by setting `verbose = TRUE` in [galah\\_config\(\)](#).

**Value**

An object of class `tbl_df` and `data.frame` (aka a tibble) of metadata of the requested media.

**See Also**

[atlas\\_counts\(\)](#) to find the number of records with media; but note this is not necessarily the same as the number of media files, as each record can have more than one media file associated with it (see examples section for how to do this).

**Examples**

```
## Not run:
# Download Regent Honeyeater records with multimedia attached
galah_call() |>
  galah_identify("Regent Honeyeater") |>
  galah_filter(year == 2011) |>
```

```
atlas_media()

# Download multimedia
galah_call() |>
  galah_identify("Regent Honeyeater") |>
  galah_filter(year == 2011) |>
  atlas_media() |>
  collect_media(path = "folder/your-directory")

# Specify a single media type to download
galah_call() |>
  galah_identify("Eolophus Roseicapilla") |>
  galah_filter(multimedia == "Sound") |>
  atlas_media()

# It's good to check how many records have media files before downloading
galah_call() |>
  galah_filter(multimedia == c("Image", "Sound", "Video")) |>
  galah_group_by(multimedia) |>
  atlas_counts()

## End(Not run)
```

---

atlas_occurrences	<i>Return occurrence records</i>
-------------------	----------------------------------

---

## Description

The most common form of data stored by living atlases are observations of individual life forms, known as 'occurrences'. This function allows the user to search for occurrence records that match their specific criteria, and return them as a data.frame for analysis. Optionally, the user can also request a DOI for a given download to facilitate citation and re-use of specific data resources.

## Usage

```
atlas_occurrences(
  request = NULL,
  identify = NULL,
  filter = NULL,
  geolocate = NULL,
  data_profile = NULL,
  select = NULL,
  mint_doi = FALSE,
  doi = NULL,
  refresh_cache = FALSE
)
```

**Arguments**

request	optional data_request object: generated by a call to <a href="#">galah_call()</a> .
identify	data.frame: generated by a call to <a href="#">galah_identify()</a> .
filter	data.frame: generated by a call to <a href="#">galah_filter()</a>
geolocate	string: generated by a call to <a href="#">galah_geolocate()</a>
data_profile	string: generated by a call to <a href="#">galah_apply_profile()</a>
select	data.frame: generated by a call to <a href="#">galah_select()</a>
mint_doi	logical: by default no DOI will be generated. Set to TRUE if you intend to use the data in a publication or similar
doi	<b>[Deprecated]</b> Use collect_occurrences instead. string: this argument enables retrieval of occurrence records previously downloaded from the ALA, using the DOI generated by the data.
refresh_cache	logical: if set to TRUE and <a href="#">galah_config(caching = TRUE)</a> then files cached from a previous query will be replaced by the current query

**Details**

Note that unless care is taken, some queries can be particularly large. While most cases this will simply take a long time to process, if the number of requested records is >50 million the call will not return any data. Users can test whether this threshold will be reached by first calling [atlas\\_counts\(\)](#) using the same arguments that they intend to pass to [atlas\\_occurrences\(\)](#). It may also be beneficial when requesting a large number of records to show a progress bar by setting `verbose = TRUE` in [galah\\_config\(\)](#).

**Value**

An object of class `tbl_df` and `data.frame` (aka a tibble) of occurrences, containing columns as specified by [galah\\_select\(\)](#). The `data.frame` object has the following attributes:

- a listing of the user-supplied arguments of the `data_request` (i.e., `identify`, `filter`, `geolocate`, `select`)
- a `doi` of the data download
- the `search_url` of the query to ALA API

**Examples**

```
## Not run:
# Download occurrence records for a specific taxon
galah_config(email = "your_email_here")
galah_call() |>
  galah_identify("Reptilia") |>
  atlas_occurrences()

# Download occurrence records in a year range
galah_call() |>
  galah_identify("Litoria") |>
  galah_filter(year >= 2010 & year <= 2020) |>
```

```

atlas_occurrences()

# Download occurrences records in a WKT-specified area
polygon <- "POLYGON((146.24960 -34.05930,
                    146.37045 -34.05930,
                    146.37045 -34.152549,
                    146.24960 -34.15254,
                    146.24960 -34.05930))"

galah_call() |>
  galah_identify("Reptilia") |>
  galah_filter(year >= 2010, year <= 2020) |>
  galah_geolocate(polygon) |>
  atlas_occurrences()

## End(Not run)

```

---

atlas\_species

*Return species lists*


---

## Description

While there are reasons why users may need to check every record meeting their search criteria (i.e. using [atlas\\_occurrences\(\)](#)), a common use case is to simply identify which species occur in a specified region, time period, or taxonomic group. This function returns a `data.frame` with one row per species, and columns giving associated taxonomic information.

## Usage

```

atlas_species(
  request = NULL,
  identify = NULL,
  filter = NULL,
  geolocate = NULL,
  data_profile = NULL,
  refresh_cache = FALSE
)

```

## Arguments

request	optional <code>data_request</code> object: generated by a call to <a href="#">galah_call()</a> .
identify	<code>data.frame</code> : generated by a call to <a href="#">galah_identify()</a> .
filter	<code>data.frame</code> : generated by a call to <a href="#">galah_filter()</a>
geolocate	string: generated by a call to <a href="#">galah_geolocate()</a>
data_profile	string: generated by a call to <a href="#">galah_apply_profile()</a>
refresh_cache	logical: if set to <code>TRUE</code> and <code>galah_config(caching = TRUE)</code> then files cached from a previous query will be replaced by the current query



## Details

The primary use case of this function is to extract species-level information given a set of criteria defined by `search_taxa()`, `galah_filter()` or `galah_geolocate()`. If the purpose is simply to get taxonomic information that is not restricted by filtering, then `search_taxa()` is more efficient. Similarly, if counts are required that include filter but without returning taxonomic detail, then `atlas_counts()` is more efficient (see examples).

## Value

An object of class `tbl_df` and `data.frame` (aka a tibble), returning matching species. The `data.frame` object has attributes listing of the user-supplied arguments of the `data_request` (i.e., `identify`, `filter`, `geolocate`, `columns`)

## Examples

```
# First register a valid email address
galah_config(email = "ala4r@ala.org.au")

# Get a list of species within genus "Heleioporus"
# (every row is a species with associated taxonomic data)
galah_call() |>
  galah_identify("Heleioporus") |>
  atlas_species()

# Get a list of species within family "Peramelidae"
galah_call() |>
  galah_identify("peramelidae") |>
  atlas_species()

# It's good idea to find how many species there are before downloading
galah_call() |>
  galah_identify("Heleioporus") |>
  atlas_counts(type = "species")
```

---

atlas\_taxonomy

*Search taxonomic trees*


---

## Description

The ALA has its' own internal taxonomy that is derived from authoritative sources. `atlas_taxonomy` provides a means to query that taxonomy, returning a tree (class `Node`) showing which lower clades are contained within the specified taxon.

## Usage

```
atlas_taxonomy(request = NULL, identify = NULL, down_to = NULL)
```

## Arguments

request	optional data_request object: generated by a call to <a href="#">galah_call()</a> .
identify	data.frame: generated by a call to <a href="#">galah_identify()</a> .
down_to	The identity of the clade at which the downwards search should stop. Should be specified using an object of class character and <a href="#">galah_down_to</a> , as returned from <a href="#">galah_down_to()</a> . Also accepts a string.

## Details

The approach used by this function is recursive, meaning that it becomes slow for large queries such as `atlas_taxonomy(search_taxa("Plantae"), down_to = galah_down_to(species))`. Although the inputs to `search_taxa` and `down_to` are case-insensitive, node names are always returned in title case.

## Value

A tree consisting of objects of class `Node`, containing the requested taxonomy. Each node contains the following attributes:

- name: The scientific name of the taxon in question
- rank: The taxonomic rank to which that taxon belongs
- guid: A unique identifier used by the ALA
- authority: The source of the taxonomic name & identifier

## See Also

[search\\_taxa\(\)](#) to search for an individual taxon; [show\\_all\(ranks\)](#) for valid ranks used to specify the `down_to` argument.

## Examples

```
# Get a taxonomic tree of *Chordata* down to the class level
galah_call() |>
  galah_identify("chordata") |>
  galah_down_to(class) |>
  atlas_taxonomy()
```

---

clear_cached_files	<i>Clear previously cached files</i>
--------------------	--------------------------------------

---

**Description**

Deletes cached files within the cached file directory and their query metadata

**Usage**

```
clear_cached_files()
```

**Value**

No return value; called for side effect of removing files

**Examples**

```
## Not run:
# First set caching to true with [galah_config()]
galah_config(caching = TRUE)

# Then create a data query.
# The data you download will be cached in a temporary directory.
dat <- atlas_counts(group_by = galah_group_by(year))

# To clear your cached files directory, use `clear_cached_files()`
clear_cached_files()

## End(Not run)
```

---

collect_media	<i>Collect media files</i>
---------------	----------------------------

---

**Description**

This function downloads full-sized or thumbnail images and media files using information from atlas\_media to a local directory.

**Usage**

```
collect_media(
  df,
  type = c("full", "thumbnail"),
  path,
  download_dir,
  refresh_cache
)
```

**Arguments**

df	tibble returned by atlas_media() or show_all(media)
type	string: either "full" to download original images, or "thumbnail" to download thumbnails
path	string: path to directory where downloaded media will be stored
download_dir	<b>[Deprecated]</b> Use path instead.
refresh_cache	logical: if set to TRUE and galah_config(caching = TRUE) then files cached from a previous query will be replaced by the current query. NOTE: Unclear that this works right now.

**Value**

Available image & media files downloaded to a user local directory.

**Examples**

```
## Not run:
# Use `atlas_media()` to return a `tibble` of records that contain media
galah_call() |>
  galah_identify("perameles") |>
  galah_filter(year == 2015) |>
  atlas_media()

# To download media files, add `collect_media()` to the end of a query
galah_call() |>
  galah_identify("perameles") |>
  galah_filter(year == 2015) |>
  atlas_media() |>
  collect_media(path = here::here("folder", "subfolder"))

## End(Not run)
```

---

collect\_occurrences     *Collect occurrence records from a pre-existing DOI or URL*

---

**Description****[Experimental]**

Download occurrence records using an existing DOI or URL. Pre-existing DOIs and URLs come from previously generated downloads using atlas\_occurrences or online.

**Usage**

```
collect_occurrences(url, doi)
```

**Arguments**

`url` string: Retrieve occurrence records previously downloaded from the ALA, using the URL provided via email.

`doi` string: Retrieve occurrence records previously downloaded from the ALA, using the DOI generated by the data.

**Value**

An object of class `tbl_df` and `data.frame` (aka a tibble) of occurrences

**Examples**

```
## Not run:
# Download previously retrieved records using an existing DOI or URL
collect_occurrences(doi = "your-doi")

# DOIs can be minted by adding `mint_doi = TRUE` to `atlas_occurrences()`
records <-
  galah_call() |>
  galah_identify("perameles") |>
  galah_filter(year == 2001) |>
  atlas_occurrences(mint_doi = TRUE)

attributes(records)$doi # return minted doi

## End(Not run)
```

---

count.data\_request      *Count for object of class data\_request*

---

**Description**

**[Experimental]**

**Usage**

```
## S3 method for class 'data_request'
count(x, ..., wt, sort, name, type = c("record", "species"))
```

**Arguments**

`x` An object of class `data_request`, created using [galah\\_call\(\)](#)

`...` currently ignored

`wt` currently ignored

`sort` currently ignored

`name` currently ignored

type                    string: one of c("record", "species"). Defaults to "record". If "species", the number of species matching the criteria will be returned, if "record", the number of records matching the criteria will be returned.

### See Also

[atlas\\_counts\(\)](#), with which this function is synonymous.

---

`filter.data_request`    *Narrow a query by specifying filters*

---

### Description

"Filters" are arguments of the form `field logical value` that are used to narrow down the number of records returned by a specific query. For example, it is common for users to request records from a particular year (`year == 2020`), or to return all records except for fossils (`basisOfRecord != "FossilSpecimen"`).

**[Experimental]**

### Usage

```
## S3 method for class 'data_request'
filter(.data, ...)
```

### Arguments

`.data`                    An object of class `data_request`, created using [galah\\_call\(\)](#)  
`...`                      filters, in the form `field logical value`

### See Also

[galah\\_filter\(\)](#), with which this function is synonymous.

---

`galah_apply_profile`    *Apply a data quality profile*

---

### Description

A 'profile' is a group of filters that are pre-applied by the ALA. Using a data profile allows a query to be filtered quickly to the most relevant or quality-assured data that is fit-for-purpose. For example, the "ALA" profile is designed to exclude lower quality records, whereas other profiles apply filters specific to species distribution modelling (e.g. CDSM).

### Usage

```
galah_apply_profile(...)
```

## Arguments

... a profile name. Should be a string - the name or abbreviation of a data quality profile to apply to the query. Valid values can be seen using `show_all(profiles)`

## Details

Note that only one profile can be loaded at a time; if multiple profiles are given, the first valid profile is used.

For more bespoke editing of filters within a profile, use `galah_filter()`

## Value

A tibble containing a valid data profile value.

## See Also

`show_all()` and `search_all()` to look up available data profiles. `galah_filter()` can be used for more bespoke editing of individual data profile filters.

## Examples

```
# Apply a data quality profile to a query
galah_call() |>
  galah_identify("reptilia") |>
  galah_filter(year == 2021) |>
  galah_apply_profile(ALA) |>
  atlas_counts()
```

---

galah\_call

*Start building a data query*

---

## Description

To download data from the ALA (or another atlas), one must construct a data query. This query tells the atlas API what data to download and return, as well as how it should be filtered.

## Usage

```
galah_call(
  identify = NULL,
  filter = NULL,
  select = NULL,
  geolocate = NULL,
  data_profile = NULL,
  group_by = NULL,
  down_to = NULL,
```

```

    ...
  )

  ## S3 method for class 'data_request'
  print(x, ...)

```

### Arguments

identify	data.frame: generated by a call to <a href="#">galah_identify()</a>
filter	data.frame: generated by a call to <a href="#">select_filters()</a>
select	data.frame: generated by a call to <a href="#">galah_select()</a>
geolocate	string: generated by a call to <a href="#">galah_geolocate()</a>
data_profile	string: generated by a call to <a href="#">galah_apply_profile()</a>
group_by	data.frame: generated by a call to <a href="#">galah_group_by()</a>
down_to	data.frame: generated by a call to <a href="#">galah_down_to()</a>
...	other function-specific request parameters
x	an object of class <code>data_request</code>

### Details

The `galah` package enables users to construct their data queries using piping syntax (i.e., `%>%` from `magrittr`, or `|>` from `base`).

Start a query with `galah_call()`. Pipe functions like [galah\\_identify\(\)](#), [galah\\_filter\(\)](#), [[galah\\_select\(\)](#)], and [galah\\_group\\_by\(\)](#) to narrow your query and specify filters. Finish a query with an `atlas_` function to identify which type of data is downloaded (i.e., [atlas\\_occurrences\(\)](#), [atlas\\_counts\(\)](#), [atlas\\_species\(\)](#), [atlas\\_taxonomy\(\)](#) or [atlas\\_media\(\)](#)).

Using `galah_call()` with pipes allows you to build & filter a query to download data in the same way that you would wrangle data with `dplyr` and the `tidyverse`.

### Value

An object of class `data_request`.

### Examples

```

# Begin your query with `galah_call()`, then pipe using `%>%` or `|>`

# Get number of records of *Aves* from 2001 to 2004 by year
galah_call() |>
  galah_identify("Aves") |>
  galah_filter(year > 2000 & year < 2005) |>
  galah_group_by() |>
  atlas_counts()

# Get information for all species in *Cacatuidae* family
galah_call() |>
  galah_identify("Cacatuidae") |>

```



```

    atlas_species()
## Not run:
# Download records of genus *Eolophus* from 2001 to 2004
galah_config(email = "your-email@email.com")

galah_call() |>
  galah_identify("Eolophus") |>
  galah_filter(year > 2000 & year < 2005) |>
  atlas_occurrences()

## End(Not run)

```

---

galah\_config

*Get or set configuration options that control galah behaviour*


---

## Description

The galah package supports large data downloads, and also interfaces with the ALA which requires that users of some services provide a registered email address and reason for downloading data. The galah\_config function provides a way to manage these issues as simply as possible.

## Usage

```

galah_config(..., profile_path = NULL)

## S3 method for class 'galah_config'
print(x, ...)

```

## Arguments

... Options can be defined using the form name = "value". Valid arguments are:

- atlas string: Living Atlas to point to, Australia by default. Can be an organisation name, acronym, or region (see [show\\_all\\_atlases\(\)](#) for admissible values)
- caching logical: if TRUE, results will be cached, and any cached results will be re-used). If FALSE, data will be downloaded.
- cache\_directory string: the directory to use for the cache. By default this is a temporary directory, which means that results will only be cached within an R session and cleared automatically when the user exits R. The user may wish to set this to a non-temporary directory for caching across sessions. The directory must exist on the file system.
- download\_reason\_id numeric or string: the "download reason" required. by some ALA services, either as a numeric ID (currently 0–13) or a string (see [show\\_all\(reasons\)](#) for a list of valid ID codes and names). By default this is NA. Some ALA services require a valid download\_reason\_id code, either specified here or directly to the associated R function.

- email string: An email address that has been registered with the chosen atlas. For the ALA, you can register at [this address](#).
- password string: A registered password (GBIF only)
- run\_checks logical: should galah run checks for filters and columns. If making lots of requests sequentially, checks can slow down the process and lead to HTTP 500 errors, so should be turned off. Defaults to TRUE.
- send\_email logical: should you receive an email for each query to [atlas\\_occurrences\(\)](#)? Defaults to FALSE; but can be useful in some instances, for example for tracking DOIs assigned to specific downloads for later citation.
- username string: A registered username (GBIF only)
- verbose logical: should galah give verbose such as progress bars? Defaults to FALSE.

profile\_path **[Deprecated]**  
 Keeping for compatibility with older package versions. It is preferable to not save galah\_config options to a .Rprofile file.

x an object of class galah\_config

## Value

For galah\_config(), a list of all options. When galah\_config(...) is called with arguments, nothing is returned but the configuration is set.

## Examples

```
## Not run:
# To download occurrence records, enter your email in `galah_config()`.
# This email should be registered with the ALA.
# You can register at:
# https://auth.ala.org.au/userdetails/registration/createAccount
galah_config(email = "your-email@email.com")

# Turn on caching in your session
galah_config(caching = TRUE)

# Some ALA services require that you add a reason for downloading data.
# Add your selected reason using the option `download_reason_id`
galah_config(download_reason_id = 0)

# To look up all valid reasons to enter, use `show_all(reasons)`
show_all(reasons)

# Make debugging in your session easier by setting `verbose = TRUE`
galah_config(verbose = TRUE)

## End(Not run)
```

---

galah_down_to	<i>Specify the lowest taxonomic rank required in a downwards search</i>
---------------	---

---

**Description**

atlas\_taxonomy generates a downwards search of the taxonomic tree. Use galah\_down\_to() to specify the taxonomic level to search to. galah\_down\_to() uses non-standard evaluation (NSE).

**Usage**

```
galah_down_to(...)
```

**Arguments**

... the name of a single taxonomic rank

**Value**

A string with the named rank

**See Also**

[galah\\_select\(\)](#), [galah\\_filter\(\)](#) and [galah\\_geolocate\(\)](#) for related methods.

**Examples**

```
# Return a taxonomic tree of *Chordata* down to the class level
## Not run:
galah_call() |>
  galah_identify("Vertebrata") |>
  galah_down_to(class) |>
  atlas_taxonomy()

## End(Not run)
```

---

galah_filter	<i>Narrow a query by specifying filters</i>
--------------	---

---

**Description**

"Filters" are arguments of the form field logical value that are used to narrow down the number of records returned by a specific query. For example, it is common for users to request records from a particular year (year == 2020), or to return all records except for fossils (basisOfRecord != "FossilSpecimen").

The result of galah\_filter() can be passed to the filter argument in [atlas\\_occurrences\(\)](#), [atlas\\_species\(\)](#), [atlas\\_counts\(\)](#) or [atlas\\_media\(\)](#).

**Usage**

```
galah_filter(..., profile = NULL)
```

**Arguments**

`...` filters, in the form `field logical value`

`profile` **[Soft-deprecated]** Use `galah_apply_profile` instead. If supplied, should be a string recording a data quality profile to apply to the query. See [show\\_all\\_profiles\(\)](#) for valid profiles. By default no profile is applied.

**Details**

`galah_filter` uses non-standard evaluation (NSE), and is designed to be as compatible as possible with `dplyr::filter()` syntax.

All statements passed to `galah_filter()` (except the `profile` argument) take the form of field - logical - value. Permissible examples include:

- `=` or `==` (e.g. `year = 2020`)
- `!=`, e.g. `year != 2020`)
- `>` or `>=` (e.g. `year >= 2020`)
- `<` or `<=` (e.g. `year <= 2020`)
- OR statements (e.g. `year == 2018 | year == 2020`)
- AND statements (e.g. `year >= 2000 & year <= 2020`)

In some cases R will fail to parse inputs with a single equals sign (`=`), particularly where statements are separated by `&` or `|`. This problem can be avoided by using a double-equals (`==`) instead.

*Notes on behaviour*

Separating statements with a comma is equivalent to an AND statement; Ergo `galah_filter(year >= 2010 & year < 2020)` is the same as `galah_filter(year >= 2010, year < 2020)`.

All statements must include the field name; so `galah_filter(year == 2010 | year == 2021)` works, as does `galah_filter(year == c(2010, 2021))`, but `galah_filter(year == 2010 | 2021)` fails.

It is possible to use an object to specify required values, e.g. `year_value <- 2010; galah_filter(year > year_value)`

`solr` supports range queries on text as well as numbers; so this is valid: `galah_filter(cl22 >= "Tasmania")`

**Value**

A tibble containing filter values.

**See Also**

[search\\_taxa\(\)](#) and [galah\\_geolocate\(\)](#) for other ways to restrict the information returned by [atlas\\_occurrences\(\)](#) and related functions. Use [search\\_all\(fields\)](#) to find fields that you can filter by, and [show\\_values\(\)](#) to find what values of those filters are available.

**Examples**

```
# Filter query results to return records of interest
galah_call() |>
  galah_filter(year >= 2019,
               basisOfRecord == "HumanObservation") |>
  atlas_counts()
```

---

galah_geolocate	<i>Narrow a query to within a specified area</i>
-----------------	--

---

**Description**

Restrict results to those from a specified area. Areas can be specified as either polygons or bounding boxes, depending on type.

**Usage**

```
galah_geolocate(..., type = c("polygon", "bbox"))
```

**Arguments**

...	a single sf object, WKT string or shapefile. Bounding boxes can be supplied as a tibble/data.frame or a bbox
type	string: one of c("polygon", "bbox"). Defaults to "polygon". If type = "polygon", a multipolygon will be built via <a href="#">galah_polygon()</a> . If type = "bbox", a multipolygon will be built via <a href="#">galah_bbox()</a> . The multipolygon is used to narrow a query to the ALA.

**Details**

By default, type is set to "polygon" which narrows queries to within an area supplied as a POLYGON. Polygons must be specified as either an sf object, a 'well-known text' (WKT) string, or a shapefile. Shapefiles must be simple to be accepted by the ALA.

Alternatively, set type = "bbox" to narrow queries to within a bounding box. Bounding boxes can be extracted from a supplied sf object or a shapefile. A bounding box can also be supplied as a bbox object (via `sf::st_bbox()`) or a tibble/data.frame.

If type = "polygon", WKT strings longer than 10000 characters and sf objects with more than 500 vertices will not be accepted by the ALA. Some polygons may need to be simplified. If type = "bbox", sf objects and shapefiles will be converted to a bounding box to query the ALA.

**Value**

length-1 object of class character and galah\_geolocate, containing a multipolygon WKT string representing the area provided.

**See Also**

[galah\\_polygon\(\)](#) and [galah\\_bbox\(\)](#) for specific functions to narrow queries by a specified area. [search\\_taxa\(\)](#), [galah\\_filter\(\)](#) and [galah\\_select\(\)](#) for other ways to restrict the information returned by [atlas\\_occurrences\(\)](#) and related functions.

**Examples**

```
## Not run:
# Search for records within a polygon using a shapefile
location <- sf::st_read("path/to/shapefile.shp")
galah_call() |>
  galah_identify("vulpes") |>
  galah_geolocate(location) |>
  atlas_counts()

# Search for records within the bounding box of a shapefile
location <- sf::st_read("path/to/shapefile.shp")
galah_call() |>
  galah_identify("vulpes") |>
  galah_geolocate(location, type = "bbox") |>
  atlas_counts()

## End(Not run)

# Search for records within a polygon using an `sf` object
location <-
"POLYGON((143.32 -18.78,145.30 -20.52,141.52 -21.50,143.32 -18.78))" |>
  sf::st_as_sfc()
galah_call() |>
  galah_identify("reptilia") |>
  galah_polygon(location) |>
  atlas_counts()

# Search for records using a Well-known Text string (WKT)
wkt <- "POLYGON((142.36228 -29.00703,
                142.74131 -29.00703,
                142.74131 -29.39064,
                142.36228 -29.39064,
                142.36228 -29.00703))"
galah_call() |>
  galah_identify("vulpes") |>
  galah_geolocate(wkt) |>
  atlas_counts()

# Search for records within the bounding box extracted from an `sf` object
location <-
"POLYGON((143.32 -18.78,145.30 -20.52,141.52 -21.50,143.32 -18.78))" |>
  sf::st_as_sfc()
galah_call() |>
  galah_identify("vulpes") |>
  galah_geolocate(location, type = "bbox") |>
  atlas_counts()
```

```

# Search for records using a bounding box of coordinates
b_box <- sf::st_bbox(c(xmin = 143, xmax = 148, ymin = -29, ymax = -28),
                    crs = sf::st_crs("WGS84"))
galah_call() |>
  galah_identify("reptilia") |>
  galah_geolocate(b_box, type = "bbox") |>
  atlas_counts()

# Search for records using a bounding box in a `tibble` or `data.frame`
b_box <- tibble::tibble(xmin = 148, ymin = -29, xmax = 143, ymax = -21)
galah_call() |>
  galah_identify("vulpes") |>
  galah_geolocate(b_box, type = "bbox") |>
  atlas_counts()

```

---

galah_group_by	<i>Specify fields to group when downloading record counts</i>
----------------	---

---

## Description

`atlas_counts` supports server-side grouping of data. Grouping can be used to return record counts grouped by multiple, valid fields (found by `search_all(fields)`). Use `galah_group_by` when using the `group_by` argument of `atlas_counts` to return record counts summed by one or more valid fields.

## Usage

```
galah_group_by(..., expand = TRUE)
```

## Arguments

<code>...</code>	zero or more individual column names to include
<code>expand</code>	logical: When passed to <code>group_by</code> argument of <code>atlas_counts</code> , should factor levels be expanded? Defaults to TRUE.

## Value

If any arguments are provided, returns a `data.frame` with columns name and type, as per `galah_select()`; if no arguments are provided, returns NULL.

## See Also

[galah\\_select\(\)](#), [galah\\_filter\(\)](#) and [galah\\_geolocate\(\)](#) for related methods.

**Examples**

```
galah_call() |>
  galah_group_by(basisOfRecord) |>
  atlas_counts()
```

---

galah_identify	<i>Narrow a query by passing taxonomic identifiers</i>
----------------	--

---

**Description**

When conducting a search or creating a data query, it is common to identify a known taxon or group of taxa to narrow down the records or results returned.

**Usage**

```
galah_identify(..., search = TRUE)
```

**Arguments**

...	one or more scientific names (if <code>search = TRUE</code> ) or taxonomic identifiers (if <code>search = FALSE</code> ); or an object of class <code>ala_id</code> (from <code>search_taxa</code> ).
<code>search</code>	(logical); should the results in question be passed to <code>search_taxa</code> ?

**Details**

`galah_identify()` is used to identify taxa you want returned in a search or a data query. Users to pass scientific names or taxonomic identifiers with pipes to provide data only for the biological group of interest.

It is good to use [search\\_taxa\(\)](#) and [search\\_identifiers\(\)](#) first to check that the taxa you provide to `galah_identify()` return the correct results.

**Value**

A tibble containing identified taxa.

**See Also**

[search\\_taxa\(\)](#) to find identifiers from scientific names; [search\\_identifiers\(\)](#) for how to get names if taxonomic identifiers are already known.



**Examples**

```
# Specify a taxon. A valid taxon will return an identifier.
galah_identify("reptilia")

# Specify more than one taxon at a time.
galah_identify("reptilia", "mammalia", "aves", "pisces")

# Use `galah_identify()` to narrow your queries
galah_call() |>
  galah_identify("Eolophus") |>
  atlas_counts()

# If you know a valid taxon identifier, add it and set `search = FALSE`.
galah_call() |>
  galah_identify("https://biodiversity.org.au/afd/taxa/009169a9-a916-40ee-866c-669ae0a21c5c",
    search = FALSE) |>
  atlas_counts()
```

galah\_select

*Specify fields for occurrence download***Description**

The living atlases store content in hundreds of different fields, and users often require thousands or millions of records at a time. To reduce time taken to download data, and limit complexity of the resulting data.frame, it is sensible to restrict the fields returned by `atlas_occurrences()`. This function allows easy selection of fields, or commonly-requested groups of columns, following syntax shared with `dplyr::select()`.

**Usage**

```
galah_select(..., group = c("basic", "event", "media", "assertions"))
```

**Arguments**

...	zero or more individual column names to include
group	string: (optional) name of one or more column groups to include. Valid options are "basic", "event" and "assertions"

**Details**

The full list of available fields can be viewed with `show_all(fields)`.

Calling the argument `group = "basic"` returns the following columns:

- decimalLatitude
- decimalLongitude

- eventDate
- scientificName
- taxonConceptID
- recordID
- dataResourceName
- occurrenceStatus

Using group = "event" returns the following columns:

- eventRemarks
- eventTime
- eventID
- eventDate
- samplingEffort
- samplingProtocol

Using group = "media" returns the following columns:

- multimedia
- multimedialicence
- images
- videos
- sounds

Using group = "assertions" returns all quality assertion-related columns. The list of assertions is shown by `show_all_assertions()`.

### Value

A tibble specifying the name and type of each column to include in the call to `atlas_counts()` or `atlas_occurrences()`.

### See Also

[search\\_taxa\(\)](#), [galah\\_filter\(\)](#) and [galah\\_geolocate\(\)](#) for other ways to restrict the information returned by `atlas_occurrences()` and related functions; `atlas_counts()` for how to get counts by levels of variables returned by `galah_select`; `show_all(fields)` to list available fields.

### Examples

```
## Not run:  
# Download occurrence records of *Perameles*,  
# Only return scientificName and eventDate columns  
galah_config(email = "your-email@email.com")  
galah_call() |>  
  galah_identify("perameles")|>  
  galah_select(scientificName, eventDate) |>
```

```
atlas_occurrences()

# Only return the "basic" group of columns and the basisOfRecord column
galah_call() |>
  galah_identify("perameles") |>
  galah_select(basisOfRecord, group = "basic") |>
  atlas_occurrences()

## End(Not run)
```

---

group\_by.data\_request *Specify fields to group when downloading record counts*

---

## Description

atlas\_counts supports server-side grouping of data. Grouping can be used to return record counts grouped by multiple, valid fields (found by `search_all(fields)`). Use `galah_group_by` when using the `group_by` argument of `atlas_counts` to return record counts summed by one or more valid fields. **[Experimental]**

## Usage

```
## S3 method for class 'data_request'
group_by(.data, ...)
```

## Arguments

<code>.data</code>	An object of class <code>data_request</code>
<code>...</code>	zero or more individual column names to include

## Value

If any arguments are provided, returns a `data.frame` with columns name and type, as per `galah_select()`; if no arguments are provided, returns `NULL`.

## See Also

[galah\\_group\\_by\(\)](#), with which this function is synonymous.

---

identify.data\_request *Narrow a query by passing taxonomic identifiers*

---

### Description

When conducting a search or creating a data query, it is common to identify a known taxon or group of taxa to narrow down the records or results returned.

### Usage

```
## S3 method for class 'data_request'  
identify(x, ..., search = TRUE)
```

### Arguments

x	An object of class <code>data_request</code> , created using <code>galah_call()</code>
...	one or more scientific names (if <code>search = TRUE</code> ) or taxonomic identifiers (if <code>search = FALSE</code> ); or an object of class <code>ala_id</code> (from <code>search_taxa</code> ).
search	(logical); should the results in question be passed to <code>search_taxa</code> ?

### Details

`galah_identify()` is used to identify taxa you want returned in a search or a data query. Users to pass scientific names or taxonomic identifiers with pipes to provide data only for the biological group of interest.

It is good to use `search_taxa()` and `search_identifiers()` first to check that the taxa you provide to `galah_identify()` return the correct results.

### Value

A tibble containing identified taxa.

### See Also

`galah_identify()`, with which this function is synonymous; `search_taxa()` to find identifiers from scientific names; `search_identifiers()` for how to get names if taxonomic identifiers are already known.

---

`search_all`*Search for record information*

---

### Description

The living atlases store a huge amount of information, above and beyond the occurrence records that are their main output. In *galah*, one way that users can investigate this information is by searching for a specific option or category for the type of information they are interested in. Functions prefixed with `search_` do this, displaying any matches to a search term within the valid options for the information specified by the suffix.

**[Experimental]** `search_all()` is a helper function that can do searches within multiple types of information from `search_` sub-functions. See *Details* (below) for accepted values.

### Usage

`search_all(type, query)``search_apis(query)``search_assertions(query)``search_atlases(query)``search_collections(query)``search_datasets(query)``search_providers(query)``search_fields(query)``search_licences(query)``search_reasons(query)``search_ranks(query)``search_profiles(query)``search_lists(query)`

### Arguments

`type`            A string to specify what type of parameters should be searched.

`query`            A string specifying a search term. Searches are not case-sensitive.

## Details

There are five categories of information, each with their own specific sub-functions to look-up each type of information. The available types of information for `search_all()` are:

Category	Type	Description	Sub-fun
configuration	atlases	Search for what atlases are available	search_
	apis	Search for what APIs & functions are available for each atlas	search_
	reasons	Search for what values are acceptable as 'download reasons' for a specified atlas	search_
taxonomy	taxa	Search for one or more taxonomic names	search_
	identifiers	Take a universal identifier and return taxonomic information	search_
	ranks	Search for valid taxonomic ranks (e.g. Kingdom, Class, Order, etc.)	search_
filters	fields	Search for fields that are stored in an atlas	search_
	assertions	Search for results of data quality checks run by each atlas	search_
	licenses	Search for copyright licences applied to media	search_
group filters	profiles	Search for what data profiles are available	search_
	lists	Search for what species lists are available	search_
data providers	providers	Search for which institutions have provided data	search_
	collections	Search for the specific collections within those institutions	search_
	datasets	Search for the data groupings within those collections	search_

## Value

An object of class `tbl_df` and `data.frame` (aka a tibble) containing all data that match the search query.

## References

- Darwin Core terms <https://dwc.tdwg.org/terms/>
- ALA fields <https://api.ala.org.au/#ws72>
- ALA assertions fields <https://api.ala.org.au/#ws81>

## See Also

See `search_taxa()` and `search_identifiers()` for more information on taxonomic searches. Use the `show_all()` function and `show_all_()` sub-functions to show available options of information. These functions are used to pass valid arguments to `galah_select()`, `galah_filter()`, and related functions.

## Examples

```
# Search for fields that include the word "date"
search_all(fields, "date")

# Search for fields that include the word "marine"
search_all(fields, "marine")

# Search using a single taxonomic term
# (see `?search_taxa()` for more information)
```

```
search_all(taxa, "Reptilia") # equivalent

# Look up a unique taxon identifier
# (see `?search_identifiers()` for more information)
search_all(identifiers,
            "https://id.biodiversity.org.au/node/apni/2914510")

# Search for species lists that match "endangered"
search_all(lists, "endangered") # equivalent

# Search for a valid taxonomic rank, "subphylum"
search_all(ranks, "subphylum")
```

---

search\_identifiers      *Search for taxa with taxonomic identifiers*

---

## Description

In the ALA, all records are associated with an identifier that uniquely identifies the taxon to which that record belongs. Once those identifiers are known, this function allows you to use them to look up further information on the taxon in question. Effectively this is the inverse function to [search\\_taxa\(\)](#), which takes names and provides identifiers. The resulting tibble of taxonomic information can also be passed to [galah\\_identify\(\)](#) to filter queries to the specified taxon or taxa.

## Usage

```
search_identifiers(query)
```

## Arguments

query                      string: A vector containing one or more taxonomic identifiers, given as strings.

## Value

An object of class `tbl_df`, `data.frame` (aka a tibble) and `ala_id` containing taxonomic information.

## See Also

[search\\_taxa\(\)](#) for how to find species by (scientific) names. [galah\\_identify\(\)](#), [galah\\_select\(\)](#), [galah\\_filter\(\)](#) and [galah\\_geolocate\(\)](#) for other ways to restrict the information returned by [atlas\\_occurrences\(\)](#) and related functions.

## Examples

```
# Look up a unique taxon identifier
search_identifiers(query = "https://id.biodiversity.org.au/node/apni/2914510")
```

---

search_media	<i>Search for associated media of occurrence records</i>
--------------	--

---

### Description

Search for media files for a set of occurrence records downloaded using [atlas\\_occurrences\(\)](#). `search_media()` also accepts a set of media IDs (parsed or unparsed).

### Usage

```
search_media(df)
```

### Arguments

`df` A tibble of species occurrence records or media IDs.

### Value

a tibble of matching media files of occurrence records or media ids

### Examples

```
## Not run:
# Search for media files for a set of species occurrence records
occs <- galah_call() |>
  galah_identify("perameles") |>
  galah_filter(year == 2001) |>
  atlas_occurrences()

search_media(occs)

## End(Not run)
```

---

search_taxa	<i>Look up taxon information</i>
-------------	----------------------------------

---

### Description

Look up taxonomic names before downloading data from the ALA, using [atlas\\_occurrences\(\)](#), [atlas\\_species\(\)](#) or [atlas\\_counts\(\)](#). Taxon information returned by `search_taxa()` may be passed to [galah\\_identify\(\)](#) to provide the `identify` argument of `atlas_` functions. `search_taxa()` allows users to disambiguate homonyms (i.e. where the same name refers to taxa in different clades) prior to downloading data.



**Usage**

```
search_taxa(...)
```

**Arguments**

... : A string of one or more scientific names, separated by commas, or a data frame specifying taxonomic levels. Note that searches are not case-sensitive.

**Details**

Users can also specify taxonomic levels in a search using a data frame (tibble). Taxa may be specified using either the `specificEpithet` argument to designate the second element of a Latin binomial, or the `scientificName` argument to specify the scientific name (which may include the subspecific epithet if required).

**Value**

An object of class `tbl_df`, `data.frame` (aka a tibble) and `ala_id` containing taxonomic information.

**See Also**

[search\\_identifiers\(\)](#) for how to get names if taxonomic identifiers are already known. [galah\\_identify\(\)](#), [galah\\_select\(\)](#), [galah\\_filter\(\)](#), and [galah\\_geolocate\(\)](#) for ways to restrict the information returned by [atlas\\_occurrences\(\)](#) and related functions. [atlas\\_taxonomy\(\)](#) to look up taxonomic trees.

**Examples**

```
# Search using a single string.
# Note that `search_taxa()` isn't case sensitive
search_taxa("Reptilia")

# Search using multiple strings.
# `search_taxa()` will return one row per taxon
search_taxa("reptilia", "mammalia")

# Specify taxonomic levels in a tibble using "specificEpithet"
search_taxa(tibble::tibble(
  class = "aves",
  family = "pardalotidae",
  genus = "pardalotus",
  specificEpithet = "punctatus"))

# Specify taxonomic levels in a tibble using "scientificName"
search_taxa(tibble::tibble(
  family = c("pardalotidae", "maluridae"),
  scientificName = c("Pardalotus striatus striatus", "malurus cyaneus")))

# `galah_identify()` uses `search_taxa()` to narrow data queries
taxa <- search_taxa("reptilia", "mammalia")
```

```
galah_call() |>
  galah_identify(taxa) |>
  atlas_counts()
```

---

select.data\_request    *Specify fields for occurrence download*

---

## Description

The living atlases store content in hundreds of different fields, and users often require thousands or millions of records at a time. To reduce time taken to download data, and limit complexity of the resulting data.frame, it is sensible to restrict the fields returned by `atlas_occurrences()`. This function allows easy selection of fields, or commonly-requested groups of columns, following syntax shared with `dplyr::select()`.

## Usage

```
## S3 method for class 'data_request'
select(.data, ..., group = c("basic", "event", "media", "assertions"))
```

## Arguments

<code>.data</code>	An object of class <code>data_request</code> , created using <code>galah_call()</code>
<code>...</code>	zero or more individual column names to include
<code>group</code>	string: (optional) name of one or more column groups to include. Valid options are "basic", "event" and "assertions"

## Details

The full list of available fields can be viewed with `show_all(fields)`. **[Experimental]**

Calling the argument `group = "basic"` returns the following columns:

- decimalLatitude
- decimalLongitude
- eventDate
- scientificName
- taxonConceptID
- recordID
- dataResourceName
- occurrenceStatus

Using `group = "event"` returns the following columns:

- eventRemarks

- eventTime
- eventID
- eventDate
- samplingEffort
- samplingProtocol

Using `group = "media"` returns the following columns:

- multimedia
- multimedialicence
- images
- videos
- sounds

Using `group = "assertions"` returns all quality assertion-related columns. The list of assertions is shown by `show_all_assertions()`.

### Value

A tibble specifying the name and type of each column to include in the call to `atlas_counts()` or `atlas_occurrences()`.

### See Also

[galah\\_select\(\)](#), with which this function is synonymous.

---

show\_all

*Show valid record information*

---

### Description

The living atlases store a huge amount of information, above and beyond the occurrence records that are their main output. In `galah`, one way that users can investigate this information is by showing all the available options or categories for the type of information they are interested in. Functions prefixed with `show_all_` do this, displaying all valid options for the information specified by the suffix.

**[Experimental]** `show_all()` is a helper function that can display multiple types of information from `show_all_` sub-functions. See `Details` (below) for accepted values.

**Usage**

```

show_all(type, limit = NULL)

show_all_assertions(limit = NULL)

show_all_atlases(limit = NULL)

show_all_cached_files(limit = NULL)

show_all_apis(limit = NULL)

show_all_collections(limit = NULL)

show_all_datasets(limit = NULL)

show_all_providers(limit = NULL)

show_all_fields(limit = NULL)

show_all_licences(limit = NULL)

show_all_reasons(limit = NULL)

show_all_ranks(limit = NULL)

show_all_profiles(limit = NULL)

show_all_lists(limit = NULL)

```

**Arguments**

type	A string to specify what type of parameters should be shown.
limit	Optional number of values to return. Defaults to NULL, i.e. all records

**Details**

There are five categories of information, each with their own specific sub-functions to look-up each type of information. The available types of information for show\_all\_ are:

Category	Type	Description	Sub-function
configuration	atlases	Show what atlases are available	show_all_at
	apis	Show what APIs & functions are available for each atlas	show_all_ap
	reasons	Show what values are acceptable as 'download reasons' for a specified atlas	show_all_re
taxonomy	ranks	Show valid taxonomic ranks (e.g. Kingdom, Class, Order, etc.)	show_all_ra
filters	fields	Show fields that are stored in an atlas	show_all_fi
	assertions	Show results of data quality checks run by each atlas	show_all_as
	licenses	Show what copyright licenses are applied to media	show_all_li
group filters	profiles	Show what data profiles are available	show_all_pr

	lists	Show what species lists are available	show_all_li
data providers	providers	Show which institutions have provided data	show_all_pr
	collections	Show the specific collections within those institutions	show_all_co
	datasets	Shows all the data groupings within those collections	show_all_da

## Value

An object of class `tbl_df` and `data.frame` (aka a tibble) containing all data of interest.

## References

- Darwin Core terms <https://dwc.tdwg.org/terms/>
- ALA fields <https://api.ala.org.au/#ws72>
- ALA assertions fields <https://api.ala.org.au/#ws81>

## See Also

Use the `search_all()` function and `search_()` sub-functions to search for information. These functions are used to pass valid arguments to `galah_select()`, `galah_filter()`, and related functions.

## Examples

```
# See all supported atlases
show_all(atlases)

# Show a list of all available data quality profiles
show_all(profiles)

# Show a listing of all accepted reasons for downloading occurrence data
show_all(reasons)

# Show a listing of all taxonomic ranks
show_all(ranks)
```

---

show\_values

*Show or search for values within a specified field*

---

## Description

Users may wish to see the specific values *within* a chosen field, profile or list to narrow queries or understand more about the information of interest. `show_values()` provides users with these values. `search_values()` allows users for search for specific values within a specified field.

## Usage

```
show_values(df)
```

```
search_values(df, query)
```

## Arguments

`df` A search result from `search_fields()`, `search_profiles()` or `search_lists()`.  
`query` A string specifying a search term. Not case sensitive.

## Details

Each **Field** contains categorical or numeric values. For example:

- The field "year" contains values 2021, 2020, 2019, etc.
- The field "stateProvince" contains values New South Wales, Victoria, Queensland, etc. These are used to narrow queries with `galah_filter()`.

Each **Profile** consists of many individual quality filters. For example, the "ALA" profile consists of values:

- Exclude all records where spatial validity is FALSE
- Exclude all records with a latitude value of zero
- Exclude all records with a longitude value of zero

Each **List** contains a list of species, usually by taxonomic name. For example, the Endangered Plant species list contains values:

- *Acacia curranii* (Curly-bark Wattle)
- *Brachyscome papillosa* (Mossgiel Daisy)
- *Solanum karsense* (Menindee Nightshade)

## Value

A tibble of values for a specified field, profile or list.

## Examples

```
# Show values in field 'cl22'  
search_fields("cl22") |>  
  show_values()  
  
# Search for any values in field 'cl22' that match 'tas'  
search_fields("cl22") |>  
  search_values("tas")  
  
# See items within species list "dr19257"  
search_lists("dr19257") |>  
  show_values()
```

---

 slice\_head.data\_request

*Slice for object of class data\_request*


---

### Description

**[Experimental]** This is a simple function to set the 'limit' argument in `atlas_counts()` using dplyr syntax.

### Usage

```
## S3 method for class 'data_request'
slice_head(.data, ..., n, prop)
```

### Arguments

<code>.data</code>	An object of class <code>data_request</code> , created using <code>galah_call()</code>
<code>...</code>	currently ignored
<code>n</code>	The number of rows to be returned. If data are grouped (using <code>group_by</code> ), this operation will be performed on each group.
<code>prop</code>	currently ignored

---

 st\_crop.data\_request *Narrow a query to within a specified polygon*


---

### Description

Restrict results to those from a specified area. Areas must be polygons. Polygons must be supplied as an sf object, a 'well-known text' (WKT) string, or a shapefile. Polygons and shapefiles must not be overly complex (i.e. have too many characters or too many vertices) or they will not be accepted in a query to the ALA.

`st_crop` is masked from `sf`, but when piped after `galah_call()`, is functionally synonymous with `galah_polygon()`

### Usage

```
## S3 method for class 'data_request'
st_crop(x, y, ...)
```

**Arguments**

x	An object of class <code>data_request</code> , created using <code>galah_call()</code>
y	A single <code>sf</code> object, WKT string or shapefile
...	currently ignored

**Details**

[Experimental]

**See Also**

`galah_polygon()`, with which this function is synonymous.



# Index

atlas\_citation, 2  
atlas\_counts, 3  
atlas\_counts(), 5, 7, 9, 14, 16, 19, 26, 32, 39  
atlas\_media, 4  
atlas\_media(), 5, 16, 19  
atlas\_occurrences, 6  
atlas\_occurrences(), 2, 3, 8, 16, 18–20, 22, 25, 26, 31–34  
atlas\_species, 8  
atlas\_species(), 16, 19, 32  
atlas\_taxonomy, 9  
atlas\_taxonomy(), 16, 33

clear\_cached\_files, 11  
collect\_media, 11  
collect\_media(), 5  
collect\_occurrences, 12  
count.data\_request, 13

filter.data\_request, 14

galah\_apply\_profile, 14  
galah\_apply\_profile(), 4, 5, 7, 8, 16  
galah\_bbox(), 21, 22  
galah\_call, 15  
galah\_call(), 4, 5, 7, 8, 10, 13, 14, 28, 34, 39, 40  
galah\_config, 17  
galah\_config(), 5, 7  
galah\_down\_to, 19  
galah\_down\_to(), 10, 16  
galah\_filter, 19  
galah\_filter(), 4, 5, 7–9, 14–16, 19, 22, 23, 26, 30, 31, 33, 37, 38  
galah\_geolocate, 21  
galah\_geolocate(), 4, 5, 7–9, 16, 19, 20, 23, 26, 31, 33  
galah\_group\_by, 23  
galah\_group\_by(), 4, 16, 27  
galah\_identify, 24  
galah\_identify(), 4, 5, 7, 8, 10, 16, 28, 31–33  
galah\_polygon(), 21, 22, 39, 40  
galah\_select, 25  
galah\_select(), 7, 16, 19, 22, 23, 27, 30, 31, 33, 35, 37  
group\_by, 39  
group\_by.data\_request, 27

identify.data\_request, 28

print.data\_request (galah\_call), 15  
print.galah\_config (galah\_config), 17

search\_all, 29  
search\_all(), 15, 37  
search\_api (search\_all), 29  
search\_assertions (search\_all), 29  
search\_atlases (search\_all), 29  
search\_collections (search\_all), 29  
search\_datasets (search\_all), 29  
search\_fields (search\_all), 29  
search\_fields(), 38  
search\_identifiers, 31  
search\_identifiers(), 24, 28, 30, 33  
search\_licences (search\_all), 29  
search\_lists (search\_all), 29  
search\_lists(), 38  
search\_media, 32  
search\_profiles (search\_all), 29  
search\_profiles(), 38  
search\_providers (search\_all), 29  
search\_ranks (search\_all), 29  
search\_reasons (search\_all), 29  
search\_taxa, 32  
search\_taxa(), 9, 10, 20, 22, 24, 26, 28, 30, 31  
search\_values (show\_values), 37  
select.data\_request, 34  
select\_filters(), 16

- show\_all, [35](#)
- show\_all(), [15](#), [30](#)
- show\_all\_apis (show\_all), [35](#)
- show\_all\_assertions (show\_all), [35](#)
- show\_all\_atlases (show\_all), [35](#)
- show\_all\_atlases(), [17](#)
- show\_all\_cached\_files (show\_all), [35](#)
- show\_all\_collections (show\_all), [35](#)
- show\_all\_datasets (show\_all), [35](#)
- show\_all\_fields (show\_all), [35](#)
- show\_all\_licences (show\_all), [35](#)
- show\_all\_lists (show\_all), [35](#)
- show\_all\_profiles (show\_all), [35](#)
- show\_all\_profiles(), [20](#)
- show\_all\_providers (show\_all), [35](#)
- show\_all\_ranks (show\_all), [35](#)
- show\_all\_reasons (show\_all), [35](#)
- show\_values, [37](#)
- show\_values(), [20](#)
- slice\_head.data\_request, [39](#)
- st\_crop.data\_request, [39](#)