

# Package ‘ArctosR’

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**Title** An Interface to the 'Arctos' Database

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**Description** Performs requests to the 'Arctos' API to download data. Provides a set of builder classes for performing complex requests, as well as a set of simple functions for automating many common requests and workflows. More information about 'Arctos' can be found in Cicero et al. (2024) <[doi:10.1371/journal.pone.0296478](https://doi.org/10.1371/journal.pone.0296478)> or on their website <<https://arctosdb.org/>>.

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**BugReports** <https://github.com/hrhwilliams/arctosr/issues>

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ArctosR-package

*ArctosR: An Interface to the Arctos Database*

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### Description

The ArctosR package provides a set of functions to help users perform requests to the Arctos API to download data. It provides a set of builder classes for performing complex requests, as well as a set of simple functions for automating many common requests and workflows.

### About Arctos

Arctos is community and an online collection management information system. Arctos is a consortium of museums and organizations that collaborate to serve data on over 5 million records from natural and cultural history collections. Arctos integrates access to information from diverse disciplines: anthropology, botany, entomology, ethnology, herpetology, geology, ichthyology, mammalogy, mineralogy, ornithology, paleontology, parasitology as well as archival and cultural collections. The web interface to the Arctos database can be found at <https://arctos.database.museum/>. For more information about Arctos, see <https://arctosdb.org/about/>, and Cicero et al. (2024) doi: [10.1371/journal.pone.0296478](https://doi.org/10.1371/journal.pone.0296478).

**Functions in ArctosR**

[get\\_query\\_parameters](#), [get\\_result\\_parameters](#), [get\\_record\\_count](#), [get\\_records](#), [response\\_data](#), [save\\_response\\_rds](#), [read\\_response\\_rds](#), [save\\_response\\_csv](#), [expand\\_column](#)

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**See Also**

Useful links:

- <https://github.com/hrhwilliams/arctosr>
- Report bugs at <https://github.com/hrhwilliams/arctosr/issues>

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CatalogRequestBuilder *CatalogRequestBuilder*

---

**Description**

CatalogRequestBuilder

CatalogRequestBuilder

**Super class**

[ArctosR::RequestBuilder](#) -> CatalogRequestBuilder

**Methods****Public methods:**

- [CatalogRequestBuilder\\$set\\_limit\(\)](#)
- [CatalogRequestBuilder\\$set\\_query\(\)](#)
- [CatalogRequestBuilder\\$set\\_filter\(\)](#)
- [CatalogRequestBuilder\\$set\\_parts\(\)](#)
- [CatalogRequestBuilder\\$set\\_attributes\(\)](#)
- [CatalogRequestBuilder\\$set\\_components\(\)](#)
- [CatalogRequestBuilder\\$set\\_columns\(\)](#)
- [CatalogRequestBuilder\\$set\\_columns\\_list\(\)](#)

- [CatalogRequestBuilder\\$from\\_previous\\_response\(\)](#)
- [CatalogRequestBuilder\\$build\\_request\(\)](#)
- [CatalogRequestBuilder\\$clone\(\)](#)

**Method** `set_limit()`: Sets the limit on how many records to initially request from Arctos.

*Usage:*

```
CatalogRequestBuilder$set_limit(limit)
```

*Arguments:*

limit (integer(1)).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_query()`: Sets the query parameters to use to search Arctos.

*Usage:*

```
CatalogRequestBuilder$set_query(...)
```

*Arguments:*

query (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_filter()`: Sets the result parameters to use to filter out results.

*Usage:*

```
CatalogRequestBuilder$set_filter(...)
```

*Arguments:*

query (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_parts()`: Set parts to query over.

*Usage:*

```
CatalogRequestBuilder$set_parts(...)
```

*Arguments:*

parts (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_attributes()`: Set attributes to query over.

*Usage:*

```
CatalogRequestBuilder$set_attributes(...)
```

*Arguments:*

attributes (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_components()`: Set components to query over.

*Usage:*

```
CatalogRequestBuilder$set_components(...)
```

*Arguments:*

components (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_columns()`: Sets the columns in the dataframe returned by Arctos.

*Usage:*

```
CatalogRequestBuilder$set_columns(...)
```

*Arguments:*

cols (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `set_columns_list()`: Sets the columns in the dataframe returned by Arctos.

*Usage:*

```
CatalogRequestBuilder$set_columns_list(l)
```

*Arguments:*

cols (list).

*Returns:* [CatalogRequestBuilder](#).

**Method** `from_previous_response()`: Sets the columns in the dataframe returned by Arctos.

*Usage:*

```
CatalogRequestBuilder$from_previous_response(response)
```

*Arguments:*

response a response object from a previous request

*Returns:* [FromResponseRequestBuilder](#).

**Method** `build_request()`: Send a request for data to Arctos with parameters specified by the other methods called on this class.

*Usage:*

```
CatalogRequestBuilder$build_request()
```

*Returns:* [Response](#).

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
CatalogRequestBuilder$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

check_for_status	<i>Check if the query object ends with a successful response</i>
------------------	--

---

### Description

Checks if a response failed as part of a query.

### Usage

```
check_for_status(query)
```

### Arguments

query	A query object to check the return status of
-------	--

### Value

TRUE if the query succeeded, FALSE otherwise

### Examples

```
library(ArctosR)

# query with an invalid column name 'paarts'
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "paarts", "partdetail")
)

check_for_status(query)
```

---

expand_column	<i>Expand information of columns in JSON format</i>
---------------	---

---

### Description

Expand all information contained in a JSON formatted column in a query object. Information is presented as nested data frames if needed.

### Usage

```
expand_column(query, column_name)
```

### Arguments

query	The query object with a JSON formatted column to be expanded.
column_name	(character) The name of the column to be expanded.

**Value**

Nothing.

**Examples**

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

# The partdetail column is a JSON list of parts and their attributes
# This will convert the column to dataframes:
expand_column(query, "partdetail")
```

---

FromResponseRequestBuilder

*FromResponseRequestBuilder*

---

**Description**

Builder for the case where a request is made with the context of a previous response.

**Super class**

[ArctosR::RequestBuilder](#) -> FromResponseRequestBuilder

**Methods****Public methods:**

- [FromResponseRequestBuilder\\$new\(\)](#)
- [FromResponseRequestBuilder\\$request\\_more\(\)](#)
- [FromResponseRequestBuilder\\$build\\_request\(\)](#)
- [FromResponseRequestBuilder\\$clone\(\)](#)

**Method new():**

*Usage:*

```
FromResponseRequestBuilder$new(response, records)
```

**Method request\_more():** Request at most count more records from this response's original query

*Usage:*

```
FromResponseRequestBuilder$request_more(count)
```

*Arguments:*

count number of additional records to request

*Returns:* FromResponseRequestBuilder

**Method** build\_request(): Perform the request.

*Usage:*

FromResponseRequestBuilder\$build\_request()

*Returns:* Request

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

FromResponseRequestBuilder\$clone(deep = FALSE)

*Arguments:*

deep Whether to make a deep clone.

---

get\_error\_response      *Get the last error message of a query object*

---

**Description**

Returns the error string returned from Arctos if the last response in a query object returned a status code other than HTTP 200 for debugging purposes.

**Usage**

```
get_error_response(query)
```

**Arguments**

query                    A query object to return the error string of

**Value**

The error string of a failing response object, or "No error" if the query didn't fail

**Examples**

```
library(ArctosR)

# query with an invalid column name 'paarts'
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "paarts", "partdetail")
)

get_error_response(query)
```

---

get\_last\_response\_url *Get the last URL used by a request in a query object*

---

**Description**

Returns the last URL used by a request in a query object

**Usage**

```
get_last_response_url(query)
```

**Arguments**

query            A query object to return the URL for

**Value**

The URL of the last performed request in a query object

**Examples**

```
library(ArctosR)

query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

get_last_response_url(query)
```

---

get\_query\_parameters *Get parameters to perform queries*

---

**Description**

Request information about all valid query parameters for querying Arctos.

**Usage**

```
get_query_parameters()
```

**Value**

Data frame listing valid query parameters and associated description and category. The returned columns are: display, obj\_name, category, subcategory, description. All entries in obj\_name are valid parameters to pass to [get\\_records](#) as keys.

**Examples**

```
library(ArctosR)

q <- get_query_parameters()
```

---

get\_records

*Get records from Arctos based on a query*


---

**Description**

Make a request to Arctos to return data based on a query. The columns (fields) returned are specified in the list defined in `columns`. A list of possible query keys can be obtained from the output of [get\\_query\\_parameters](#).

**Usage**

```
get_records(..., api_key = NULL, columns = NULL, limit = NULL,
            filter_by = NULL, all_records = FALSE)
```

**Arguments**

<code>...</code>	Query parameters and their values to pass to Arctos to search. For example, <code>scientific_name = "Canis lupus"</code>
<code>api_key</code>	(character) The API key to use for this request. The default, <code>NULL</code> , uses the package's default API key.
<code>columns</code>	A list of columns to be returned in the table of records to be downloaded from Arctos.
<code>limit</code>	(numeric) The maximum number of records to download at once. Default is 100.
<code>filter_by</code>	An optional list of record attributes to filter results by.
<code>all_records</code>	(logical) If true, the request is performed multiple times to obtain data from Arctos until all records matching the query have been downloaded.

**Value**

A query object consisting of metadata for each request sent to Arctos to fulfill the user's query, and a data frame of records.

**Examples**

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
```

```

  columns = list("guid", "parts", "partdetail")
)

```

---

get\_record\_count      *Count number of records in a query*

---

### Description

Request from Arctos the total number of records that match a specific query. A list of possible query keys can be obtained from the output of [get\\_query\\_parameters](#).

### Usage

```
get_record_count(..., api_key = NULL)
```

### Arguments

...                    Query parameters and their values to pass to Arctos to search. For example, ‘scientific\_name = "Canis lupus"’

api\_key                (character) The API key to use for this request. The default, NULL, uses the package’s default API key.

### Value

The number of records matching the given query, as an integer.

### Examples

```

library(ArctosR)

count <- get_record_count(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm"
)

```

---

get\_result\_parameters    *Get parameters to define valid results in queries*

---

### Description

Request information about all valid result columns to request from Arctos.

### Usage

```
get_result_parameters()
```

**Value**

Data frame listing valid result columns and associated description and category. The returned columns are: `display`, `obj_name`, `query_cost`, `category`, `description`, `default_order`. The names in `obj_name` are passed to `get_records` in the `columns` parameter as a list.

**Examples**

```
library(ArctosR)

r <- get_result_parameters()
```

---

InfoRequestBuilder      *InfoRequestBuilder*

---

**Description**

Builder for a request for query parameter or result parameter documentation from Arctos. For a valid request, only one method to specify the type of request can be called.

**Super class**

`ArctosR::RequestBuilder` -> InfoRequestBuilder

**Methods****Public methods:**

- `InfoRequestBuilder$build_request()`
- `InfoRequestBuilder$clone()`

**Method** `build_request()`:

*Usage:*

```
InfoRequestBuilder$build_request()
```

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
InfoRequestBuilder$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

---

Metadata

*Metadata*

---

### Description

Metadata for a specific HTTP response from Arctos.

### Methods

#### Public methods:

- [Metadata\\$to\\_list\(\)](#)
- [Metadata\\$clone\(\)](#)

#### Method `to_list()`:

*Usage:*

`Metadata$to_list()`

**Method `clone()`:** The objects of this class are cloneable with this method.

*Usage:*

`Metadata$clone(deep = FALSE)`

*Arguments:*

`deep` Whether to make a deep clone.

---

Query

*Query*

---

### Description

The results of a user query. Able to accept multiple responses to increase the record count, or to add columns.

### Methods

#### Public methods:

- [Query\\$catalog\\_request\(\)](#)
- [Query\\$from\\_response\\_request\(\)](#)
- [Query\\$info\\_request\(\)](#)
- [Query\\$perform\(\)](#)
- [Query\\$save\\_metadata\\_json\(\)](#)
- [Query\\$save\\_records\\_csv\(\)](#)
- [Query\\$expand\\_col\(\)](#)
- [Query\\$get\\_responses\(\)](#)

- [Query\\$clone\(\)](#)

**Method** `catalog_request():`

*Usage:*

`Query$catalog_request()`

**Method** `from_response_request():`

*Usage:*

`Query$from_response_request()`

**Method** `info_request():`

*Usage:*

`Query$info_request()`

**Method** `perform():`

*Usage:*

`Query$perform(api_key = NULL)`

**Method** `save_metadata_json():`

*Usage:*

`Query$save_metadata_json(file_path)`

**Method** `save_records_csv():`

*Usage:*

`Query$save_records_csv(file_path, expanded = FALSE)`

**Method** `expand_col():`

*Usage:*

`Query$expand_col(column_name)`

**Method** `get_responses():`

*Usage:*

`Query$get_responses()`

**Method** `clone():` The objects of this class are cloneable with this method.

*Usage:*

`Query$clone(deep = FALSE)`

*Arguments:*

`deep` Whether to make a deep clone.

---

read_response_rds	<i>Read query records previously saved as an RDS file</i>
-------------------	---

---

**Description**

Load in a query object saved to an RDS file.

**Usage**

```
read_response_rds(filename)
```

**Arguments**

filename (character) The name of the file to load in.

**Value**

A query object

**Examples**

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

# Save the data in a .RDS file
save_response_rds(query, "wolves.RDS")

# Load the data from the .RDS just saved
read_response_rds("wolves.RDS")
```

---

Records	<i>Records</i>
---------	----------------

---

**Description**

A (possibly nested) data frame of records returned by a static set of query and result parameters

## Methods

### Public methods:

- [Records\\$new\(\)](#)
- [Records\\$append\(\)](#)
- [Records\\$save\\_flat\\_csv\(\)](#)
- [Records\\$save\\_nested\\_csvs\(\)](#)
- [Records\\$expand\\_col\(\)](#)
- [Records\\$clone\(\)](#)

### Method new():

*Usage:*

```
Records$new(df, tbl)
```

### Method append():

*Usage:*

```
Records$append(other)
```

**Method save\_flat\_csv():** Writes the data in the response object to a CSV file.

*Usage:*

```
Records$save_flat_csv(file_path)
```

### Method save\_nested\_csvs():

*Usage:*

```
Records$save_nested_csvs(file_path)
```

**Method expand\_col():** Expand a column of nested JSON tables in the response to a list of dataframes.

*Usage:*

```
Records$expand_col(column)
```

*Arguments:*

```
col (string)
```

**Method clone():** The objects of this class are cloneable with this method.

*Usage:*

```
Records$clone(deep = FALSE)
```

*Arguments:*

```
deep Whether to make a deep clone.
```

---

Request

*Request*

---

## Description

A generic Arctos request. Not intended to be used directly. See `InfoRequestBuilder` and `CatalogRequestBuilder`.

## Methods

### Public methods:

- `Request$with_endpoint()`
- `Request$add_param()`
- `Request$add_params()`
- `Request$serialize()`
- `Request$perform()`
- `Request$from_raw_response()`
- `Request$clone()`

### Method `with_endpoint()`:

*Usage:*

```
Request$with_endpoint(endpoint)
```

### Method `add_param()`:

*Usage:*

```
Request$add_param(...)
```

### Method `add_params()`:

*Usage:*

```
Request$add_params(l)
```

### Method `serialize()`:

*Usage:*

```
Request$serialize()
```

### Method `perform()`:

*Usage:*

```
Request$perform(api_key = NULL)
```

### Method `from_raw_response()`:

*Usage:*

```
Request$from_raw_response(raw_response)
```

**Method `clone()`:** The objects of this class are cloneable with this method.

*Usage:*

```
Request$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

RequestBuilder

*RequestBuilder*

---

**Description**

A builder for a generic Arctos request. Not to be used directly.

**Methods****Public methods:**

- [RequestBuilder\\$debug\(\)](#)
- [RequestBuilder\\$build\\_request\(\)](#)
- [RequestBuilder\\$clone\(\)](#)

**Method** `debug()`: Turn on printing of debug information.

*Usage:*

```
RequestBuilder$debug()
```

**Method** `build_request()`:

*Usage:*

```
RequestBuilder$build_request()
```

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
RequestBuilder$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

Response

*Response*

---

## Description

Response returned from Arctos.

## Methods

### Public methods:

- [Response\\$new\(\)](#)
- [Response\\$set\\_start\\_index\(\)](#)
- [Response\\$was\\_success\(\)](#)
- [Response\\$is\\_empty\(\)](#)
- [Response\\$has\\_json\\_content\(\)](#)
- [Response\\$to\\_list\(\)](#)
- [Response\\$to\\_records\(\)](#)
- [Response\\$clone\(\)](#)

### Method new():

*Usage:*

`Response$new(request, raw_response)`

### Method set\_start\_index():

*Usage:*

`Response$set_start_index(start)`

### Method was\_success():

*Usage:*

`Response$was_success()`

### Method is\_empty():

*Usage:*

`Response$is_empty()`

### Method has\_json\_content():

*Usage:*

`Response$has_json_content()`

### Method to\_list():

*Usage:*

`Response$to_list()`

### Method to\_records():

*Usage:*

```
Response$to_records(start = 0)
```

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```
Response$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

response\_data

*Get query records as a data frame*

---

## Description

Obtain the data frame with the records from a successful query.

## Usage

```
response_data(query)
```

## Arguments

query            The query object to extract the data frame from.

## Value

A data frame with the information requested in the query.

## Examples

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

# Grab the dataframe of records from the query
df <- response_data(query)
```

---

save_response_csv	<i>save_response_csv</i>
-------------------	--------------------------

---

### Description

Save the records inside the query object as a CSV file, optionally alongside metadata relating to the requests made to download the data.

### Usage

```
save_response_csv(query, filename, expanded = FALSE, with_metadata = TRUE)
```

### Arguments

query	The query object to be saved
filename	(character) Name of the file to be saved.
expanded	(logical) Setting this option to TRUE will create a folder of CSVs representing hierarchical data. See details.
with_metadata	Whether to save the metadata of the response as a JSON file along side the CSV or folder of CSVs.

### Details

Some columns from Arctos are themselves tables, so to accurately represent the structure of the data, these inner tables can be saved as separate CSVs that are named according to which record they belong.

### Value

Nothing.

### Examples

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

# Save the response in a flat CSV with an additional metadata file in JSON
save_response_csv(query, "msb-wolves.csv", with_metadata = TRUE)
```

---

save\_response\_rds      *Write query records as an RDS file*

---

**Description**

Save the query object as an RDS file, which stores the entire state of the query and can be loaded at a later time.

**Usage**

```
save_response_rds(query, filename)
```

**Arguments**

query	The query object to be saved.
filename	(character) Name of the file to be saved.

**Value**

Nothing.

**Examples**

```
library(ArctosR)

# Request to download all available data
query <- get_records(
  scientific_name = "Canis lupus", guid_prefix = "MSB:Mamm",
  columns = list("guid", "parts", "partdetail")
)

# Save the data in a .RDS file
save_response_rds(query, "wolves.RDS")
```

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