Package ‘worrms’

July 8, 2020

Type Package

Title World Register of Marine Species (WoRMS) Client

Description Client for World Register of Marine Species
(<http://www.marinespecies.org/>). Includes functions for each
of the API methods, including searching for names by name, date and
common names, searching using external identifiers, fetching
synonyms, as well as fetching taxonomic children and
taxonomic classification.

Version 0.4.2

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URL https://docs.ropensci.org/worrms,
    https://github.com/ropensci/worrms (devel), https://taxize.dev
    (user manual)

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

LazyData true

VignetteBuilder knitr

Encoding UTF-8

Language en-US

Imports crul (>= 0.6.0), tibble (>= 1.2), jsonlite (>= 1.1),
data.table

Suggests roxygen2 (>= 7.1.0), knitr, rmarkdown, testthat, vcr (>=
0.2.0)

RoxygenNote 7.1.0

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    worms, species

X-schema.org-isPartOf https://ropensci.org

NeedsCompilation no

Author Scott Chamberlain [aut, cre] (<https://orcid.org/0000-0003-1444-9135>)
Description

World Register of Marine Species Client

Fail behavior

The WoRMS REST API doesn’t have sophisticated error messaging, so most errors will result in a (204) - No Content or in (400) - Bad Request

Because WoRMS doesn’t do comprehensive error reporting, we do a fair amount of checking user inputs to help prevent errors that will be meaningless to the user. Let us know if we can improve on this.
Author(s)
Scott Chamberlain <myrmecocystus@gmail.com>

wm_attr_aphia

Get AphiaIDs by attribute definition ID

Usage

wm_attr_aphia(id, offset = 1, ...)

wm_attr_aphia_(id = NULL, name = NULL, ...)

Arguments

id (numeric/integer) a attribute ID. For wm_attr_aphia it's required and must be
length(id) == 1, for wm_attr_aphia_ it's optional and can be length(id) >= 1

offset (integer) record to start at. default: 1

... named curl options. see curl::curl_options

name (character) one or more taxonomic names. optional

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together,
but can be split by id column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the
relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.
The sister function with the underscore at the end is the plural version, accepting more than one
input. Internally this function loops over the non-underscore method, and labels output (whether
it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by
your inputs.
Examples

```r
## Not run:
w_m_attr_aphia(id = 7)
w_m_attr_aphia(id = 4)
w_m_attr_aphia(id = 4, offset = 50)
w_m_attr_aphia_(id = c(7, 2))
## End(Not run)
```

wm_attr_category

Get attributes grouped by a CategoryID

Description

Get attributes grouped by a CategoryID

Usage

```r
wm_attr_category(id, ...)
w_m_attr_category_(id = NULL, name = NULL, ...)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>(numeric/integer) a CategoryID. For <code>wm_attr_category</code> it’s required and must be <code>length(id) == 1</code>, for <code>wm_attr_category_</code> it’s optional and can be <code>length(id) &gt;= 1</code></td>
</tr>
<tr>
<td>...</td>
<td>named curl options. see <code>curl::curl_options</code></td>
</tr>
<tr>
<td>name</td>
<td>(character) one or more taxonomic names. optional</td>
</tr>
</tbody>
</table>

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relavant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_attr_data

Examples

```r
## Not run:
wm_attr_category(id = 7)
wm_attr_category(id = 2)
wm_attr_category_(id = c(7, 2))
## End(Not run)
```

wm_attr_data

Get attribute data by AphiaID

Description

Get attribute data by AphiaID

Usage

```r
wm_attr_data(id, include_inherited = FALSE, ...)
wm_attr_data_(id = NULL, name = NULL, ...)
```

Arguments

- `id` (numeric/integer) an AphiaID. For `wm_attr_data` it’s required and must be `length(id) == 1`, for `wm_attr_data_` it’s optional and can be `length(id) >= 1`
- `include_inherited` (logical) Include attributes inherited from its parent taxon. Default: `FALSE`
- `...` named curl options. see `curl::curl_options`
- `name` (character) one or more taxonomic names. optional

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by `id` column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_attr_def

Examples

```r
## Not run:
wm_attr_data(id = 127160)
wm_attr_data(id = 126436)

wm_attr_data_(id = c(127160, 126436))

## End(Not run)
```

---

**wm_attr_def**  Get attribute definition by ID

Description

Get attribute definition by ID

Usage

```r
wm_attr_def(id, include_inherited = FALSE, ...)
wm_attr_def_(id = NULL, name = NULL, ...)
```

Arguments

- **id** (numeric/integer) an attribute ID. For `wm_attr_def` it’s required and must be `length(id) == 1`, for `wm_attr_def_` it’s optional and can be `length(id) >= 1`
- **include_inherited** (logical) Include attributes inherited from its parent taxon. Default: `FALSE`
- **...** named curl options. see `curl::curl_options`
- **name** (character) one or more taxonomic names. optional

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by `id` column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_children

Examples

## Not run:
wm_attr_def(id = 1)
wmm_attr_def(id = 4)
wmm_attr_def(id = 4, include_inherited = TRUE)

wm_attr_def_(id = c(4, 1))

## End(Not run)

wm_children

Get children for an AphiaID

Description

Get children for an AphiaID

Usage

wm_children(id, marine_only = TRUE, offset = 1, ...)

wm_children_(id = NULL, name = NULL, marine_only = TRUE, offset = 1, ...)

Arguments

id (numeric/integer) an AphiaID. For wm_children it's required and must be length(id) == 1, for wm_children_ it's optional and can be length(id) >= 1

marine_only (logical) marine only or not. default: TRUE

offset (integer) record to start at. default: 1

name (character) one or more taxonomic names. optional

... named curl options. see curl::curl_options

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relavant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
Examples

```r
## Not run:
wm_children(343613)
w_om_children(id = 105706)
w_om_children(id = 105706, FALSE)
w_om_children(id = 105706, offset = 5)

# plural version, via id or name
wm_children_(id = c(105706, 343613))
w_om_children_(name = c('Mesodesma', 'Leucophaeus'))

## End(Not run)
```

wm_classification

Get classification for an AphiaID

Description

Get classification for an AphiaID

Usage

```r
wm_classification(id, ...)
wm_classification_(id = NULL, name = NULL, ...)
```

Arguments

- `id` (numeric/integer) an AphiaID. For `wm_children` it's required and must be `length(id) == 1`, for `wm_children_` it's optional and can be `length(id) >= 1`
- `...` named curl options. see `curl::curl_options`
- `name` (character) one or more taxonomic names. optional

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by `id` column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_common_id

Examples

```r
## Not run:
wm_classification(id = 105706)
wm_classification(id = 126436)

wm_classification(254967)
wm_classification(344089)

# plural version, via id or name
wm_classification_(id = c(254967, 344089))
wm_classification_(name = c('Platanista gangetica', 'Leucophaeus scoresbii'))

## End(Not run)
```

wm_common_id  

Get vernacular names from an AphialID

Description
Get vernacular names from an AphialID

```r
wm_common_id(id, ...)

wm_common_id_(id = NULL, name = NULL, ...)
```  

Arguments

- `id`  
  (numeric/integer) an AphialID. For `wm_common_id` it's required and must be `length(id) == 1`, for `wm_common_id_` it's optional and can be `length(id) >= 1`

- `...`  
  named curl options. see `curl::curl_options`

- `name`  
  (character) one or more taxonomic names. optional

Value
A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by `id` column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphialID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_distribution

Get distribution data by AphiaID

Description
Get distribution data by AphiaID

Usage
wm_distribution(id, ...)

wm_distribution_(id = NULL, name = NULL, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>(numeric/integer) an AphiaID. For <code>wm_distribution</code> it's required and must be <code>length(id) == 1</code>, for <code>wm_distribution_</code> it's optional and can be <code>length(id) &gt;= 1</code></td>
</tr>
<tr>
<td>...</td>
<td>named curl options. see <code>curl::curl_options</code></td>
</tr>
<tr>
<td>name</td>
<td>(character) one or more taxonomic names. optional</td>
</tr>
</tbody>
</table>

Value
A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural
Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Examples
## Not run:
wm_common_id(id = 105706)
wmm_common_id(id = 156806)
wmm_common_id(id = 397065)

wm_common_id_(id = c(105706, 156806, 397065))

nms <- c("Rhincodontidae", "Mesodesma deauratum", "Cryptomya californica")
wmm_common_id_(name = nms)

## End(Not run)
wm_external

Examples

```r
## Not run:
wm_distribution(id = 156806)
wm_distribution(id = 126436)

wm_distribution_(id = c(156806, 126436))

## End(Not run)
```

wm_external

Get an external ID via an AphiaID

Description

Get an external ID via an AphiaID

Usage

```r
wm_external(id, type = "tsn", ...)

wm_external_(id = NULL, name = NULL, type = "tsn", ...)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>(numeric/integer) an AphiaID. For <code>wm_external</code> it’s required and must be <code>length(id) == 1</code>, for <code>wm_external_</code> it’s optional and can be <code>length(id) &gt;= 1</code></td>
</tr>
<tr>
<td>type</td>
<td>(character) the type of external id. one of: tsn, bold, dyntaxa, eol, fishbase, iucn, lsid, ncbi, gisd. default: tsn</td>
</tr>
<tr>
<td>...</td>
<td>named curl options. see <code>curl::curl_options</code></td>
</tr>
<tr>
<td>name</td>
<td>(character) one or more taxonomic names. optional</td>
</tr>
</tbody>
</table>

Value

An integer that is the ID. When using underscore method, a list, named by the input IDs

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
Examples

## Not run:
# by default, get a TSN (an ITIS code)
wm_external(id = 1080)

## get many
wm_external_(id = c(1080, 126436))

# BOLD code
wm_external(id = 278468, type = "bold")

# NCBI code
wm_external(id = 278468, type = "ncbi")

# fishbase code
wm_external(id = 278468, type = "fishbase")

# curl options
library(crul)
wm_external(id = 105706, verbose = TRUE)

## End(Not run)

---

wm_id2name  
Get taxonomic name for an AphiaID

Description

Get taxonomic name for an AphiaID

Usage

wm_id2name(id, ...)
wm_id2name_(id, ...)

Arguments

id (numeric/integer) an AphiaID, required. For wm_id2name must be length(id) == 1, but for wm_id2name_ can be length(id) >= 1
... named curl options. see curl::curl_options

Value

An character string that is the taxonomic name. When using underscore method, a list, named by the input IDs
**Singular vs. plural**

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

**Examples**

```r
# Not run:
wm_id2name(id = 105706)
wm_id2name_(id = c(105706, 126436))

# End(Not run)
```

---

**wm_name2id**

*Get AphiaID from a taxonomic name*

**Description**

Get AphiaID from a taxonomic name

**Usage**

```r
wm_name2id(name, ...)
wm_name2id_(name, ...)
```

**Arguments**

- `name` (character) a taxonomic name, required. For `wm_name2id` must be `length(name) == 1`, but for `wm_name2id_` can be `length(name) >= 1`
- `...` named curl options. see `curl::curl_options`

**Value**

An integer that is the AphiaID. When using underscore method, a list, named by the input names

**Singular vs. plural**

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.
wm_ranks

Get taxonomic ranks by their identifier

Description

Get taxonomic ranks by their identifier

Usage

wm_ranks_id(rank_id, id = NULL, offset = 1, ...)

wm_ranks_name(rank_name, id = NULL, offset = 1, ...)

Arguments

rank_id (numeric/integer) a rank identifier. length==1
id an AphiaID. length==1
offset (integer) record to start at. default: 1
... named curl options. see curl::curl_options
rank_name (character) a rank name. length==1

Value

A tibble/data.frame

Examples

## Not run:
wm_ranks_id(220)
wm_ranks_id(180)
wm_ranks_id(180, id = 4)
wm_ranks_name("genus")
wm_ranks_name("genus", id = 4)

## End(Not run)
wm_record

Get complete AphiaRecord for an AphiaID

Description

Get complete AphiaRecord for an AphiaID

Usage

wm_record(id, ...)

wm_record_(id = NULL, name = NULL, ...)

Arguments

id (numeric/integer) an AphiaID. For wm_record it's required and must be length(id) == 1, for wm_record_ it's optional and can be length(id) >= 1

... named curl options. see curl::curl_options

name (character) one or more taxonomic names. optional

Value

A named list. When using underscore method, each output is named by the input ID, and can be separated by the list names

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Note

wm_record_ is defunct, wm_record can do plural requests now

Examples

```r
## Not run:
wm_record(id = 105706)
wm_record(id = c(105706, 126436))
wm_record_(id = c(105706, 126436))

## End(Not run)
```
wm_records_common  
Get records by vernacular name, optional fuzzy matching

Description
Get records by vernacular name, optional fuzzy matching

Usage
wm_records_common(name, fuzzy = FALSE, offset = 1, ...)
wm_records_common_(name, fuzzy = FALSE, offset = 1, ...)

Arguments
name (character) a species common name. required. For `wm_records_common` must be length(name) == 1; for `wm_records_common_` can be length(name) >= 1
fuzzy (logical) fuzzy search. default: FALSE
offset (integer) record to start at. default: 1
... named curl options. see `curl::curl_options`

Value
A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural
Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.
The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Examples
```r
## Not run:
wm_records_common(name = 'dolphin')
wm_records_common(name = 'clam')
wm_records_common_(name = c('dolphin', 'clam'))
wm_records_common(name = 'dolphin', fuzzy = TRUE)
wm_records_common(name = 'clam', fuzzy = TRUE, offset = 5)
## End(Not run)
```
wm_records_date

Get records by date

Description
Get records by date

Usage
wm_records_date(
  start_date,
  end_date = NULL,
  marine_only = TRUE,
  offset = 1,
  ...
)

Arguments
start_date (character) start date. required.
end_date (character) end date. optional
marine_only (logical) marine only or not. default: TRUE
offset (integer) record to start at. default: 1
... named curl options. see curl::curl_options

Value
A tibble/data.frame

Examples
## Not run:
a_date <- format(Sys.Date() - 1, "%Y-%m-%dT%H:%M:%S+00:00")
wm_records_date(a_date)

## End(Not run)
wm_records_name

Get records by single name, optional fuzzy matching

Description

Get records by single name, optional fuzzy matching

Usage

wm_records_name(name, fuzzy = TRUE, marine_only = TRUE, offset = 1, ...)

Arguments

name  (character) a taxonomic name, required.
fuzzy  (logical) fuzzy search. default: TRUE
marine_only  (logical) marine only or not. default: TRUE
offset  (integer) record to start at. default: 1
...  named curl options. see curl::curl_options

Value

A tibble/data.frame

Note

there is no underscore method like other functions in this package as there is already a plural version:
wm_records_names()

Examples

## Not run:
wm_records_name(name = 'Leucophaeus')
wm_records_name(name = 'Leucophaeus', fuzzy = FALSE)
wm_records_name(name = 'Leucophaeus', marine_only = FALSE)
wm_records_name(name = 'Platanista', marine_only = FALSE)
wm_records_name(name = 'Platanista', marine_only = FALSE, offset = 5)

## End(Not run)
wm_records_names

Get records for one or more taxonomic name(s)

Description
Get records for one or more taxonomic name(s)

Usage
wm_records_names(name, fuzzy = FALSE, marine_only = TRUE, ...)

Arguments
name (character) start date. required.
fuzzy (logical) fuzzy search. default: FALSE
marine_only (logical) marine only or not. default: TRUE
... named curl options. see curl::curl_options

Value
A list of tibble’s/data.frame’s, one for each of the input names

Note
there is no underscore method like other functions in this package as this is the plural version for
wm_records_name()

Examples
## Not run:
wm_records_names(name = 'Leucophaeus scoresbii')
wm_records_names(name = 'Leucophaeus scoresbii', fuzzy = TRUE)
wm_records_names(name = c('Leucophaeus scoresbii', 'Coryphaena'))

## End(Not run)
wm_records_rank

Get AphiaRecords for a given taxonRankID

Description

Get AphiaRecords for a given taxonRankID

Usage

wm_records_rank(rank_id, id = NULL, offset = 1, ...)

Arguments

  rank_id     (numeric/integer) a rank id
  id          (character) a single AphialD
  offset      (integer) record to start at. default: 1
  ...         named curl options. see curl::curl_options

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relavant WoRMS API method - and only accepts one thing (i.e., name or AphialD) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Examples

## Not run:
wm_records_rank(rank_id = 180, id = 106776)
wm_records_rank(rank_id = 180, id = 106776, offset = 50)

## End(Not run)
wm_records_taxamatch  

Get records for one or more taxonomic name(s) using the TAXAMATCH fuzzy matching algorithm

Description

Get records for one or more taxonomic name(s) using the TAXAMATCH fuzzy matching algorithm

Usage

wm_records_taxamatch(name, marine_only = TRUE, ...)

Arguments

name  

(character) taxon name. required.

marine_only  

(logical) marine only or not. default: TRUE

...  

named curl options. see curl::curl_options

Value

A list of tibble's/data.frame's, one for each of the input names

Note

there is no underscore method like other functions in this package as this function already accepts many names

Examples

## Not run:
wm_records_taxamatch(name = 'Leucophaeus')
wm_records_taxamatch(name = c('Leucophaeus', 'Coryphaena'))

## End(Not run)

wm_record_by_external  

Get record by external ID

Description

Get record by external ID
Usage

wm_record_by_external(id, type = "tsn", ...)
wm_record_by_external_(id = NULL, name = NULL, type = "tsn", ...)

Arguments

id (numeric/integer) an AphiaID. For `wm_record_by_external` it's required and must be `length(id) == 1`, for `wm_record_by_external_` it's optional and can be `length(id) >= 1`

type (character) the type of external id. one of: tsn, bold, dyntaxa, eol, fishbase, iucn, lsid, ncbi, gisd. default: tsn

... named curl options. see `curl::curl_options`

name (character) one or more taxonomic names. optional

Value

A named list. When using underscore method, each output is named by the input ID, and can be separated by the list names

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it's a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Examples

```r
## Not run:
wm_record_by_external(id = 85257)
wms_record_by_external(id = 159854)
wms_record_by_external_(id = c(85257, 159854))
## End(Not run)
```

wm_sources

Get sources for an AphiaID

Description

Get sources for an AphiaID
**wm_synonyms**

**Usage**

```r
wm_sources(id, ...)  
wm_sources_(id = NULL, name = NULL, ...)
```

**Arguments**

- **id** (numeric/integer) an AphiaID. For `wm_sources` it’s required and must be `length(id) == 1`, for `wm_sources_` it’s optional and can be `length(id) >= 1`
- **...** named curl options. see `curl::curl_options`
- **name** (character) one or more taxonomic names. optional

**Value**

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by `id` column

**Singular vs. plural**

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request.

The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

**Examples**

```r
## Not run:  
wm_sources(id = 105706)  
wm_sources_(id = 105706)  
wm_sources_(id = c(105706, 126436))  
wm_sources_(name = c("Rhincodontidae", "Gadus morhua"))
## End(Not run)
```

---

**wm_synonyms**  
*Get synonyms for an AphiaID*

**Description**

Get synonyms for an AphiaID

**Usage**

```r
wm_synonyms(id, offset = 1, ...)  
wm_synonyms_(id = NULL, name = NULL, ...)
```
Arguments

id (numeric/integer) an AphiaID. For `wm_synonyms` it’s required and must be `length(id) == 1`, for `wm_synonyms_` it’s optional and can be `length(id) >= 1`

offset (integer) record to start at. default: 1

... named curl options. see `curl::curl_options`

name (character) one or more taxonomic names. optional

Value

A tibble/data.frame. when using underscore method, outputs from each input are binded together, but can be split by id column

Singular vs. plural

Of the two sister functions, the one without the underscore is the original function that wraps the relevant WoRMS API method - and only accepts one thing (i.e., name or AphiaID) per request. The sister function with the underscore at the end is the plural version, accepting more than one input. Internally this function loops over the non-underscore method, and labels output (whether it’s a list or data.frame rows) with the input names or IDs so that you can easily parse output by your inputs.

Examples

```r
## Not run:
wm_synonyms(id = 105706)
wm_synonyms_(id = 105706)
wm_synonyms(id = 126436)
wm_synonyms(id = 126436, offset = 10)
wm_synonyms_(id = c(105706, 126436))

## End(Not run)
```
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