

Package ‘AntWeb’

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Type Package

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Title programmatic interface to the AntWeb

Description A complete programmatic interface to the AntWeb database from the California Academy of Sciences.

Version 0.7

Depends R (>= 3.0.1)

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URL <https://github.com/ropensci/AntWeb>

BugReports <https://github.com/ropensci/AntWeb/issues>

LazyData true

Imports rjson, plyr, assertthat, httr, leafletR (>= 0.1-1)

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AntWeb	<i>AntWeb</i>
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Description

AntWeb

Details

The **AntWeb** world's largest online database of images, specimen records, and natural history information on ants. The database is maintained and hosted by the **California Academy of Sciences**.

aw_cbind	<i>aw_cbind</i>
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Description

Allows for combining split AntWeb calls (e.g. paginated calls) back into one single result object

Usage

```
aw_cbind(results)
```

Arguments

results A list of objects of class antweb

Examples

```
## Not run:  
x1 <- aw_data(genus = "crematogaster", georeferenced = TRUE)  
x2 <- aw_data(genus = "crematogaster", georeferenced = TRUE, offset = 1000)  
x12 <- aw_cbind(list(x1, x2))  
  
## End(Not run)
```

aw_code	<i>aw_code</i>
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Description

Retrieve data by specimen id

Usage

```
aw_code(occurrenceid = NULL, catalogNumber = NULL)
```

Arguments

occurrenceid	A unique id in the AntWeb database identifying a particular specimen
catalogNumber	Specimen catalogue number

Value

list

See Also

[aw_data](#)

Examples

```
# data_by_code <- aw_code(occurrenceid = "CAS:ANTWEB:alas188691")
# data_by_code <- aw_code(catalognumber="inb0003695883")
```

aw_coords	<i>aw_coords</i>
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Description

Retrieve AntWeb data by location. A radius argument can be supplied as a search radius around a point on the map.

Usage

```
aw_coords(coord = NULL, r = NULL)
```

Arguments

coord	Latitude and Longitude. Should be supplied as lat, long. Example: 37.76, -122.45
r	A radius in kilometers. For 2 km add r = 2

Value`aw_data`**Examples**

```
# data_by_loc <- aw_coords(coord = "37.76,-122.45", r = 2)
```

<code>aw_data</code>	<i>Retrieve data from the AntWeb</i>
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Description

This function allows a user to query the AntWeb database by any taxonomic rank or full species name.

Usage

```
aw_data(genus = NULL, species = NULL, scientific_name = NULL,
        georeferenced = NULL, min_elevation = NULL, max_elevation = NULL,
        type = NULL, habitat = NULL, country = NULL, min_date = NULL,
        max_date = NULL, bbox = NULL, limit = NULL, offset = NULL,
        quiet = FALSE)
```

Arguments

<code>genus</code>	An ant genus name
<code>species</code>	a species name
<code>scientific_name</code>	An easier way to pass the Genus and species name together, especially when the data are derived from other packages.
<code>georeferenced</code>	Default is FALSE. Set to TRUE to return only data with lat/long information. Note that this filtering takes place on the client-side, not server side.
<code>bbox</code>	A lat long bounding box. Format is lat, long, lat, long. Use this website: http://boundingbox.klokantech.com/ to quickly grab a bbox (set format on bottom left to csv and be sure to switch the order from long, lat, long, lat to lat, long, lat, long) Just set the format on the bottom left to CSV.
<code>type</code>	A holotype
<code>habitat</code>	A fuzzy search by any habitat
<code>country</code>	A country name
<code>min_date</code>	A lower date bound in the format yyyy-mm-dd
<code>max_date</code>	An upper date bound in the format yyyy-mm-dd
<code>min_elevation</code>	A lower elevation bound
<code>max_elevation</code>	An upper elevation bound
<code>limit</code>	A numeric value to limit number of records
<code>offset</code>	An offset best used with limit as a way to paginate records
<code>quiet</code>	If true, any informative messages will be suppressed

Value

data.frame

Examples

```
# data <- aw_data(genus = "acanthognathus", species = "brevicornis")
# data3 <- aw_data(genus = "acanthognathus", species = "brevicornis", georeferenced = TRUE)
# data2 <- aw_data(scientific_name = "acanthognathus brevicornis")
# sandstone <- aw_data(genus = "Aphaenogaster", habitat = "sandstone")
# data_genus_only <- aw_data(genus = "acanthognathus", limit = 25)
# leaf_cutter_ants <- aw_data(genus = "acromyrmex")
# data <- aw_data(genus = "Technomyrmex", bbox = '37.77,-122.46,37.76,-122.47')
# Search just using a bounding box
# data <- aw_data(bbox = '37.77,-122.46,37.76,-122.47')
# Search by a elevation band
# aw_data(min_elevation = 1500, max_elevation = 2000)
# When you throw a really specimen rich band like below, you'll get a huge number of requests.
# Only the first 1000 records will download first.
# aw_data(min_elevation = 200, max_elevation = 400)
# aw_data(min_date = '1980-01-01', max_date = '1981-01-01')
# fail <- aw_data(scientific_name = "auberti levithorax") # This should fail gracefully
```

aw_data_all

Download all aw_data available for any request

Description

This is a thin wrapper around aw_data

Usage

```
aw_data_all(..., progress = "text")
```

Arguments

...	All the same arguments that get passed to aw_data
progress	Default is on and set to text. Set to none to suppress

See Also

aw_data

Examples

```
## Not run:
# crem <- aw_data_all(genus = "crematogaster", georeferenced = TRUE)

## End(Not run)
```

aw_distinct

aw_distinct

Description

Retrieves a data.frame of distinct ranks based on various restrictions

Usage

```
aw_distinct(rank = "genus", habitat = NULL, country = NULL,
  min_elevation = NULL, max_elevation = NULL, limit = 1000,
  offset = NULL)
```

Arguments

rank	= "genus" Default is genus. But you can also use phylum, sub-phylum etc
habitat	The habitat type
country	Country name
min_elevation	Min elevation recorded for specimen
max_elevation	Max elevation recorded for specimen
limit	= 1000 Default limit. Set higher if necessary
offset	To be used in conjunction with limit

Examples

```
## Not run:
aw_distinct(rank = "genus", country = "Madagascar")

## End(Not run)
```

aw_images

aw_images

Description

Download ant images based on time elapsed and/or type.

Usage

```
aw_images(since = NULL, img_type = NULL)
```

Arguments

since number of days in the past to query
img_type h for head, d for dorsal, p for profile, and l for label. If a img_type is not specified, all images are retrieved.

Value

data.frame

Examples

```
## Not run:
z <- aw_images(since = 5)
z1 <- aw_images(since = 5, img_type = "d")

## End(Not run)
```

aw_map	<i>LeafletJS Map</i>
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Description

Builds an interactive map of locations for any list of species

Usage

```
aw_map(aw_obj, dest = tempdir(), title = "AntWeb species map",
incl.data = TRUE)
```

Arguments

aw_obj Result from a search on AntWeb
dest Location where the html file and geojson file should be stored. Default is the temp directory
title Title of the map.
incl.data Default is TRUE. Writes geoJSON data into the html file to get around security restrictions in browsers like Google Chrome. Set to FALSE to read from a separate local geoJSON file.

Examples

```
## Not run:
acanthognathus_df <- aw_data(genus = "acanthognathus", georeferenced = TRUE)
aw_map(acanthognathus_df)
# Or just plot data by habitat. So for e.g. using sandstone as a substrate
sandstone <- aw_data(habitat = "sandstone")
aw_map(sandstone)

## End(Not run)
```

aw_unique *aw_unique*

Description

Get a list of unique names within any taxonomic rank

Usage

```
aw_unique(rank = NULL, name = NULL)
```

Arguments

rank	A taxonomic rank. Allowed values are subfamily, genus or species
name	Optional. If left blank, the query will return a list of all unique names inside the supplied rank.

Value

data.frame

See Also

[aw_data](#)

Examples

```
## Not run:  
subfamily_list <- aw_unique(rank = "subfamily")  
# genus_list <- aw_unique(rank = "genus")  
# species_list <- aw_unique(rank = "species")  
  
## End(Not run)
```

print.antweb *Print a summary for an antweb object*

Description

Print a summary for an antweb object

Usage

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


print.antweb

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Arguments

x	An object of class antweb
...	additional arguments

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