

Package ‘raquamaps’

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Type Package

Title Aqua Maps Implemented Using R

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URL <https://github.com/raquamaps/raquamaps>

BugReports <https://github.com/raquamaps/raquamaps/issues>

Description This package is a programmatic interface to Aquamaps.org

LazyData true

Depends R (>= 3.0)

Imports stringr (>= 1.0.0),
crayon (>= 1.3.1),
RColorBrewer (>= 1.1),
methods,
utils,
RSQLite (>= 1.0.0),
foreign (>= 0.8),
raster (>= 2.5),
sp (>= 1.2),
rgdal (>= 1.1),
classInt (>= 0.1),
rgbif (>= 0.9),
leaflet (>= 1.0.0),
shiny (>= 0.13.0),
shinythemes (>= 1.0.1),
DT (>= 0.1),
ggplot2 (>= 2.0.0),
ggthemes (>= 3.0.1),
ggmap (>= 2.6.1),
maps (>= 3.1.0),
tufte (>= 0.2),

```

purrr (>= 0.2.1),
httr (>= 1.0.0),
dplyr (>= 0.4.0),
tidyr (>= 0.4.1),
reshape2 (>= 1.4),
xml2 (>= 0.1.2),
rvest (>= 0.3.1)

```

Suggests devtools,
testthat,
knitr,
rmarkdown

VignetteBuilder knitr

RoxygenNote 5.0.1

R topics documented:

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raqumaps-package	<i>raqumaps</i>
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Description

raqumaps provides tools that make it easier to produce Aqua Maps.

Details

AquaMaps is a project involving tools for generating model-based, large-scale predictions of natural occurrences of species. For marine species, the model uses estimates of environmental preferences with respect to depth, water temperature, salinity, primary productivity, and association with sea ice or coastal areas. These estimates of species preferences, called environmental envelopes, are derived from large sets of occurrence data available from online collection databases.

References

Kaschner, K., R. Watson, A.W. Trites and D. Pauly. 2006. Mapping worldwide distributions of marine mammals using a Relative Environmental Suitability (RES) model. *Mar. Ecol. Prog. Ser.* 316:285-310.

Ready, J., K. Kaschner, A.B. South, P.D. Eastwood, T. Rees, J. Rius, E. Agbayani, S. Kullander, and R. Froese. 2010. Predicting the distributions of marine organisms at the global scale. *Ecol. Model.* 221: 467-478, doi:10.1016/j.ecolmodel.2009.10.025

Kesner-Reyes, K., K. Kaschner, S. Kullander, C. Garilao, J. Barile, and R. Froese. 2012. AquaMaps: algorithm and data sources for aquatic organisms. In: Froese, R. and D. Pauly. Editors. 2012. Fish-Base. World Wide Web electronic publication. www.fishbase.org, version (04/2012).

Östergren J, Kullander S O, Prud’homme O, Reyes K K, Kaschner K and Froese R (in preparation) Predicting freshwater-dependent species distributions in Europe

Examples

#see functions.

adjust_spreads	<i>Adjustment of climate summary stat values during envelope parameter calculation</i>
----------------	--

Description

This function takes a data frame with bioclimate parameter spread data and returns a similar data frame but with various adjustments for extreme values. This function works using a set of correction rules defined inline and reflecting adjustment limits as described in a separate paper (ref: Tamas Jantevik)

Usage

```
adjust_spreads(spreads)
```

Arguments

spreads	data frame with spread data to adjust
---------	---------------------------------------

Examples

```
## Not run:
adjusted_spreads <- adjust_spreads(spreads)

## End(Not run)
```

aquamaps_galemys_pyrenaicus	<i>Example grid cell data for one specific species (Galemys pyrenaicus), approx 359 rows</i>
-----------------------------	--

Description

A dataset that should be possible to get from rgbif, should show how to do it.

Usage

```
aquamaps_galemys_pyrenaicus
```

Format

A data frame [359 x 5]

CsquareCod CsquareCod

LOICZID LOICZID

InBasin InBasin

GoodCell GoodCell

Species Species ...

Source

<https://www.aquamaps.org/>

aquamaps_hc

Half degree cell metadata (only identifiers and coordinates)

Description

A dataset containing metadata such as identifiers (CsquareCod, LOICZID) and bbox coords

Usage

aquamaps_hc

Format

A data frame [8,593 x 12]

CsquareCod CsquareCod

LOICZID LOICZID

NLimit NLimit

Slimit Slimit

WLimit WLimit

ELimit ELimit

CenterLat CenterLat

CenterLong CenterLong ...

Source

<https://www.aquamaps.org/>

aquamaps_hcaf_eu

Half degree cell authority file for EU with bioclimate data (8,493 cells)

Description

A dataset containing reference data for bioclimate variables

Usage

aquamaps_hcaf_eu

Format

A data frame [8,593 x 12]

CsquareCod CsquareCod

LOICZID LOICZID

Elevation Elevation

TempMonthM TempMonthM

PrecipAnMe PrecipAnMe

SoilpH SoilpH

SoilMoistu SoilMoistu

SoilCarbon SoilCarbon

CTI_Max CTI_Max

NPP NPP

Islands Islands

Basins Basins ...

Source

<https://www.aquamaps.org/>

aquamaps_hcaf_world	<i>Half degree cell authority file for the world (259,200 cells) with bio-climate data</i>
---------------------	--

Description

A dataset containing reference data for bioclimate variables

Usage

aquamaps_hcaf_world

Format

A data frame [259,200 x 16]

LOICZID LOICZID

FAO FAO

CountryMain CountryMain

CountrySecond CountrySecond

CountryThird CountryThird

CsquareCod CsquareCod

Islands Islands
Basins Basins
SoilpH SoilpH
SoilCarbon SoilCarbon
CTI_Max CTI_Max
Elevation Elevation
TempMonthM TempMonthM
NPP NPP
SoilMoistu SoilMoistu
PrecipAnMe PrecipAnMe ...

Source

<https://www.aquamaps.org/>

aquamaps_presence_basins

Example grid cell data for various species of a certain category with presence in a basin (approx 410 000 rows)

Description

A dataset that should be possible to get via rgbif, would be nice to show that instead?

Usage

aquamaps_presence_basins

Format

A data frame [410,288 x 5]

loiczid loiczid is the unique cell identifier

csquarecode csquarecode is also a cell identifier

lname lname is the latin name for a species

category category is a category for a species

inbassin inbassin states whether the presence is in a basin ...

Source

<https://www.aquamaps.org/>

aquamaps_presence_occurrences

Example grid cell data for various species (approx 40 000 rows)

Description

A dataset that should be possible to get from rgbif, should show how to do it.

Usage

aquamaps_presence_occurrences

Format

A data frame [39,307 x 4]

loiczid loiczid

csquarecode csquarecode

lname lname

occurrence occurrence ...

Source

<https://www.aquamaps.org/>

aquamaps_qc

Quarter degree cell metadata (only identifiers and coordinates)

Description

A dataset containing metadata such as identifiers and bbox coords

Usage

aquamaps_qc

Format

A data frame

OBJECTID OBJECTID

Quadrant Quadrant

Global_Quadrant Global_Quadrant

c_square_code c_square_code

N_limit N_limit
E_limit E_limit
S_limit S_limit
W_limit W_limit
area_km2 area_km2_
centrelatitude centrelatitude
centrelongitude centrelongitude
Northern Northern
Southern Southern
Eastern Eastern
Western Western
Area Area
CenterLat CenterLat
CenterLon CenterLon
Shape Shape ...

Source

<https://www.aquamaps.org/>

aquatic_hcaf	<i>Half degree cell data (various bioclimate layers)</i>
--------------	--

Description

A dataset containing identifiers and bioclimate layers

Usage

aquatic_hcaf

Format

A data frame
CsquareCode CsquareCode
Basin Basin
BasinOther BasinOther
TempAnMean TempAnMean
TempMonthMean TempMonthMean
PrecipAnTotal PrecipAnTotal
PrecipAnMean PrecipAnMean

SoilpH SoilpH
SoilMoisture SoilMoisture
SoilCarbon SoilCarbon
RunoffAnnual RunoffAnnual
CTI CTI
NPPAnnual NPPAnnual
NPPAnnualAmericas NPPAnnualAmericas
ID ID
LOICZID LOICZID
NLimit NLimit
Slimit Slimit
WLimit WLimit
ELimit ELimit
CenterLat CenterLat
CenterLong CenterLong
CellArea CellArea
OceanArea OceanArea
CellType CellType
PWater PWater
FAOAreaM FAOAreaM
FAOAreaIn FAOAreaIn
CountryMain CountryMain
CountrySecond CountrySecond
CountryThird CountryThird
CountrySubMain CountrySubMain
CountrySubSecond CountrySubSecond
CountrySubThird CountrySubThird
EEZFirst EEZFirst
EEZSecond EEZSecond
EEZThird EEZThird
EEZFourth EEZFourth
EEZFifth EEZFifth
EEZSixth EEZSixth
EEZAll EEZAll
EEZRemark EEZRemark
LME LME
LME_2013_but never updated LME_2013_but never updated

LME_2010 LME_2010
LMEBorder LMEBorder
OceanBasin OceanBasin
Longhurst Longhurst
IslandsNo IslandsNo
Area0_20 Area0_20
Area20_40 Area20_40
Area40_60 Area40_60
Area60_80 Area60_80
Area80_100 Area80_100
AreaBelow100 AreaBelow100
ElevationMin ElevationMin
ElevationMax ElevationMax
ElevationMean ElevationMean
ElevationSD ElevationSD
DepthMin DepthMin
DepthMax DepthMax
DepthMean DepthMean
DepthSD DepthSD
SSTMnMin SSTMnMin
SSTMnMax SSTMnMax
SSTAnMean SSTAnMean
SSTAnSD SSTAnSD
SSTMnRange SSTMnRange
SBTAnMean SBTAnMean
SalinityMin SalinityMin
SalinityMax SalinityMax
SalinityMean SalinityMean
SalinitySD SalinitySD
SalinityBMean SalinityBMean
PrimProdMean PrimProdMean
IceConAnn IceConAnn
Shelf Shelf
Slope Slope
IceConSpr IceConSpr
IceConSum IceConSum
IceConFal IceConFal

IceConWin IceConWin
LandDist LandDist
WaveHeight WaveHeight
TidalRange TidalRange
Abyssal Abyssal
Coral Coral
Estuary Estuary
Seamount Seamount
MPA MPA
SST1950 SST1950
SBT1950 SBT1950
Salinity1950 Salinity1950
SalinityB1950 SalinityB1950
PrimProd1950 PrimProd1950
IceCon1950 IceCon1950
SST1999 SST1999
SBT1999 SBT1999
Salinity1999 Salinity1999
SalinityB1999 SalinityB1999
PrimProd1999 PrimProd1999
IceCon1999 IceCon1999
SST2050 SST2050
SBT2050 SBT2050
Salinity2050 Salinity2050
SalinityB2050 SalinityB2050
PrimProd2050 PrimProd2050
IceCon2050 IceCon2050
SST2100 SST2100
SBT2100 SBT2100
Salinity2100 Salinity2100
SalinityB2100 SalinityB2100
PrimProd2100 PrimProd2100
IceCon2100 IceCon2100
SST1950c SST1950c
SBT1950c SBT1950c
Salinity1950c Salinity1950c
SalinityB1950c SalinityB1950c

PrimProd1950c PrimProd1950c
IceCon1950c IceCon1950c
SST2050c SST2050c
SBT2050c SBT2050c
Salinity2050c Salinity2050c
SalinityB2050c SalinityB2050c
PrimProd2050c PrimProd2050c
IceCon2050c IceCon2050c
SST2100c SST2100c
SBT2100c SBT2100c
Salinity2100c Salinity2100c
SalinityB2100c SalinityB2100c
IceCon2100c IceCon2100c
PrimProd2100c PrimProd2100c

Source

<https://www.aquamaps.org/>

calc_prob	<i>Function to calculate probability per individual bioclimate variable given "spread" summary stats for a single environment envelope parameter</i>
-----------	--

Description

Function to calculate probability per individual bioclimate variable given "spread" summary stats for a single environment envelope parameter

Usage

```
calc_prob(x, min, max, d1, d9)
```

Arguments

x	bioclimate parameter value
min	the min statistics for this bioclimate variable
max	the max statistics for this bioclimate variable
d1	the first decile for for this bioclimate variable
d9	the ninth decile for this bioclimate variable

Examples

```
## Not run:
p <- calc_prob(1, 1, 1, 1)

## End(Not run)
```

calc_probs	<i>Function to calculate probabilities</i>
------------	--

Description

Function to calculate probabilities

Usage

```
calc_probs(hcaf_species, spreads)
```

Arguments

hcaf_species	data frame with half degree cell parameter values for relevant bioclimate variables
spreads	data frame with environmental envelope information (spreads for relevant bioclimate variables)

Examples

```
## Not run:
p <- calc_probs(hcaf_by_species(), spreads)

## End(Not run)
```

calc_probs_by_species	<i>Retrieve environmental, determine spread and return probabilities for a given species, using the bundled reference data</i>
-----------------------	--

Description

Retrieve environmental, determine spread and return probabilities for a given species, using the bundled reference data

Usage

```
calc_probs_by_species(.latinname)
```

Arguments

.latinname character string with latin name for species

Examples

```
## Not run:
probs_default <- calc_probs_by_species(default_species())

## End(Not run)
```

calc_spreads	<i>Calculate environmental data spread summaries given environmental data for a species</i>
--------------	---

Description

Calculate environmental data spread summaries given environmental data for a species

Usage

```
calc_spreads(.hcaf_species)
```

Arguments

.hcaf_species data frame with environmental data for one species

Examples

```
## Not run:
spreads <- calc_spreads(hcaf_by_species())

## End(Not run)
```

calc_spreads_by_species	<i>Retrieve environmental data and determine spread for a given species, using the bundled reference data</i>
-------------------------	---

Description

Retrieve environmental data and determine spread for a given species, using the bundled reference data

Usage

```
calc_spreads_by_species(.latinname)
```

Arguments

.latinname character string with latin name for species

Examples

```
## Not run:
spread_default <- calc_spreads_by_species(default_species())

## End(Not run)
```

default_clim_vars	<i>Default bioclimate variable names in raquamaps</i>
-------------------	---

Description

This function returns a vector with the default relevant environmental parameter names for demonstrational purposes

Usage

```
default_clim_vars()
```

Examples

```
## Not run:
clim_vars <- default_clim_vars()

## End(Not run)
```

default_hcaf	<i>Default half degree cells reference data, including geometry and bioclimate measurements, for demonstrational purposes</i>
--------------	---

Description

This function returns a data frame with reference data

Usage

```
default_hcaf(.clim_vars = default_clim_vars())
```

Arguments

.clim_vars vector of bioclimate variables to use

Examples

```
## Not run:
hcaf <- default_hcaf()

## End(Not run)
```

default_presence	<i>Default presence data for several species, for demonstrational purposes</i>
------------------	--

Description

This function returns a data frame with reference data to indicate cells with presence of species

Usage

```
default_presence()
```

Examples

```
## Not run:
presence <- default_presence()

## End(Not run)
```

default_species	<i>Default species in raquamaps</i>
-----------------	-------------------------------------

Description

This function returns the default species latin name for demonstrational purposes

Usage

```
default_species()
```

Examples

```
## Not run:
species <- default_species()

## End(Not run)
```

default_species_list *Default set of species for demonstrational purposes*

Description

This function returns a data frame with reference data suggesting a set of species to be used in calculations

Usage

```
default_species_list()
```

Examples

```
## Not run:  
species_list <- default_species_list()  
  
## End(Not run)
```

export_am_csv_tmp *Export results from as csv (tempfile)*

Description

Export results from as csv (tempfile)

Usage

```
export_am_csv_tmp(tbl)
```

Arguments

tbl data frame with results from calc_probs

Value

filename for temp file with csv results

get_am_name_uris	<i>Get aqua maps identifiers for a latin name</i>
------------------	---

Description

aquamaps.org uses internal identifiers for species, and this function scrapes the website and resolves a given latinname into one of these identifiers, which can be used to get a specific nativerange map in the case there are several available for a specific given latinname

Usage

```
get_am_name_uris(latinname = default_species())
```

Arguments

latinname a character vector with the latin name for the species

Value

character vector with aquamaps.org internal identifier(s)

Examples

```
## Not run:
  get_am_name_uris("Gadus morhua")
  get_am_name_uris("Sphyraena sphyraena")

## End(Not run)
```

get_dropbox_file	<i>Download a dropbox folder content as a zip-file</i>
------------------	--

Description

This function downloads a dropbox folder into the given destination directory.

Usage

```
get_dropbox_file(pubshare, destfile = tempfile())
```

Arguments

pubshare a string with the dropbox public share, for example "u4ipvf1tfo4izhq/AACVIXriWFkMfoliMtIyRUDPa"
destfile path for downloaded content, defaults to tempfile()

Value

path to local file with the downloaded content

Examples

```
## Not run:
get_dropbox_file("u4ipvf1tfo4izhq/AACVIxriWfKMfoliMtIyRUDPa", "/tmp/test.zip")

## End(Not run)
```

hcaf_by_species	<i>Default half degree cells reference data, including geometry and bioclimate measurements, for demonstrational purposes, filtered for a specific species and for specific bioclimate measurements</i>
-----------------	---

Description

This function returns a data frame with reference data consisting of environmental data for only those cells that have a specific species present

Usage

```
hcaf_by_species(.latinname = default_species(), .vars = default_clim_vars())
```

Arguments

.latinname	character string with latin name for species
.vars	vector of climate variable names to use

Examples

```
## Not run:
hcaf <- hcaf_by_species(default_species(), default_clim_vars())

## End(Not run)
```

nativerange	<i>Get native range dataset from aquamaps.org given latin name</i>
-------------	--

Description

aquamaps.org provides native range data downloads on a per species basis and this function scrapes the website for this information and returns it as a dataframe

Usage

```
nativerange(latinname = default_species(), identifier)
```

Arguments

latinname	a character vector with the latin name for the species
identifier	aquamaps.org sometimes provide several internal identifiers for the same latin name, if missing the first match will be used, but this can be overridden by using this parameter...

Value

dplyr layouted data frame with lat, long, native range p-value (0..1) and species name

Examples

```
## Not run:
  native_range_df <- nativerange("Gadus morhua")
  native_range_df <- nativerange("Sphyræna sphyræna")

## End(Not run)
```

occs_ggmap_gridded	<i>Plots a raster layer as a gridded map using ggplot</i>
--------------------	---

Description

Plots a raster layer as a gridded map using ggplot

Usage

```
occs_ggmap_gridded(r, legend = TRUE, legend_title = "Occurrences (n)",
  center, padding = 10)
```

Arguments

<code>r</code>	a raster layer with with occurrence points
<code>legend</code>	a boolean indicting whether to include the color legend
<code>legend_title</code>	a character string explaining which variable is displayed
<code>center</code>	optional coordinate from geocode to center the map on
<code>padding</code>	distance in degrees around the center to include in the map

Value

a ggplot

`occs_ggmap_gridded_polys`

Plots a raster grid using ggplot and polygons

Description

Plots a raster grid using ggplot and polygons

Usage

```
occs_ggmap_gridded_polys(raster)
```

Arguments

<code>raster</code>	a raster layer
---------------------	----------------

Value

a ggplot

`occs_ggmap_points`

Plots an occurrence data frame with points as a map using ggplot

Description

Plots an occurrence data frame with points as a map using ggplot

Usage

```
occs_ggmap_points(occs)
```

Arguments

<code>occs</code>	a data frame with occurrence points
-------------------	-------------------------------------

Value

a ggplot

occs_webmap_gridded *Plots a raster grid using leaflet*

Description

Plots a raster grid using leaflet

Usage

```
occs_webmap_gridded(r, legend_title = NA)
```

Arguments

`r` a raster layer
`legend_title` the title for the color legend, default is NA

Value

a web map using leaflet

plot_stepped_raster *Plot raster data in raquamaps style*

Description

Plot raster data in raquamaps style

Usage

```
plot_stepped_raster(raster, breaks, trim = FALSE)
```

Arguments

`raster` raster layer
`breaks` vector with character strings describing intervals
`trim` boolean to indicate whether the raster layer should be cropped

Value

plot of the raster

presence_rgbif	<i>Get presence data using rgbif</i>
----------------	--------------------------------------

Description

Get presence data using rgbif

Usage

```
presence_rgbif(latinname = default_species(), maxlimit = 10000)
```

Arguments

latinname	string with latin name for species
maxlimit	upper limit for number of rows to return

Value

data frame with coordinates, country and vernacular name

r2df_points	<i>Converts a raster grid into a dataframe of points which can be plotted with ggplot</i>
-------------	---

Description

Converts a raster grid into a dataframe of points which can be plotted with ggplot

Usage

```
r2df_points(raster)
```

Arguments

raster	a raster layer
--------	----------------

Value

a data frame with the cell grid coordinates and values in a data frame with columns x, y, z

r2df_polygons	<i>Converts a raster grid into a dataframe of closed polygons which can be plotted with ggplot</i>
---------------	--

Description

Converts a raster grid into a dataframe of closed polygons which can be plotted with ggplot

Usage

```
r2df_polygons(raster)
```

Arguments

raster	a raster layer
--------	----------------

Value

a data frame with the cell grid as polygons

rasterize_occs	<i>Converts points in data frame into raster</i>
----------------	--

Description

Converts points in data frame into raster

Usage

```
rasterize_occs(df)
```

Arguments

df	data frame with coordinates in decimalLongitude, decimalLatitude columns
----	--

Value

a half degree raster grid with individual cell values representing the count of occurrences within the grid cells

rasterize_presence	<i>Converts presence data from rgbif into raster data</i>
--------------------	---

Description

Converts presence data from rgbif into raster data

Usage

```
rasterize_presence(occs = presence_rgbif())
```

Arguments

occs	data frame with coordinates, from rgbif
------	---

Value

a raster grid with individual cell values representing the count of occurrences within the grid cells

rgbif_galemys_pyrenaicus	<i>Example grid cell data for one specific species (Galemys pyrenaicus)</i>
--------------------------	---

Description

A dataset fetched using rgbif on 31st of May 2015

Usage

```
rgbif_galemys_pyrenaicus
```

Format

A data frame

decimalLatitude	decimalLatitude
decimalLongitude	decimalLongitude
geodeticDatum	geodeticDatum
countryCode	countryCode
vernacularName	vernacularName ...

Source

<https://www.aquamaps.org/>

 rgbif_great_white_shark

Example grid cell data for one specific species (Great White Shark)

Description

A dataset fetched using rgbif on 31st of May 2015

Usage

```
rgbif_great_white_shark
```

Format

A data frame

decimalLatitude decimalLatitude

decimalLongitude decimalLongitude

geodeticDatum geodeticDatum

countryCode countryCode

vernacularName vernacularName ...

Source

<https://www.aquamaps.org/>

 stepped_raster

Discretize a raster into intervals or steps for chloropeth maps

Description

Discretize a raster into intervals or steps for chloropeth maps

Usage

```
stepped_raster(r, n = 5, interval_style = "fisher")
```

Arguments

r raster

n number of steps to use, default being five steps

interval_style a character string with classInt interval styles, defaulting to "fisher", but can be "quantile", "equal" (see classIntervals docs)

Value

a list with the raster (discretized) and breaks (intervals)

which_cells	<i>Return all grid cells identifiers where the specified species occurs</i>
-------------	---

Description

Return all grid cells identifiers where the specified species occurs

Usage

```
which_cells(.presence = default_presence(), .latinname = default_species())
```

Arguments

.presence	dataset with presence data for various species
.latinname	latin name for species

which_cells_in_raster	<i>Raster grid cell identifiers with presence</i>
-----------------------	---

Description

Raster grid cell identifiers with presence

Usage

```
which_cells_in_raster(r, lower_limit = 0)
```

Arguments

r	raster
lower_limit	raster cell values higher than this parameter is interpreted as presence

Value

a vector of raster grid cell identifiers (loiczids)

Index

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