

Package ‘defrostR’

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Type Package

Title A tool for standardizing amphibian taxonomy

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Author H. Christoph Liedtke

Maintainer H. Christoph Liedtke <christoph.liedtke@ebd.csic.es>

Description This package provides a workflow for combining amphibian taxonomic data sets from different sources that use different taxonomic nomenclature, by suggesting the most current nomenclature used by the Amphibian Species of the World online reference for a given input query of species names. It can also be used to extract specific systematic information (e.g. species downstream of a given taxonomic level).

Depends R (>= 3.0.1), XML

Suggests knitr, rmarkdown

VignetteBuilder knitr

License GPL (>= 2.0)

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

URL <http://github.com/hcliedtke/defrostR>

BugReports <http://github.com/hcliedtke/defrostR/issues>

NeedsCompilation no

R topics documented:

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 amphweb

AmphibiaWeb Taxonomy

Description

Data table of taxonomy downloaded from <http://amphibiaweb.org/>. The dataset contains a list of species and species names used by AmphibiaWeb as well as higher level taxonomy and more (IUCN red list status etc.). A version is stored internally for the purpose of running examples, but users should be aware that this may be outdated depending both on how recently the defrostR package as well as the AmphibiaWeb website has been updated.

Usage

```
amphweb
```

Format

```
R dataset
```

Examples

```
head(amphweb)
amphweb<-defrostR::amphweb
```

 aswStats

Get summary statistics of current taxonomy

Description

This function uses the ASW taxonomy table created with the function `getTaxonomy()` and summarizes counts of units per taxonomic level

Usage

```
aswStats(asw_taxonomy = defrostR::asw_taxonomy, verbose = F, Order = NA,
         Superfamily = NA, Family = NA, Subfamily = NA, Genus = NA)
```

Arguments

| | |
|---------------------------|--|
| <code>asw_taxonomy</code> | output of the function <code>frostScraper()</code> default will take defrostR's stored version, which might be outdated |
| <code>verbose</code> | logical arguments can be turned on to summarize at given taxonomic levels or to give numbers of each unit per taxonomic level. default is switched off (FALSE) |
| <code>Order</code> | string to specify summary statistics of only a specific order |
| <code>Superfamily</code> | string to specify summary statistics of only a specific superfamily |
| <code>Family</code> | string to specify summary statistics of only a specific Family |
| <code>Subfamily</code> | string to specify summary statistics of only a specific subfamily |
| <code>Genus</code> | string to specify summary statistics of only a specific genus |

Details

One logical arguments can be turned on to summarize at given taxonomic levels or to give numbers of each unit per taxonomic level

Value

returns either a data frame or list of summary statistics

Examples

```
aswStats()  
aswStats(verbose=TRUE, Family="Rhacophoridae")
```

asw_synonyms

Amphibian Species of the World synonyms

Description

Data table generated using the getSynonyms() function. The dataset contains a full list of synonyms listed on the Amphibian Species of the World (ASW) website and the current accepted name of the species. A version is stored internally for the purpose of running examples, but users should be aware that this may be outdated depending both on how recently the defrostR package as well as the ASW website has been updated.

Usage

```
asw_synonyms
```

Format

R dataset

Details

dataset last updated on 12th July 2017

Examples

```
head(asw_synonyms)  
str(asw_synonyms)  
asw_synonyms<-defrostR::asw_synonyms
```

`asw_taxonomy`*Amphibian Species of the World Taxonomy*

Description

Data table generated using the `getTaxonomy()` function. The dataset contains a full list of species listed on the Amphibian Species of the World (ASW) website along with all higher level taxonomy and the URLs for each species. A version is stored internally for the purpose of running examples, but users should be aware that this may be outdated depending both on how recently the `defrostR` package as well as the ASW website has been updated.

Usage

`asw_taxonomy`

Format

`R dataset`

Details

`dataset last updated on 12th July 2017`

Examples

```
head(asw_taxonomy)
str(asw_taxonomy)
asw_taxonomy<-defrostR::asw_taxonomy
```

`defrost`*Submit query to find updates in nomenclature*

Description

This function takes a query (a list of taxon names to be assessed) and the amphibian species of the world synonym table (preferably generated with the function `getSynonyms()`, or loaded from the data set stored internally) as input and returns an updated list of names.

Usage

```
defrost(query, asw = defrostR::asw_synonyms, interactive = F,
        return.no.matches = F)
```

Arguments

| | |
|-------------------|--|
| query | vector of taxon names to be processed (can also be tip labels of a phylogeny for example) |
| asw | amphibian species of the world synonym reference table on which to base new names on. Default setting will use the internally stored data set that may not be the most up-to-date. |
| interactive | logical argument (default=FALSE) of whether to allow an "on the fly" decision to be made on what name to take if synonym matches multiple names. FALSE will return all possible names for a given query as a string, TRUE will ask the user to select one. |
| return.no.matches | logical argument of whether to leave taxa not found in the reference table blank or whether to fill in the names provided by the query. default is FALSE |

Details

Two logical arguments can be turned on to a) allow an "on the fly" decision to be made on what name to take if synonym matches multiple names (if not, it will return all possible names) and to b) return the original query name if no match is found

Value

this function returns a data frame with the following information/columns: original/input names, "stripped" names with no formatting, status of what action has been taken, updated names as recommended by the reference table

| | |
|-------------|---|
| getSynonyms | <i>Compile dataframe of all synonyms listed on Amphibian Species of the World</i> |
|-------------|---|

Description

This function looks up any listed synonyms on the ASW website (<http://research.amnh.org/vz/herpetology/amphibia/index.html>). It takes a minimum of one argument: the asw_taxonomy table generated with the function getTaxonomy(). If a full search is performed, this can take quite long (looking through ~7000 species webpages for upwards of 20 000 synonyms), but additional arguments can be included to restrict searches to a specified taxonomic group.

Usage

```
getSynonyms(asw_taxonomy = defrostR::asw_taxonomy, Order = NA,
             Superfamily = NA, Family = NA, Subfamily = NA, Genus = NA,
             Species = NA)
```

Arguments

| | |
|--------------|---|
| asw_taxonomy | the ASW taxonomy table obtained with getTaxonomy(). If no table is provided, by default it will use the internally stored data set. WARNING! this version of the amphibian taxonomy may be outdated |
| Order | limit search to a user-specified amphibian order |

| | |
|-------------|--|
| Superfamily | limit search to a user-specified amphibian superfamily |
| Family | limit search to a user-specified amphibian family |
| Subfamily | limit search to a user-specified amphibian subfamily |
| Genus | limit search to a user-specified amphibian genus |
| Species | limit search to a user-specified amphibian species |

Details

Users may experience issues with umlauts that are not supported by their system language. On Mac OSX, this can be changed by running the following line of code in R:

```
system("defaults write org.R-project.R force.LANG en_US.UTF-8")
```

and then restarting the session. Read more here: https://cran.r-project.org/bin/macosx/RMacOSX-FAQ.html#Internationalization-of-the-R_002eapp

Value

returns a dataframe listing all species and their listed synonyms

Examples

```
#to get a full list of synonyms for all species, run: asw_synonyms<-getSynonyms()
breviceptid_synonyms<-getSynonyms(Family="Breviceptidae")
```

| | |
|-------------|--|
| getTaxonomy | <i>Compile amphibian taxonomy following the Amphibian Species of the World</i> |
|-------------|--|

Description

This function takes no arguments. It cycles through the ASW website (<http://research.amnh.org/vz/herpetology/amphibia>) to scrap all taxonomic information from Order to Species. As there are 5 taxonomic levels within each Order (Superfamily/Family/Subfamily/Genus/Species), one can expect the function to require 1 initial loop followed by 4 more, but it is designed to keep going until all lineages have reached the species level.

Usage

```
getTaxonomy()
```

Value

returns a dataframe listing all species and their taxonomic backbone as well as all URLs per species.

Examples

```
#run asw_taxonomy_table<-getTaxonomy() to scrape the ASW website for the most current taxonomy
```

| | |
|---------------|--|
| synonymReport | <i>Get summary report of "defrosted" query</i> |
|---------------|--|

Description

This function produces a report of an undertaken defrost() query

Usage

```
synonymReport(defrosted, verbose = F)
```

Arguments

| | |
|-----------|--|
| defrosted | output of the function defrost() |
| verbose | logical arguments can be turned on to list species which result in conflict. Default=FALSE |

Details

One logical arguments can be turned on to summarize in terms of numbers of cases, or to provide species names of conflicting issues.

Value

returns either a data frame or list of summary statistics

Examples

```
amphweb<-defrostR::amphweb
head(amphweb$species)
amphweb.bufoidae<-amphweb[amphweb$family=="Bufoidae",]
bufoidae.defrosted<-defrost(query=amphweb.bufoidae$species)
synonymReport(bufoidae.defrosted)
```

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