

defrostR

July 12, 2017

Type Package

Title deforstR lets you update your amphibian taxonomy based on ASW

Version 1.0.0

Date 2017-05-21

Author H. Christoph Liedtke

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

Description This package is designed to help update amphibian taxonomy

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>

R topics documented:

amphweb	2
aswStats	2
asw_synonyms	3
asw_taxonomy	3
defrost	4
getSynonyms	4
getTaxonomy	5
synonymReport	6
Index	7

amphweb

Current version of Frost synonyms

Description

most current datasets

Usage

amphweb

Format

R dataset

Examples

```
head(amphweb)
```

aswStats

Get summary statistics of current taxonomy

Description

This function uses the ASW taxonomy table created with the function `frostScraper()` 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

asw_taxonomy	output of the function <code>frostScraper()</code> default will take <code>defrostR</code> 's stored version, which might be outdated
verbose	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)
Order	string to specify summary statistics of only a specific order
Superfamily	string to specify summary statistics of only a specific superfamily
Family	string to specify summary statistics of only a specific Family
Subfamily	string to specify summary statistics of only a specific subfamily
Genus	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=T, Family="Rhacophoridae")
```

asw_synonyms

Current version of Frost synonyms

Description

most current datasets

Usage

```
asw_synonyms
```

Format

R dataset

Examples

```
head(asw_synonyms)
```

asw_taxonomy

Current version of Frost 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

Examples

```
head(asw_taxonomy)
```

defrost	<i>Suggest currently accepted nomenclature (sensu ASW)</i>
---------	--

Description

This function takes a query (a list of taxon names to be assessed) and the amphibian species of the world synonym table (either generated with the function XXXX or loaded from the defrostR data set) 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 is to use defrostR's 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. TRUE will return all possible names for a given query
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 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 a data frame of all synonyms listed on ASW</i>
-------------	---

Description

This function looks up any listed synonyms on the ASW website (<http://research.amnh.org/vz/herpetology/amphibia/index.html>). It takes only a single argument, the asw_taxonomy table generated with the function getTaxonomy(). If a full search is performed, this can take quite long (looking through ~7000 websites for upwards of 20 000 synonyms).

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, the default is to use `defrostR`'s internally stored version. **WARNING!** this version may be outdated

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

```
asw_synonyms<-getSynonyms()
breviceptid_synonyms<-getSynonyms(Family="Brevicipitidae")
```

`getTaxonomy`

Compile a data frame of all currently listed ASW species

Description

This function takes no arguments. It cycles through the ASW website (<http://research.amnh.org/vz/herpetology/amphibia>) in an attempt 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

```
asw_taxonomy_table<-getTaxonomy()
```

synonymReport	<i>Get summary report for defrosting</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)
synonymReport(bufoidae.defrosted,)
```

Index

*Topic **datasets**

amphweb, [2](#)

asw_synonyms, [3](#)

asw_taxonomy, [3](#)

amphweb, [2](#)

asw_synonyms, [3](#)

asw_taxonomy, [3](#)

aswStats, [2](#)

defrost, [4](#)

getSynonyms, [4](#)

getTaxonomy, [5](#)

synonymReport, [6](#)