Package 'AmphiSync'

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Type Package

Title An Amphibian Systematics Tool

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Description 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: an Online Reference, Frost (2017) <http://research.amnh.org/herpetology/amphibia/index.html> (Amphibian Species of the World: an online reference. Version 6 (DATE OF ACCESS). Electronic Database accessible at http://research.amnh.org/herpetology/amphibia/index.html. American Museum of Natural History, New York, USA.) 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/amphisync

BugReports http://github.com/hcliedtke/amphisync/issues

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 A version is stored internally for the purpose of running examples, but users should be aware that this may be outdated depending both on how recently the defrostR package as well as the AmphibiaWeb website has been updated.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

asw_taxonomy	output of the function frostScraper() default will take defrostR's stored version, which might be outdated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 statitics

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 nomenclautre*

Description

This function takes a query (a list of taxon names to be assessed) and the amphibian species of the world synonym table (preferrably 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. FLASE 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

Examples

```
defrost(query=c("Bufo calamita", "Bufo viridis"))
```

---

getSynonyms	*Compile dataframe of all synonyms listed on Amphibian Species of the World*

Description

This function looks up any listed synonyms on the ASW website (http://research.amnh.org/vz/herpetology/amphibia/inde 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:
## Not run: asw_synonyms<-getSynonyms()
#to get synonyms for a specific taxonomic group only:
## Not run: breviceptid_synonyms<-getSynonyms(Family="Brevicipitidae")
```

---

getTaxonomy	*Compile amphibian taxonomy following the Amphibian Species of the World*

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

```
## Not run: asw_taxonomy_table<-getTaxonomy()
```

---

searchASW   *Search the Amphibian Species of the World database (Species search)*

Description

This function searches species accounts on the ASW website (http://research.amnh.org/vz/herpetology/amphibia/index.pl)
and returns all available information listed. The URL per species is taken from defrostR's internally
stored records, unless specified otherwise.

Usage

```
searchASW(query, asw_taxonomy = defrostR::asw_taxonomy)
```

Arguments

query	search term. Binomial species name either separated by a space or "_"
asw_taxonomy	version of taxonomy to use (output of getTaxonomy()). By default, internally stored version is used (which may be out of data)

Value

returns all available information in list form

Examples

```
searchASW("Pleurodeles waltl")
```

---

synonymReport   *Get summary report of "defrosted" query*

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 statitics

Examples

```
#check out amphibiaweb taxonomy and extract only Bufonidae
head(amphweb$species)
amphweb.bufonidae<-amphweb[amphweb$family=="Bufonidae",]
#defrost bufonidae and inspect
bufonidae.defrosted<-defrost(query=amphweb.bufonidae$species)
synonymReport(bufonidae.defrosted)
```

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