Package ‘flora’

December 4, 2017

Type Package
Title Tools for Interacting with the Brazilian Flora 2020
Version 0.3.0
Author Gustavo Carvalho
Maintainer Gustavo Carvalho <gustavo.bio@gmail.com>
Depends R (>= 3.0.0)
Imports httr, dplyr, utils, jsonlite, stringdist
Suggests testthat, shiny
Description Tools to quickly compile taxonomic and distribution data from the Brazilian Flora 2020.
License GPL (>= 2)
URL http://www.github.com/gustavobio/flora
BugReports http://www.github.com/gustavobio/flora/issues
RoxygenNote 6.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2017-12-04 19:50:03 UTC

R topics documented:

   df2phytaxa ................................................................. 2
   fixCase ............................................................... 2
   flora ................................................................. 3
   get.synonyms ......................................................... 3
   get.taxa ............................................................. 4
   get_domains ......................................................... 5
   get_lifeform ......................................................... 6
   get_vegtype ......................................................... 6
   lower.taxa .......................................................... 7
   occurrence ......................................................... 7
Description

Convert the results of get.taxa() to the phylomatic sample format

Usage

df2phytaxa(taxaL uppercase = true)

Arguments

taxa A data frame with columns named family, genus, and species.
uppercase logical. Should the function capitalize first letters?

Description

Fix the name case of a taxon

Usage

fixCase(x)

Arguments

x a unit character vector with a taxon

Examples

fixCase("myrcia lingua")
fixCase("Myrcia Lingua")
fixCase("COFFEA ARABICA")
**Description**

Collect data from the Brazilian Flora checklist (http://floradobrasil.jbrj.gov.br).

**Details**

This package contains a set of tools solving problems that arise when one has to collect taxonomic and distribution information for large datasets of plants. Interacting with the Brazilian Flora Checklist website from a web browser is often a slow and somewhat cumbersome process, especially if you are not sure about the correct spelling of a name. With flora, however, you can:

- get a suggestion for the correct spelling of a name from an incorrect one
- search for its current taxonomic status
- get its author(s), synonym(s), family, distribution, and lower taxa
- process lists of names and automatically solve synonyms and typing errors

flora now holds all the data it needs. All functions can be used whilst offline.

---

### get.synonyms

*List all synonyms of a given taxa*

**Description**

This function returns all the synonyms of a given taxon according to the Brazilian Flora 2020.

**Usage**

```
get.synonyms(taxon)
```

**Arguments**

- `taxon` a character vector containing a name.

**Value**

a character vector

**Examples**

```r
## Not run:
synonyms("Myrcia lingua")

## End(Not run)
```
get.taxa

Get plant taxonomical and distribution data

Description

This function collects taxonomic information and distribution from the Brazilian Flora Checklist. Synonyms and misspelled names are resolved automatically. Results can be combined with life form, habitat, vernacular name, and occurrence data.

Usage

```r
get.taxa(taxa, replace.synonyms = TRUE, suggest.names = TRUE,
         life.form = FALSE, habitat = FALSE, vernacular = FALSE,
         states = FALSE, establishment = FALSE, drop = c("authorship", "genus",
                "specific.epiteth", "infra.epiteth", "name.status"),
         suggestion.distance = 0.9, parse = FALSE)
```

Arguments

- `taxa`: a character vector containing one or more taxa, without authors see `remove.authors` if you have a list with authorities.
- `replace.synonyms`: should the function automatically replace synonyms?
- `suggest.names`: should the function try to correct misspelled names?
- `life.form`: include the life form of the taxon?
- `habitat`: include the habitat of the taxon?
- `vernacular`: include vernacular names and localities?
- `states`: include occurrence data?
- `establishment`: include the establishment type (native, cultivated or naturalized)?
- `drop`: NULL or character vector with names of columns with taxonomic information to be removed from the returned data frame. Available names: "id", "scientific.name", "accepted.name", "family", "genus", "specific.epiteth", "infra.epiteth", "taxon.rank", "authorship", "taxon.status", "name.status", "threat.status", and "search.str".
- `suggestion.distance`: a value between 0 and 1 indicating how conservative the name suggestion algorithm should be. Values closer to 1 are very conservative. Be very careful, lower values can give wrong suggestions.
- `parse`: Parse names through the GBIF parser to remove authors?

Details

The returned data frame will contain a variable number of rows and columns depending on how the function was called. For instance, since there might be more than one vernacular name for each taxon, some rows will be duplicated if ` vernacular` is set to `TRUE`. All misspelled taxa are automatically corrected if the function can come up with a reasonable guess for the name. Conservation status follows the IUCN nomenclature.
Value

a data frame

Examples

```r
## Not run:
data(plants)
get.taxa(plants)
get.taxa(plants, life.form = TRUE, establishment = TRUE)

## End(Not run)
```

Description

Get the phytogeographic domain of a list of taxa

Usage

```r
get_domains(taxa)
```

Arguments

- `taxa`: A data frame with taxon names as returned by `get.taxa()`

Value

A data frame as returned by `get.taxa` with an extra column named domain.

Examples

```r
## Not run:
taxa <- get.taxa(c("Myrcia guianensis", "bleh", "Xylopa", "Miconia albicans", "bleh", "Poa annua"))
get_domains(taxa)

## End(Not run)
```
get_lifeform  
*Get the listed vegetation life forms for a list of taxa*

**Description**
Get the listed vegetation life forms for a list of taxa

**Usage**
```
get_lifeform(taxa)
```

**Arguments**
- **taxa**: A data frame with taxon names as returned by get.taxa()

**Value**
A data frame as returned by get.taxa with an extra column named life.form

**Examples**
```r
## Not run
taxa <- get.taxa(c("Myrcia guianensis", "bleh", "Xylopia", "Miconia albicans", "bleh", "Poa annua"))
get_lifeform(taxa)
## End(Not run)
```

---

get_vegtype  
*Get the listed vegetation types for a list of taxa*

**Description**
Get the listed vegetation types for a list of taxa

**Usage**
```
get_vegtype(taxa)
```

**Arguments**
- **taxa**: A data frame with taxon names as returned by get.taxa()

**Value**
A data frame as returned by get.taxa with an extra column named vegtype.

---

get_vegtype  
*Get the listed vegetation types for a list of taxa*
lower.taxa

Get downstream taxa

Description

Get all downstream taxa from a family or genus name.

Usage

lower.taxa(taxon, accepted = TRUE)

Arguments

taxon a character vector with either a family or genus name
accepted list only accepted names?

Examples

## Not run:
lower.taxa("Acosmium")
lower.taxa("Zygophyllaceae")

## End(Not run)

occurrence

Taxa occurrence

Description

Find the taxa that occur in a given state of Brazil.

Usage

occurrence(states, type = c("any", "only", "all"), taxa = NULL)
Arguments

states   a character vector with one or more state abbreviations following. See notes for abbreviations.

type    type of matching to be used. any will return the taxa that occur in any of the passed states. only matches taxa that occur only in all provided (no more, no less) states and all matches taxa that occur at least in all states passed. See examples.

taxa    optional character vector to match against the states

Value

a data frame

Note


Examples

```r
## Not run:
occ.any <- occurrence(c("SP", "BA", "MG"), type = "any")
occ.only <- occurrence(c("SP", "BA", "MG"), type = "only")
occ.all <- occurrence(c("SP", "BA", "MG"), type = "all")
occ.taxa <- occurrence(c("SP", "BA", "MG"), type = "all", taxa = lower.taxa("Myrcia"))

head(occ.any)
head(occ.only)
head(occ.all)
head(occ.taxa)

## End(Not run)
```

plants

<table>
<thead>
<tr>
<th>Plant names</th>
</tr>
</thead>
<tbody>
<tr>
<td>plants</td>
</tr>
</tbody>
</table>

Description

A small character vector containing 16 plant names. Contains accepted names, synonyms, and misspelled taxa.

Format

A character vector with 16 names
remove.authors

Remove the author(s) from a taxon name.

Description
This attempts to remove the authorities of a taxonomic name.

Usage
remove.authors(taxon)

Arguments
taxon  a character vector containing a single taxon

Value
a character vector

Examples
## Not run:
remove.authors("Coffea arabica L.")
remove.authors("Chrysophyllum argenteum subsp. nitidum (G.F.W.Meyer) T.D.Penn.")
## End(Not run)

standardize.names
Standardize taxonomic names

Description
This function standardizes taxa names. It is used mainly internally, but might be helpful to the end user in some situations.

Usage
standardize.names(taxon)

Arguments
taxon  a character vector containing a single name

Value
a character vector
suggest.names

Suggest a valid name from a misspelled one

Description

This function tries to suggest a valid name according to the Brazilian Flora Checklist using a possibly incorrect one as a starting point.

Usage

suggest.names(taxon, max.distance = 0.75, return.na = TRUE, ignore.words = NULL)

Arguments

taxon a character vector containing a single name
max.distance a numeric value indicating how conservative the function should be when searching for suggestions. Values close to 1 are very conservative
return.na a logical indicating whether to return a NA or the original input when no suggestion is found
ignore.words NULL or a character vector with words to be ignored by the function. Useful if you are automatizing a workflow and wants the function to ignore words or phrases such as "not found", "dead", "undetermined", and so on

Value

A character vector or NA

Examples

## Not run:
suggest.names("Cofea arabyca")
suggest.names("Myrcia bela")

## End(Not run)
trim

Trim a name and remove duplicate tabs and whitespaces

Description
Remove duplicate and misplaced whitespace characters

Usage
trim(taxon)

Arguments
taxon a character vector with a single taxon name

Value
a character vector

Examples
## Not run:
trim(" Myrcia lingua")

## End(Not run)

vernacular

Vernacular name search

Description
Search for taxa using vernacular names

Usage
vernacular(name, exact = FALSE)

Arguments
name a vernacular name
exact approximate or exact match?

Value
a data frame of results or NA
Examples

```r
## Not run:
vernacular("pimenta", exact = TRUE)
vernacular("pimenta", exact = FALSE)
## End(Not run)
```

Description

This function starts a local webserver to run the shiny app distributed with the package.

Usage

```r
web.flora()
```
Index

*Topic datasets
  plants, 8

df2phytaxa, 2
fixCase, 2
flora, 3
flora-package (flora), 3
get.synonyms, 3
get.taxa, 4
get_domains, 5
get_lifeform, 6
get_vegtype, 6
lower.taxa, 7
occurrence, 7
plants, 8
remove.authors, 4, 9
standardize.names, 9
suggest.names, 10
trim, 11
vernacular, 11
web.flora, 12