Package 'flora'

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Type Package

Title tools for interacting with the Brazilian Flora Checklist

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Depends R (>= 3.0.2)

Description Tools to quickly compile taxonomic and distribution data from the Brazilian Flora Checklist. No internet connection needed.

License GPL (>= 2)

SysDataCompression gzip

NeedsCompilation no

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R topics documented:

fixCase *Fix the name case of a taxon*

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")
```

flora *Package flora*

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.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

```
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"))
```

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", and "search.str".

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.

Value

a data frame

Examples

```
data(plants)
get.taxa(plants)
get.taxa(plants, life.form = TRUE, establishment = TRUE)
```

lower.taxa *Get downstream taxa*

Description

Get all downstream taxa from a family or genus name.

Usage

```
lower.taxa(taxon)
```

Arguments

taxon	a character vector with either a family or genus name

Examples

```
lower.taxa("Acosmium")
lower.taxa("Zygophyllaceae")
```

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

List of abbreviations: http://en.wikipedia.org/wiki/States_of_Brazil

Examples

```
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)
```

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plants *Plant names*

Description

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

Format

A character vector with 16 names

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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

```
remove.authors("Coffea arabica L.")
remove.authors("Chrysophyllum argenteum subsp. nitidum (G.F.W.Meyer) T.D.Penn.")
```

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

Examples

```
standardize.names("Miconia sp 01")
standardize.names("Miconia Sp 2")
standardize.names("Sp18")
```

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

```
suggest.names("Cofea arabyca")
suggest.names("Myrcia bela")
```

`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

```
trim("   Myrcia  lingua")
```

`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

```
vernacular("pimenta", exact = TRUE)
vernacular("pimenta", exact = FALSE)
```

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