

Package ‘flora’

May 8, 2026

Type Package

Title Tools for Interacting with the Brazilian Flora 2020

Version 0.3.4

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 6.1.1

NeedsCompilation no

Repository CRAN

Date/Publication 2020-04-28 05:00:03 UTC

Contents

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

occurrence	8
plants	9
remove.authors	9
standardize.names	10
suggest.names	10
trim	11
vernacular	12
web.flora	12

Index **13**

df2phytaxa	<i>Phylomatic format</i>
------------	--------------------------

Description

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

Usage

```
df2phytaxa(taxa, uppercase = TRUE)
```

Arguments

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

fixCase	<i>Fix the name case of a taxon</i>
---------	-------------------------------------

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	<i>Package flora</i>
-------	----------------------

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.

<code>get.synonyms</code>	<i>List all synonyms of a given taxa</i>
---------------------------	--

Description

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

Usage

```
get.synonyms(taxon, fix = FALSE, relationship = FALSE)
```

Arguments

<code>taxon</code>	a character vector containing a name.
<code>fix</code>	should the function fix issues (synonyms, misspelled names) in taxon?
<code>relationship</code>	return the kind of relationship?

Value

a character vector

Examples

```
## Not run:
get.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

```
get.taxa(taxa, replace.synonyms = TRUE, suggest.names = TRUE,
  life.form = FALSE, habitat = FALSE, vegetation.type = FALSE,
  vernacular = FALSE, states = FALSE, establishment = FALSE,
  domain = FALSE, endemism = 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?
vegetation.type	include the listed vegetation types?
vernacular	include vernacular names and localities?
states	include occurrence data?
establishment	include the establishment type (native, cultivated or naturalized)?
domain	return phytogeographic domains?
endemism	is the taxon endemic to Brazil?
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

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

## End(Not run)
```

get_domains

Get the phytogeographic domain of a list of taxa

Description

Get the phytogeographic domain of a list of taxa

Usage

```
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

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

## End(Not run)
```

get_endemism	<i>Get the listed endemism for a list of taxa</i>
--------------	---

Description

Get the listed endemism for a list of taxa

Usage

```
get_endemism(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.

Examples

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

## End(Not run)
```

get_lifeform	<i>Get the listed vegetation life forms for a list of taxa</i>
--------------	--

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

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

## End(Not run)
```

get_vegtype	<i>Get the listed vegetation types for a list of taxa</i>
-------------	---

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.

Examples

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

## End(Not run)
```

lower.taxa	<i>Get downstream taxa</i>
------------	----------------------------

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

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

Examples

```
## 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	<i>Plant names</i>
--------	--------------------

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	<i>Remove the author(s) from a taxon name.</i>
----------------	--

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	<i>Standardize taxonomic names</i>
-------------------	------------------------------------

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

```
## Not run:
standardize.names("Miconia sp 01")
standardize.names("Miconia Sp 2")
standardize.names("Sp18")

## End(Not run)
```

suggest.names	<i>Suggest a valid name from a misspelled one</i>
---------------	---

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	<i>Vernacular name search</i>
------------	-------------------------------

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

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

web.flora	<i>Web front end</i>
-----------	----------------------

Description

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

Usage

```
web.flora()
```

Index

* datasets

plants, 9

df2phytaxa, 2

fixCase, 2

flora, 3

flora-package (flora), 3

get.synonyms, 3

get.taxa, 4

get_domains, 5

get_endemism, 6

get_lifeform, 6

get_vegtype, 7

lower.taxa, 7

occurrence, 8

plants, 9

remove.authors, 4, 9

standardize.names, 10

suggest.names, 10

trim, 11

vernacular, 12

web.flora, 12