Package ‘TR8’

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Type Package

Title A Tool for Downloading Functional Traits Data for Plant Species

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Description Plant ecologists often need to collect `traits` data about plant species which are often scattered among various databases: TR8 contains a set of tools which take care of automatically retrieving some of those functional traits data for plant species from publicly available databases (Biolflor, The Ecological Flora of the British Isles, LEDA traitbase, Ellenberg values for Italian Flora, Mycorrhizal intensity databases, Catminat, BROT, PLANTS, Jepson Flora Project).

The TR8 name, inspired by `car plates` jokes, was chosen since it both reminds of the main object of the package and is extremely short to type.

License GPL (>= 2)

LazyData true

Encoding UTF-8

URL https://github.com/GioBo/TR8

BugReports https://github.com/GioBo/TR8/issues

Depends R (>= 2.10), methods

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TR8-package

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TR8-package

TR8: a tool for retrieving functional traits data for plant species.

Description

This package provides a set of functions for extracting traits data for plant species from the following sources:

- Biolflor ‘http://www.ufz.de/biolflor/index.jsp’
- Ecological Flora of the British Isles ‘http://www.ecoflora.co.uk/’
- LEDA traitbase ‘http://www.leda-traitbase.org/LEDAportal/’
- Ellenberg values for Italian Flora
- Mycorrhizal intensity database
- MycoFlor ‘http://luirig.altervista.org/’
- ‘http://perso.wanadoo.fr/philippe.julve/catminat.htm’
- BROT ‘http://www.uv.es/jgpausas/brot.htm’
- PLANTS ‘http://www.bricol.net/’

Details
The easiest way of using the package is through the `tr8()` function, which accepts a vector of plant species names and returns a data frame containing traits data which have been found in the various sources. The TR8 name, inspired by "car plates" jokes, was chosen since it both reminds of the main object of the package and is extremely short to type.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Please always use the following citations any time you use trait data retrieved with `tr8`

**BiolFlor**

**Ecoflora**

**LEDA traitbase**

**Akhmetzhanova et al, 2012**

**Hempel et al, 2013**

**Pignatti et al., 2005**

Catminat


BROT


AND


PLANTS


See Also

bib()

Examples

## Not run:
## download some trait data for Abies alba
My_traits<-tr8(species_list=c("Abies alba"),download_list=c("life_form_P"))

## End(Not run)

available_tr8  A dataframe containing the traits available for download.

Description

The available_tr8 dataframe can be used as a reference in order to know which traits can be downloaded with the TR8 package.

Usage

data("available_tr8")

Format

A data frame with the following variables:

short_code contains the codes that should be used when using the tr8() function
description contains a short description of the traits
db indicates from which databases the traits will be downloaded
**available_traits**

Details

This dataframe can be viewed by those users who want to use the `tr8()` function in a non-interactive way (i.e. not willing to use the GUI for selecting traits to be retrieved). The users should take note of the `short_code` used for the traits of interest, since these are the codes that should be passed to `tr8` in the `download_list` parameter.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

Examples

data(available_tr8)
## Not run:
tr8(species_list=c("Salix alba","Populus nigra"),download_list=c("life_form_P"))

## End(Not run)

<table>
<thead>
<tr>
<th>available_traits</th>
<th>available_traits shows which traits are available for download</th>
</tr>
</thead>
</table>

Description

The function is meant to help users in showing which traits (and from which databases) can be downloaded

Usage

`available_traits()`

Details

Users can call the function to see what data are available for download and decide which one should be passed to the `tr8()` function (in the `download_list` argument); the codes to be used as the `download_list` argument are those contained `short_code` column.

Value

a data frame

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

`tr8`
Examples

## available_traits()
# If the traits `Maximum area` and `Leaf area` from
# Ecoflora are needed for the species Salix alba and Populus nigra, type
# Not run:
tr8(species_list=c("Salix alba","Populus nigra"),download_list=c("life_form_P"))
# End(Not run)

---

**biolflor_lookup**

---

**Description**

This dataframe is used to retrieve species URLs from the BiolFlor website (`http://www.ufz.de/biolflor/index.jsp`).

**Usage**

`biolflor_lookup`

**Format**

A data frame with 3688 observations on the following 8 variables.

- **submittedname**: a character vector containing the original species’ names as used in BiolFlor
- **acceptedname**: a character vector containing the accepted name according to the `tnrs` function
- **sourceid**: a character vector; all the names are checked against the `iPlant_TNRS` database
- **score**: a character vector expressing the score for matching submitted and accepted names
- **matchedname**: name matched by the `tnrs` function
- **authority**: a character vector
- **V1**: a character vector
- **V2**: url of the BiolFlor web page for the species of interest

**References**

Please use the follow citation ay time you use data derived from Biolflor: BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde 38: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

**Examples**

`head(biolflor_lookup)`
**Description**

A list containing a brief description of traits data retrieved by the various databases; it's used as a hash table by some internal TR8 functions.

**Format**

Each element contains a key which expresses the short name for the traits that TR8 can download and to each key a three-elements vector is associated, which contains a shorter code for the trait, a long description of the trait and the reference database

- `height_max` :c( "h_max","Maximum height","Ecoflora")
- `height_min` :c( "h_min","Minimum height","Ecoflora")
- `leaf_area` :c( "le_area","Leaf area","Ecoflora")
- `leaf_longevity` :c( "le_long","Leaf longevity","Ecoflora")
- `Photosynthetic_pathway` :c( "phot_path","Photosynthetic pathway","Ecoflora")
- `life_form` :c( "li_form","Life form","Ecoflora")
- `Vegetative_reprod_method` :c("reprod_meth","Vegetative reprod method","Ecoflora")
- `Flowering_earliest_month` :c("flw_early","Flowering earliest month","Ecoflora")
- `Flowering_latest_month` :c("flw_late","Flowering latest month","Ecoflora")
- `Pollen_vector` :c( "poll_vect","Pollen vector","Ecoflora")
- `Seed_weight_mean` :c("seed_wght","Seed weight mean","Ecoflora")
- `Method_of_propagation` :c( "propag","Method of propagation","Ecoflora")
- `Ellenberg_light_Eco` :c( "ell_light_uk","Ellenberg light","Ecoflora")
- `Ellenberg_moisture_Eco` :c( "ell_moist_uk","Ellenberg moisture","Ecoflora")
- `Ellenberg_ph_Eco` :c( "ell_pH_uk","Ellenberg pH","Ecoflora")
- `Ellenberg_nitrogen_Eco` :c( "ell_N","Ellenberg nitrogen","Ecoflora")
- `Ellenberg_salt_Eco` :c( "ell_S","Ellenberg salt","Ecoflora")
- `age_of_first_flowering` :c( "age_first_flowering","Age of first flowering","LEDA")
- `branching` :c( "branching","Branching","LEDA")
- `bud_bank_seasonality_soil` :c( "bud_bank_seasonality_soil","Bud bank seasonality at soil level","LEDA")
- `buoyancy` :c( "buoyancy","Buoyancy","LEDA")
- `canopy_height` :c( "canopy_height","Mean canopy height","LEDA")
- `dispersal` :c( "dispersal","Dispersal type","LEDA")
- `leaf_distribution` :c( "leaf_distribution","Leaf distribution along the stem","LEDA")
- `leaf_dmc` :c( "leaf_dmc","Leaf dry matter content ","LEDA")
leaf_mass :c( "leaf_mass","Leaf mass","LEDA")
leaf_size :c( "leaf_size","Leaf size","LEDA")
dispersal_morphology :c( "dispersal_morphology","Dispersal morphology","LEDA")
growth_form :c( "growth_form","Growth form","LEDA")
life_span :c( "life_span","Life span","LEDA")
releasing_height :c( "releasing_height","Releasing height","LEDA")
sbank :c( "sbank","Seed bank","LEDA")
seed_mass :c( "seed_mass","Seed mass","LEDA")
shoot_growth_form :c( "shoot_growth_form","Shoot growth form","LEDA")
seed_number_per_shoot :c( "seed_number_per_shoot","Seed number per shoot","LEDA")
woodiness :c( "woodiness","Woodiness","LEDA")
terminal_velocity :c( "terminal_velocity","Terminal velocity","LEDA")
Life_form :c( "li_form_B","Life form","BiolFlor")
Life_span :c( "li_span","Life span","BiolFlor")
Rosettes :c( "ros","Rosettes","BiolFlor")
Type_of_reproduction :c( "reprod_B","Type of reproduction","BiolFlor")
Strategy_type :c( "strategy","Strategy type","BiolFlor")
Pollen_vector :c( "poll_vekt_B","Pollen vector","BiolFlor")
L :c( "ell_L_it","Ellenberg value for light in Italy","Pignatti")
T :c( "ell_T_it","Ellenberg value for temperature in Italy","Pignatti")
C :c( "ell_C_it","Ellenberg value for continentality in Italy","Pignatti")
U :c( "ell_U_it","Ellenberg value for humidity in Italy","Pignatti")
R :c( "ell_R_it","Ellenberg value for soil reaction in Italy","Pignatti")
N :c( "ell_N_it","Ellenberg value for nitrogen in Italy","Pignatti")
S :c( "ell_S_it","Ellenberg value for salinity in Italy","Pignatti")
life_form_P :c( "life_form_P","Life form for Italian Flora","Pignatti")
corotipo :c( "distribution_p","Distributions of species for the Italian Flora","Pignatti")
IT_beg_flow :c( "IT_beg_flow","Beginning of flowering in Italy","Pignatti")
IT_end_flow :c( "IT_end_flow","End of flowering in Italy","Pignatti")
Myco_infection :c( "Myco_infection","Infection of AMF according to Akhmetzhanova et al.","AMF")
MycoFlor :c( "MycoFlor","Infection of AMF according to MycoFlor","AMF")
inflorescence_fr :c( "inflorescence_fr","Type of inflorescence","Catminat")
sex_reprod_fr :c( "sex_reprod_fr","Type of sexual reproduction","Catminat")
poll_vect_fr :c( "poll_vect_fr","Pollen vector","Catminat")
fruit_type_fr :c( "fruit_type_fr","Type of fruit","Catminat")
dissemination_fr :c( "dissemination_fr","Type of dissemination","Catminat")
flower_colour_fr :c( "flower_colour_fr","Flower colour","Catminat")
ell_L_fr :c( "ell_L_fr","Ellenberg values for Light","Catminat")
elle_T_fr :c( "elle_T_fr","Ellenberg values for temperature","Catminat")
ell_C_fr :c( "ell_C_fr","Ellenberg values for continentality","Catminat")
ell_U_atm_fr :c( "ell_U_atm_fr","Ellenberg values for atmospheric moisture","Catminat")
ell_U_fr :c( "ell_U_fr","Ellenberg values for moisture","Catminat")
ell_R_fr :c( "ell_R_fr","Ellenberg values for soil reaction","Catminat")
ell_N_fr :c( "ell_N_fr","Ellenberg values for nitrogen","Catminat")
ell_S_fr :c( "ell_S_fr","Ellenberg values for salt","Catminat")
Soil_texture_fr :c( "Soil_texture_fr","Type of soil texture","Catminat")
organic_matter_fr :c( "organic_matter_fr","Organic matter in the soil","Catminat")
beg_flow_fr :c( "beg_flow_fr","Beginning of flowering (month)","Catminat")
end_flow_fr :c( "end_flow_fr","End of flowering (month)","Catminat")

Author(s)
Gionata Bocci <boccigionata@gmail.com>

References

BiolFlor
 Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bunde-
 samt für. Bonn, Bundesamt für Naturschutz)

Ecoflora
’http://www.ecoflora.co.uk’

LEDA traitbase
Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnen-
 schein, M., Poschloid, P., Van Groenendael, J.M., Klimes, L., Klimesova, J., Klotz, S., Rusch, G.M.,
 Hermy, M., Adriaens, D., Boedeltje, G., Bossuyt, B., Dannemann, A., Endels, P., Götzenberger, L.,
 Hodgson, J.G., Jackel, A-K., Kühn, I., Kunzmann, D., Ozinga, W.A., Römermann, C., Stadler, M.,
 Schlegelmilch, J., Steendam, H.J., Tackenberg, O., Wilmann, B., Cornelissen, J.H.C., Eriksson, O.,

Akhmetzhanova et al, 2012
Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V . A.,
database for 3000 vascular plants species across the former Soviet Union. Ecology 93:689. URL:
http://esapubs.org/Archive/ecol/E093/059/default.htm

Pignatti et al., 2005
Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d’Italia. Braun-
Blanquetia 39, Camerino, pp. 97.

Julve, 1998

BROT

AND

Examples

```r
## inspect the structure of the list
str(column_list)
```

---

**ECOFLORA_df**

### Description

This dataset is not ment to be directly accessed by the final user. It is imported by the `ecoflora()` function to extrapolate the correct URL for each species of interest and download the corresponding functional traits. This dataset is used as a lookup table from the `ecoflora()` function.

### Format

A data frame containing URL for the species contained in the Ecoflora web database.

- **species** a vector containing the species names as defined on Ecoflora website
- **web_link** a character vector containing the URL of each species trait web page
- **acceptedname** a character vector containing the accepted name according to TNRS
- **sourceid** a character vector containing the source used by the `taxize::tnrs` function
- **score** a numeric vector containing the score obtained by `taxize::tnrs` function
- **matchedname** a character vector containing the matched names by `taxize::tnrs`
- **uri** a character vector containing Ecoflora-URL for each species

### References

Please alwasy cite the database according to:

imkerbond_check

Examples

```r
## observe the data for the first few species
## Not run:
head(ECOFLORA_df)

## End(Not run)
```

---

imkerbond_check  
*Set of plant species names to be corrected.*

---

**Description**

*imkerbond_check* defines a list containing pairs in the form *original plant species names in the retrieved data = corrected names*. This list is used from the `tr8` function to correct the wrong plant species names found in the original dataset retrieved from the 'http://users.telenet.be/imkerbondzoersel/bijenplanten.html' website.

**Format**

The format is: a list of pairs of plant species names, each pair contains the original name and the corrected name.

**References**

'http://users.telenet.be/imkerbondzoersel/bijenplanten.html'

**Examples**

```r
## observe the structure of the dataset
str(imkerbond_check)
```

---

leda_download_to_local_directory

*A utility to download a local copy of the LEDA data files.*

---

**Description**

Allows the user to retrieve the data files from the LEDA Traitbase website, merge them in a single R dataset and store the result in a local file; this file could be then used whenever the tr8() function is used in order to speed up the process of retrieving traits data.

**Usage**

```r
leda_download_to_local_directory(directory)
```
Arguments

directory is the directory where the downloaded data will be stored (in order to be used in future R sessions); default is NULL.

Details

The function uses a GUI created via the gWidgets package, to let the user select a folder where the datasets has to be stored.

Value

The function save a local copy of LEDA data in a file called leda_database.Rda

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References


Description

Downloads the mean floating capacity values from LEDA traitbase.

Usage

leda_fc(species_list)

Arguments

species_list a vector of plant species names

Value

Returns a dataframe where for each plant species (row) mean values of Floating Capacity are reported - if present in the LEDA database - for each category of dispersal type.
Author(s)
Gionata Bocci <boccigionata@gmail.com>

References

See Also
tr8()

| leda_lookup | List with reference variables needed to download traits from LEDA Traitbase |

Description
Contains useful references for the LEDA Traitbase: these data are used by the TR8 package to find URLs of the different .txt files containing the raw data.

Usage
data(leda_lookup)

Format
Each element contains a key which express the short name for the traits of interest (to be retrieved from the LEDA Traitbase), to each key a four-elements vector is associated, which contains the name of the .txt files hosted at the LEDA website which contain the trait data, a int which express the number of rows to be skipped when reading the txt file, a longer code for the trait, a short code for the trait.

age_of_first_flowering
branching
bud_bank_seasonality_soil
buoyancy
canopy_height
dispersal
leaf_distribution
leaf_dmc
leaf_mass
leaf_size
dispersal_morphology
growth_form
life_span
releasing_height
sbank
seed_mass
shoot_growth_form
seed_number_per_shoot
woodiness
terminal_velocity

Source
'http://www.leda-traitbase.org/LEDAportal/citation.jsp'

References
Please cite the following reference any time you use data retrieved from the LEDA traitbase:

Examples
head(leda_lookup)

---

list_of_traits_Biolflor

Description
a vector containing traits that can be downloaded from Biolflor

Format
A vector of plant traits
local_storage

Author(s)
Gionata Bocci <boccigionata@gmail.com>

References
Please use the following citation any time you use data derived from BIOLFLOR:

Examples
```r
## have a look at the first rows of the dataset
head(list_of_traits_Biolflor)
```

local_storage

A utility to store a local copy of traits data

Description
local_storage can download traits data from LEDA and Akhmetzhanova databases and store them in a local folder.

Usage
```r
local_storage(db, directory)
```

Arguments
db can contain the following values: "AMF" and "LEDA" depending on the database which should be downloaded
directory the directory where the local Rda files will be stored

Details
Downloading data from the web is time consuming, thus a local storage of some traits data will speed up future data requests; this is possible for LEDA and Akhmetzhanova databases. The function must be run only once (ideally before running the `tr8` function for the first time): thanks to the `rappdirs` package, the downloaded data will be stored in the directory commonly used for user data (which depends on the Operatim System where R is running). Users can change the destination folder through the `directory` parameter, passing the full path of the directory to be used by the function.

Value
nothing
Description

`pignatti` is a dataframe containing traits data for Italian species

Format

Contains the following traits data about Italian Flora species

- **Specie.Pignatti**: species name in the original dataset
- **numero**: numeric code
- **codice**: numeric code
- **nome.scientifico**: scientific name with authors
- **forma.biologica**: life form
- **corotipo**: distribution of species
- **L**: Ellenberg value for light
- **T**: Ellenberg value for temperature
- **C**: Ellenberg value for continentality
- **U**: Ellenberg value for soil humidity
- **R**: Ellenberg value for soil pH
- **N**: Ellenberg value for Nutrients in the soil
- **S**: Ellenberg value for soil salinity
- **Name.tnrs**: species name according to tnrs

References


Examples

```r
# inspect the first rows of the dataset
head(pignatti)
```
Description

Contains species names without authors which correspond to the ones in PLANTS traitbase.

Usage

data("ref_PLANTS")

Format

Scientific.Name: this is the name used in the original dataset
acceptedname: the accepted name of the species used obtained using taxize::tnrs
score: score for the species names’ matching, returned by taxize::tnrs
matchedname: the matched named returned by taxize::tnrs
authority: species authors’ names
Symbol: code used in the original dataset
Synonym.Symbol: code used in the original dataset

Details

This dataframe is not meant to be managed by users: it serves as a lookup table for the tr8 function in order to speed-up data retrieval

Source

‘http://www.bricol.net/’

References

‘http://www.bricol.net/’

Examples

data(ref_PLANTS)
tr8: a function for retrieving functional traits data from various databases.

Description

tr8 makes internally use of other functions provided by the TR8 package in order to query various databases and provide the user with a dataframe containing traits data for the species of interest. At the moment the following databases are available:

- Biolflor ‘http://www.ufz.de/biolflor/index.jsp’
- Ecological Flora of the British Isles ‘http://www.ecoflora.co.uk/’
- LEDA traitbase ‘http://www.leda-traitbase.org/LEDAportal/’
- Ellenberg values for Italian Flora
- Mycorrhizal intensity database ‘http://esapubs.org/Archive/ecol/E093/059/default.htm’
- MycoFlor ‘http://www.esajournals.org/doi/abs/10.1890/12-1700.1’
- Catminat ‘http://philippe.julve.pagesperso-orange.fr/catminat.htm’
- BROT ‘http://www.uv.es/jgpausas/brot.htm’
- PLANTS ‘http://www.bricol.net/’
- Imkerbond Zoersel ‘http://users.telenet.be/imkerbondzoersel/’

The function can either be used in an interactive way (i.e. if the gui_config parameter is set to TRUE, a multi-panel GUI will ask users to choose among lists of available traits) or in a non-interactive way (providing the function with a vector containing the short codes of the trait which should be downloaded - in order to have an idea of the available traits and the associated codes to be used for the download_list, see the available_traits function).

Usage

```
tr8(species_list, download_list = NULL, gui_config = FALSE, synonyms = FALSE,
    catminat_alternatives = FALSE)
```

Arguments

- `species_list`: a vector containing names of the plant species for which traits data want to be extracted.
- `download_list`: a vector containing the short codes of traits which should be downloaded (to be used as an alternative to the GUI interface).
- `gui_config`: if set to TRUE a GUI for selecting traits of interest is shown (default is FALSE).
- `synonyms`: if set to TRUE tr8 will use taxize to find synonyms for the species names provided with the `species_list` parameter and will return trait values for all those species; in that case the dataframe contained in the `results` slot will have two additional columns called `synonyms` (which contains the synonyms found using tnr5s) and another one called `original_names` which includes the original names provided with `species_list` (default is FALSE).
catminat_alternatives

if set to TRUE tr8 will search, within the Catminat traitbase, for entries which contain, in their names, the ones in the provided species_list; e.g. if "Myrtus communis" is included in the species_list, tr8 will query the following existing entries in Catminat: "Myrtus communis", "Myrtus communis v. communis" and "Myrtus communis v. leucocarpa". (default is FALSE)

Details

Not all traitbases use the most updated accepted names, thus different traitbases may use different names for the same biological entity; it is not easy to find an automatic way to solve this issue, thus users are urged to always check the results provided by the tr8 function. In order to help users, the new version of the function accepts two parameters, synonyms and catminat_alternative so that data will be retrieved also for species which are not directly requested, but may be of interest for the user (e.g. in Catminat currently there are not traits for "Myrtus communis" but there are some for its subspecies). In this case some careful manual work will be required later in order to select species and traits of interest.

Value

An object of class Tr8; the slots @results contains various traits data for the species of interest.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Please always use the following citations any time you use trait data retrieved with tr8

BiolFlor


Ecoflora


Akhmetzhanova et al, 2012

Pignatti et al., 2005


MycoFlor

Mycorrhizas in the Central European flora: relationships with plant life history traits and ecology

Catminat


BROT


AND


PLANTS


See Also

bib()

Examples

```r
## Not run:
## download some trait data for Abies alba
My_traits<-tr8(species_list=c("Abies alba"),download_list=c("life_form_P"))

## End(Not run)
```

Tr8-class

Class "Tr8"

Description

Class Tr8 is used as a "container" for all other functions and classes needed to download traits data from various databases.
Objects from the Class

Objects can be created by calls of the form `new("Tr8", ...)`.

Slots

- `species_list`: Object of class "vector" list of species for which traits data are to be searched.
- `results`: Object of class "data.frame" dataframe containing scraped traits.
- `not_valid`: Object of class "vector" species whose name were not present in the Ecoflora database.
- `double_names`: Object of class "vector" species for which more than one name was found.

Methods

- `bib` signature(.Object = "Tr8"): method to get bibliographic references for the downloaded data.
- `issues` signature(.Object = "Tr8"): method to underline 'problematic' species.
- `extract_traits` signature(object = "Tr8"): method to extract the object@results dataframe from a Tr8 object.
- `lookup` signature(.Object = "Tr8"): a method to show brief reference for the downloaded data.
- `issues` signature(.Object = "Tr8"): method to print species names for which data retrieval was problematic (e.g. double entries in remote databases).

Note

Additional datasets may be added in future.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

`tr8`

Examples

```r
## Not run:
## the bib() methods let the user have the exact
## bibliographic citations to be used for the
## retrieved data

## download some trait data for Abies alba

My_traits<-tr8(species_list=c("Abies alba"),download_list=c("life_form_P"))

## See what citations should be used for the data
## bib(My_traits)
```
tr8_setup

A function to download the most recent url-tables for some traitbases.

Description

For some traitbases tr8 uses lookup-tables which contain URLs of the species of interest; some of the traitbases queried by tr8 are uploaded from time to time thus the function may be unable to retrieve traits data for the most recently uploaded species. This function allows the user to refresh some of these lookup tables. **BEWARE:** this function takes a long time to run (nearly 20 minutes are required - on a fast connection - for retrieving lookup tables for BiolFlor).

Usage

```
tr8_setup()
```

tr8_config

tr8_config a GUI to configure TR8 package.

Description

This function will make a simple GUI appear which contains a tab for each trait database: the user can choose which traits should be downloaded by the tr8 function.

Usage

```R
tr8_config()
```

Value

Returns a list containing the selected traits for each source of information

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

tr8()
Details
At the moment BiolFlor and Ecoflora lookup tables are re-generated by this function.

Value
The values does not return anythys useful for the user; it’s used for its side effects, i.e. it stores the retrieved lookup table in one directory for later use from the tr8 function.

Warning
The function takes a lot to run; I suggest to run it just at your first installation of the TR8 package.

Author(s)
Gionata Bocci <boccigionata@gmail.com>

Examples
```r
## Not run:
tr8_setup()

## End(Not run)
```

---

**traits_eco**

Set of functional traits to be retrieved by Ecoflora.

Description
traits_eco defines a list containing pairs in the form `short_name_of_the_trait = corresponding_code_in_Ecoflora`

At the moment the package does not download all the traits available at Ecoflora; curious users can expand the number of downloadable traits simply extending the list with other 'pairs' (take care of using the right Ecoflora codes as described in 'http://www.ecoflora.org.uk/search_plantchar.php').

Format
The format is: a list containing 17 elements, where each element is a pair of the form "traits":"code used in Ecoflora HTML code":

- `height_max` : num 3.05
- `height_min` : num 3.06
- `leaf_area` : num 3.17
- `leaf_longevity` : num 3.22
- `Photosynthetic_pathway` : num 4.02
- `life_form` : num 5.01
- `Vegetative_reprod_method` : num 5.05
- `Flowering_earliest_month` : num 5.07
Flowering_latest_month : num 5.08
Pollen_vector : num 5.15
Seed_weight_mean : num 5.34
Method_of_propagation : num 5.52
Ellenberg_light_Eco : num 7.14
Ellenberg_moisture_Eco : num 7.15
Ellenberg_pH_Eco : num 7.16
Ellenberg_nitrogen_Eco : num 7.17
Ellenberg_salt_Eco : num 7.18

References

Examples
## Not run:
data(traits_eco)

## End(Not run)

Description
a vector containing traits that can be downloaded from Biolflor

Format
A vector of plant traits

Author(s)
Gionata Bocci <boccigionata@gmail.com>

References
Please use the follow citation ay time you use data derived from Biolflor:
**Description**

A vector containing traits that can be downloaded from Biolflor

**Format**

A vector of plant traits

**Author(s)**

Gionata Bocci <boccigionata@gmail.com>

**References**

Please use the follow citation ay time you use data derived from Biolflor:


**Examples**

```r
## Not run:
data(traits_special_Biolflor)

## End(Not run)
```