

Package: TR8 (via r-universe)

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Type Package

Title A Tool for Downloading Functional Traits Data for Plant Species

Version 0.9.22

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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 (Bioflor, 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 (>= 3.5.0), methods, stats, utils

Imports RCurl, XML, dplyr, plyr, reshape, rappdirs, readxl, shiny, taxize

RoxygenNote 7.1.1

Repository <https://giobo.r-universe.dev>

RemoteUrl <https://github.com/giobo/tr8>

RemoteRef HEAD

RemoteSha 10ab03648e726530d9f13c438b23ceda0adf82c4

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Description

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

- Bioflor '<http://www.ufz.de/bioflor/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

Package: TR8
Type: Package
Version: 0.9.22
Date: 2020-10-08
License: GPL>=2
Depends: XML, RCurl, plyr, readxl

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

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Ecoflora

Fitter, A . H. and Peat , H. J. (1994). The Ecological Flora Database, J. Ecol., 82, 415-425. 'http://www.ecoflora.co.uk'

LEDA traitbase

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008). The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

Akhmetzhanova et al, 2012

Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V. A., Selivanov, I.A., and Cornelissen, J. H. C. (2012): A rediscovered treasure: mycorrhizal intensity database for 3000 vascular plants species across the former Soviet Union. *Ecology* 93:689. 'http://esapubs.org/Archive/ecol/E093/059/default.htm'

Hempel et al, 2013

Hempel, S., Götzenberger, L., Kühn. I., Michalski, S.G., Rillig, M.C., Zobel, M., and Moora, M., 2013. Mycorrhizas in the Central European flora: relationships with plant life history traits and ecology. *Ecology* 94: 1389-1399.

Pignatti et al., 2005

Pignatti, S., Menegoni, P., Pietrosanti, S. (2005). Biondificazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. *Braun-Blanquetia* 39, Camerino, pp. 97.

Catminat

Julve, P., 1998 ff. - Baseflor. Index botanique, écologique et chorologique de la flore de France. Version : 26 November 2014. <http://perso.wanadoo.fr/philippe.julve/catminat.htm>

BROT

Paula S, Arianoutsou M, Kazanis D, Tavsanoğlu Ç, Lloret F, Buhk C, Ojeda F, Luna B, Moreno JM, Rodrigo A, Espelta JM, Palacio S, Fernández-Santos B, Fernandes PM, and Pausas JG. 2009. Fire-related traits for plant species of the Mediterranean Basin. *Ecology* 90: 1420.

AND

Paula S. & Pausas J.G. 2013. BROT: a plant trait database for Mediterranean Basin species. Version 2013.06. URL: <http://www.uv.es/jgpausas/brot.htm>

PLANTS

Green, W. (2009) USDA PLANTS Compilation, version 1, 09-02-02.

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

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)
```

available_traits	<i>available_traits shows which traits are available for download</i>
------------------	---

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_t_code` column.

Value

a data frame

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

`tr8`

Examples

```
## available_traits()
## If the traits \code{Maximum area} and \code{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	<i>Retrieve traits data from the BiolFlor website.</i>
----------	--

Description

This function allows the user to download some pre-defined traits from the BiolFlor website: the function returns a dataframe with species name in row and traits data in column.

Usage

```
biolflor(list_species, TRAITs)
```

Arguments

list_species	vector containing names of those plant species for which traits data need to be downloaded.
TRAITs	a vector containing the traits to be downloaded (used as a check for <code>tr8_gui()</code> created variables)

Value

dataframe with species name in row and traits data in column.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

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

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Examples

```
## Not run:  
biolflor(c("Abies alba"))  
  
## End(Not run)
```

biolflor_check	<i>biolflor_check</i>
----------------	-----------------------

Description

A lookup dataframe for checking species names on the Biolflor website confronting them with the `tnrs` function

Format

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

submittedname name of plant species submitted to `tnrs`

acceptedname accepted name according to `tnrs`

sourceid sourceid according to `tnrs`

score score of matching species names according to `tnrs`

matchedname matched name according to `tnrs`

annotations plant species authors

uri url for the plant species on the `tnrs` website

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

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

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLORE - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für Naturschutz, Bonn, Bundesamt für Naturschutz)

Examples

```
## See the first lines of the data frame
head(biolflor_check)
```

biolflor_clean	<i>Removes redundant text in traits collected from Biolflor</i>
----------------	---

Description

BiolFlor tables contains brief explanations of traits: that is ok for the website but tends to produce clumsy tables in dataframes returned by `tr8()`, thus this extra-text is removed (to improve readability of such tables). This function is internally used by `tr8()`, users do not need to run it.

Usage

```
biolflor_clean(input)
```

Arguments

`input` a intermediate dataframe retrieved by `tr8()`

Value

a dataframe with shortened names for the traits levels' values

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

[biolflor](#)

Examples

```
biolflor_clean(biolflor("Avena sativa"))
```

biolflor_lookup	<i>biolflor_lookup</i>
-----------------	------------------------

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 following citation any 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)
```

biolflor_lu

biolflor_lu

Description

A lookup dataframe for retrieving data from the BiolFlor website

Format

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

V1 name of plant species

V2 url of the BiolFlor webpage containing traits data for the species

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

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

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Examples

```
## Not run:  
data(biolflor_lu)  
  
## End(Not run)
```

biolflor_traits-class *Class "biolflor_traits" for containing traits retrieved from Biolflor*

Description

This class is used to retrieve traits data from species contained in the Biolflor web database

Objects from the Class

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

Slots

url: Object of class "character": url of the corresponding web page for the species of interest
extracted: Object of class "list" a list of traits
list_traits: Object of class "vector" a vector containing the list of traits which can be downloaded by the package
list_special_traits: Object of class "vector": some of the traits require special Xpath rules to be extracted, thus a special slots is devoted to them

Methods

extract signature(.Object = "biolflor_traits"): ...

Note

Only a subset of the traits available on BiolFlor will be downloaded from TR8

Author(s)

Gionata Bocci <boccionata@gmail.com>

References

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

See Also

See Also as [biolflor](#)

Examples

```
showClass("biolflor_traits")
```

column_conversion	<i>column_conversion</i>
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Description

Shortens up columns' names in the intermediate steps of `tr8()` retrieved data

Usage

```
column_conversion(DF)
```

Arguments

DF a intermediate dataframe built by `tr8`

Details

This function is internally used by `tr8()`.

Value

a dataframe with shortened col names

Author(s)

Gionata Bocci <boccigionata@gmail.com>

column_list	<i>column_list</i>
-------------	--------------------

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 express 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_vect_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")
ell_T_fr :c("ell_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**

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Ecoflora

Fitter, A . H. and Peat , H. J. (1994). The Ecological Flora Database, J. Ecol., 82, 415-425. 'http://www.ecoflora.co.uk'

LEDA traitbase Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008). The LEDA Traitbase: A database of life-history traits of Northwest European flora. Journal of Ecology 96: 1266-1274.

Akhmetzhanova et al, 2012

Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V. A., Selivanov, I.A., and Cornelissen, J. H. C. (2012): A rediscovered treasure: mycorrhizal intensity 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

Pignatti, S., Menegoni, P., Pietrosanti, S. (2005). Biondicazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. Braun-Blanquetia 39, Camerino, pp. 97.

Julve, 1998

Julve, P., 1998 ff. - Baseflor. Index botanique, écologique et chorologique de la flore de France. Version : 26 November 2014 . URL: <http://perso.wanadoo.fr/philippe.julve/catminat.htm>

BROT

Paula S, Arianoutsou M, Kazanis D, Tavsanoğlu Ç, Lloret F, Buhk C, Ojeda F, Luna B, Moreno JM, Rodrigo A, Espelta JM, Palacio S, Fernández-Santos B, Fernandes PM, and Pausas JG. 2009. Fire-related traits for plant species of the Mediterranean Basin. Ecology 90: 1420.

AND

Paula S. & Pausas J.G. 2013. BROT: a plant trait database for Mediterranean Basin species. Version 2013.06. URL: <http://www.uv.es/jgpausas/brot.htm>

Examples

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

control	<i>control</i>
---------	----------------

Description

A function to check if the user wants to download some traits from a certain database.

Usage

```
control(name_variable, dframe, DB)
```

Arguments

name_variable	name of the variable set up by <code>tr8_config()</code>
dframe	a dataframe containing traits definition (created by the <code>tr8()</code> function).
DB	name of the database to be used (eg. "Ecoflora")

Details

This function check whether the user has run the `tr8_config()` function and, in case he did, which traits were selected (i.e. need to be downloaded by the `tr8` function) for each database. These variables have the form "res_NAMEDB" (eg. `res_Bioflor`) and they contain the "output" of a "gWidget::notebook" window. The values of these variables can be accessed through the `svalue`

Value

a vector of selected traits (if the variable was set through the `tr8_config()` function OR NULL if `tr8_config()` was run, but no traits were chosen for that database OR an empty vector if `tr8_config()` was not run.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

`tr8()`

ecoflora	<i>Retrieves traits data from Ecoflora website</i>
----------	--

Description

The function accepts a list of plant species names, tries to download the corresponding functional traits from the Ecoflora website ('http://www.ecoflora.co.uk/') and return a data.frame with species names as rows and functional traits as columns.

Usage

```
ecoflora(species_list, reference = ECOFLORA_df, TRAITS)
```

Arguments

species_list	a vector containing list of plant species names.
reference	the reference lookup data.frame (this is not ment to be set by users; it is left here for further development)
TRAITS	a vector containing the traits to be downloaded (used as a check for tr8_gui() created variables)

Value

Return a data.frame with species as rows and traits as columns. Only those species present in the Ecoflora database will be included in this data.frame, other species will be left out.

Author(s)

Bocci Gionata

References

Fitter, A . H. and Peat , H. J., 1994, The Ecological Flora Database, J. Ecol., 82, 415-425.

See Also

[traits_eco](#)

Examples

```
## Not run:  
#My_data<-ecoflora(species_list=c("Abies alba"))  
  
## End(Not run)
```

Ecoflora-class	<i>Class "Ecoflora": Class containing traits from Ecological Flora of the british Isles</i>
----------------	---

Description

The class is a box containing url and traits data for species which are present in the Ecoflora website

Objects from the Class

Objects can be created by calls of the form `new("Ecoflora", species_list, reference, traits)`.

Slots

species_list: Object of class "vector" a list of species for which traits data are to be searched

reference: Object of class "data.frame" a data frame containing web pages of the searched species

df: Object of class "data.frame" a temporary df

not_valid: Object of class "vector" species whose name were not present in the Ecoflora database

results: Object of class "data.frame" dataframe containing scraped traits

traits: Object of class "list" codes for the traits to be searched

double_names: Object of class "vector" species for which more than one name was found

Methods

initialize signature(.Object = "Ecoflora"): when initialized, some slots will be "cleaned"

retrieve signature(.Object = "Ecoflora"): instructions to scrape data from the website

Note

Not all species listed on the Ecoflora website have all the listed traits.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Fitter, A . H. and Peat , H. J. (1994). The Ecological Flora Database, J. Ecol., 82, 415-425.

See Also

See Also [ecoflora](#)

Examples

```
showClass("Ecoflora")
```

 ECOFLORA_df

ECOFLORA_df: local lookup table for Ecoflora species' url(s)

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 always cite the database according to:

Fitter, A . H. and Peat , H. J., 1994, The Ecological Flora Database, J. Ecol., 82, 415-425.

Examples

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

## End(Not run)
```

 ellenberg_pignatti-class

Class "ellenberg_pignatti" to contain ellenberg values for Italian Flora's species

Description

The class is used to extract data from a database which contains traits data for species belonging to the italian flora.

Objects from the Class

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

Slots

`species_list`: Object of class "vector" a vector of plant species names

`results`: Object of class "data.frame" containing the results of the queries

`not_valid`: Object of class "vector" containing names of 'problematic' species

Methods

`get_traits` signature(`.Object` = "ellenberg_pignatti"): ...

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Pignatti S., Menegoni P., Pietrosanti S., 2005, Biondificazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. Braun-Blanquetia 39, Camerino, pp. 97.

See Also

See Also as [pignatti_f](#)

Examples

```
showClass("ellenberg_pignatti")
```

extract

extract data from biolflor_traits classes

Description

extract data fro biolflor_traits classes

Usage

```
extract(.Object)
```

Arguments

`.Object` an object of biolflor_traits signature

```
get_italian_flowering get_italian_flowering
```

Description

Gets the beginning and the end of the flowering phase for the italian flora. Values are based on Pignatti and retrieved from the '<http://luirig.altervista.org/>'

Usage

```
get_italian_flowering(species_list, TRAITS)
```

Arguments

`species_list` : a vector containing species names
`TRAITS` : a vector containing the traits to be downloaded (used as a check for `tr8_gui()` created variables)

Value

a dataframe with two columns, the beginning and the end month (expressed as a number from 1 to 12) of the flowering phase

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

'<http://luirig.altervista.org/>'

```
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/bijenplan>' 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

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

leda

Extracts functional traits from the LEDA traitbase.

Description

leda allows the user to extract data from *LEDA_df* which is a '<http://www.leda-traitbase.org/LEDAportal/>'. subset of the data available on the LEDA traitbase website

Usage

```
leda(species_list, TRAITS, rearranged)
```

Arguments

species_list	a vector containing names of plant species
TRAITS	a vector containing the traits to be downloaded (used as a check for <code>tr8_gui()</code> created variables)
rearranged	a variable which passes the already downloaded LEDA dataset if this is available (NULL otherwise)

Details

The function returns a data.frame with species as rows and LEDA functional traits as columns. NA will be used for those traits which do not have values in the LEDA traitbase. Species names are converted to *accepted* names (*sensu* TNRS).

Value

dataframe containing traits data and species names as row.names

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

See Also

leda_download_to_local_directory

Examples

```
## Not run:

#My_traits<-leda(species_list=c("Abies alba"))

## End(Not run)
```

LEDA_df

LEDA_df: local (partial) copy of the LEDA traitbase website.

Description

This data.frame includes a local copy of (some) of the parameters available on the LEDA website; up to now only few functional traits were taken into account. Hopefully the database will be extended in the following releases of the package. Please refer to <http://www.leda-traitbase.org/LEDAportal/plantTraits> for a detailed explanation of the traits available (definitions, units of measure, etc...) in LEDA.

Format

A data frame containing traits data for 8309 species.

SBS.name species name as used in LEDA

canopy_height.m : canopy height expressed in meters

mean.SLA..mm.2.mg. : mean value for specific leaf area expressed in $mm^2\ mm^{-1}$

mean.SM..mg. : seed mass in g

plant.growth.form : plant growth form

dispersal.type : dispersal type categories

acceptedname : accepted name according to *TNRS*

seed_longevity : longevity of the seedbank

sourceid : source of species name used by `taxize::tnrs`

score : score obtained by `taxize::tnrs`

matchedname : matched name obtained by `taxize::tnrs`

annotations :

uri : reference url for the species

Details

The original datasets are available as .TXT files in they raw form at '<http://www.leda-traitbase.org/LEDAportal/data>' what is found here is a selection of a few traits. A higher number of traits from LEDA may be included in the following releases of the package.

References

Please cite the following reference any time you use data retrieved from the LEDA traitbase (citation reported at '<http://www.leda-traitbase.org/LEDAportal/citation.jsp>'):

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

Examples

```
## Not run:
data(LEDAdf)

## End(Not run)
```

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

```
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

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Corneliss n, J.H.C., Eriksson, O., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96:1266-1274. ‘http://www.leda-traitbase.org/LEDAportal/data_files.jsp’

leda_fc

leda_fc

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

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96:1266-1274. ‘http://www.leda-traitbase.org/LEDAportal/data_files.jsp’

See Also

tr8()

leda_general

Function which takes care of downloading the .txt files composing the LEDA Traitbase

Description

Takes care of downloading the required .txt files and extract the trait (column of the table) of interest and return a dataframe with requested species' names as rows and LEDA traits as columns.

Usage

```
##leda_general(url, skip_row, species, column, out_name)
```

Arguments

url	the url of the txt file
skip_row	the number of the first rows of the file which should be left out (they contain information such as the SQL query needed to generate the file, but are of no use for the TR8 package)
species	Vector of plant species names
column	The name of the column containing the trait of interest in txt file
out_name	A short name to be used as the trait name in the returned dataframe

Value

The function returns a dataframe containing the column of interest from the original .txt file.

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Please cite the following reference any time you use data retrieved from the LEDA traitbase (citation reported at ‘<http://www.leda-traitbase.org/LEDAPortal/citation.jsp>’):

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

See Also

tr8()

Examples

```
## Not run:
age_of_first_flowering<-leda_general(url="age
  skip_row =4, column="age of first flowering", out_name="age_first_flowering",
  species=species)

## End(Not run)
```

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 contains the trait data, a int which expresses 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:

Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008): The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

Examples

```
head(leda_lookup)
```

```
list_of_traits_Biolflor
      list_of_traits_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:

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Examples

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

```
local_storage      A utility to storage 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

```
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 Operating System where R is running). Users can change the destination folder through the `directory` parameters, passing the full path of the directory to be used by the function.

Value

nothing

Author(s)

Gionata Bocci <boccigionata@gmail.com>

luirig

luirig

Description

Downloads flowering dates for Italian plant species

Usage

```
luirig(url)
```

Arguments

`url` a url provided by the function `get_italian_flowering`

Details

This function tries to retrieve the months of beginning and ending of the flowering period for species of the italian (data are collected from the website '<http://luirig.altervista.org/>'). The function is used by the `get_italian_flowering` function.

Value

a tuple of values: beginning and ending of flowering period (or NA,NA if data are not found)

Author(s)

Gionata Bocci <boccigionata@gmail.com>

See Also

`get_italian_flowering`

myco

myco

Description

A lookup dataframe for checking species names on the Bioflor website confronting them with the `tnrs` function

Format

A data frame with 2970 observations on the following 2 variables.

species name of plant species

Myco_infection score of AMF infection

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V. A., Selivanov, I.A., and Cornelissen, J. H. C. (2012): A rediscovered treasure: mycorrhizal intensity database for 3000 vascular plants species across the former Soviet Union. *Ecology* 93:689. [‘http://esapubs.org/Archive/ecol/E093/059/default.htm’](http://esapubs.org/Archive/ecol/E093/059/default.htm)

Examples

```
## Not run:  
#data(myco)  
  
## End(Not run)
```

pignatti

pignatti

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

Pignatti, S., Menegoni, P., Pietrosanti, S., 2005, Biondicazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. Braun-Blanquetia 39, Camerino, pp. 97.

Examples

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

pignatti_f	<i>Extracts ellenberg values for the Italia Flora as provided by Pignatti et al. (2005)</i>
------------	---

Description

This function is not ment to be used by the final user; it's used by the wrapper function `tr8()`

Usage

```
pignatti_f(species, TRAITS)
```


Arguments

species	a vector containing plant species names
TRAITS	a vector containing the traits to be downloaded (used as a check for tr8_gui() created variables)

Value

a data frame

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

Pignatti, S., Menegoni, P., Pietrosanti, S., 2005, Biondificazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. Braun-Blanquetia 39, Camerino, pp. 97.

 ref_PLANTS

 ref_PLANTS

Description

Contains species names without outhors 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)
```

retrieve_amf	<i>retrieve_amf</i>
--------------	---------------------

Description

Retrieve data about AMF potential inoculation for a list of plant species passed as argument

Usage

```
retrieve_amf(species, TRAITS)
```

Arguments

species	a vector containing names of plant species
TRAITS	a vector containing the traits to be downloaded (used as a check for tr8_gui() created variables)

Details

The returned dataframe comprises one column: `Myco_infection`

`Myco_infection` : a numeric vector containing percentage of infection as provided by Akhmetzhanova et al.

Value

a data frame

Author(s)

Gionata Bocci <boccigionata@gmail.com>

References

- Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V. A., Selivanov, I.A., and Cornelissen, J. H. C. (2012): A rediscovered treasure: mycorrhizal intensity database for 3000 vascular plants species across the former Soviet Union. Ecology 93:689. 'http://esapubs.org/Archive/ecol/E093/059/default.htm'

Examples

```
## Not run:  
##My_traits<-retrieve_amf(species_list=c("Abies alba"))  
  
## End(Not run)
```

seed_simplify	<i>seed_simplify a function to shorten levels for seed longevity</i>
---------------	--

Description

Used to shorten levels of Seed longevity according to LEDA traitbase

Usage

```
seed_simplify(tp)
```

Arguments

tp : a list obtained from the LEDA traitbase

Details

Short codes are obtained adopting the following rules:

LT "long-term persistent"

ST "short-term persistent"

T "transient"

P "present"

Value

a vector

Author(s)

Gionata Bocci <boccigionata@gmail.com>

tr8	<i>tr8: a function for retrieving functional traits data from various databases.</i>
-----	--

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:

- Bioflor ‘<http://www.ufz.de/bioflor/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 html-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).

When the HTML-GUI is being used, the user will have to select the traits of interest from the available lists and then click the "Send request" button and go back to the R console (NB: the browser web page will become inactive; the user will have to take care of closing it).

Usage

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

Arguments

- | | |
|----------------------------|--|
| <code>species_list</code> | a vector containing names of the plant species for which traits data want to be extracted. |
| <code>download_list</code> | a vector containing the short codes of traits which should be downloaded (to be used as an alternative to the GUI interface) |
| <code>gui_config</code> | 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 *tnrs*) 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)
- allow_persistent** if set to TRUE, tr8 will store retrieved databases from LEDA and Ecoflora into local files to speed up future queries; if FALSE, the downloaded data will be store in a temp directory that will be cleaned up at the end of the session; when NULL (default value), the user will be prompted for a choice between the two options.

Details

Not all traitbases use the most updated accepted names, thus different traibases 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

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Ecoflora

Fitter, A . H. and Peat , H. J. (1994). The Ecological Flora Database, *J. Ecol.*, 82, 415-425. 'http://www.ecoflora.co.uk'

LEDA traitbase Kleyer, M., Bekker, R.M., Knevel, I.C., Bakker, J.P, Thompson, K., Sonnenschein, M., Poschlod, 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., Garnier, E., Peco, B. (2008). The LEDA Traitbase: A database of life-history traits of Northwest European flora. *Journal of Ecology* 96: 1266-1274.

Akhmetzhanova et al, 2012

Akhmetzhanova, A.A, Soudzilovskaia, N.A., Onipchenko, V.G., Cornwell, W. K., Agafonov, V. A., Selivanov, I.A., and Cornelissen, J. H. C. (2012): A rediscovered treasure: mycorrhizal intensity database for 3000 vascular plants species across the former Soviet Union. *Ecology* 93:689. 'http://esapubs.org/Archive/ecol/E093/059/default.htm'

Pignatti et al., 2005

Pignatti, S., Menegoni, P., Pietrosanti, S. (2005). Biondicazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. *Braun-Blanquetia* 39, Camerino, pp. 97.

MycoFlor

Mycorrhizas in the Central European flora: relationships with plant life history traits and ecology Stefan Hempel, Lars Götzenberger, Ingolf Kühn, Stefan G. Michalski, Matthias C. Rillig, Martin Zobel, and Mari Moora *Ecology* 2013 94:6, 1389-1399

Catminat

Julve, P., 1998 ff. - Baseflor. Index botanique, écologique et chorologique de la flore de France. Version : 26 November 2014. <http://perso.wanadoo.fr/philippe.julve/catminat.htm>

BROT

Paula S, Arianoutsou M, Kazanis D, Tavsanoğlu Ç, Lloret F, Buhk C, Ojeda F, Luna B, Moreno JM, Rodrigo A, Espelta JM, Palacio S, Fernández-Santos B, Fernandes PM, and Pausas JG. 2009. Fire-related traits for plant species of the Mediterranean Basin. *Ecology* 90: 1420.

AND

Paula S. & Pausas J.G. 2013. BROT: a plant trait database for Mediterranean Basin species. Version 2013.06. URL: <http://www.uv.es/jgpausas/brot.htm>

PLANTS

Green, W. (2009) USDA PLANTS Compilation, version 1, 09-02-02.

Pignatti S., Menegoni P., Pietrosanti S., 2005, Biondicazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d'Italia. *Braun-Blanquetia* 39, Camerino, pp. 97.

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"),allow_persistent=TRUE)

## 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 <boccionata@gmail.com>

See Also

[tr8](#)

Examples

```
## 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)

## to see a short explanation for the codes used to identify
## the traits use lookup()

lookup(My_traits)

## End(Not run)
```

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

```
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()

tr8_setup	<i>A function to download the most recent url-tables for some traitbases.</i>
-----------	---

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 BioFlor).

Usage

```
tr8_setup()
```

Details

At the moment BioFlor and Ecoflora lookup tables are re-generated by this function.

Value

The values does not return anything 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

```
## 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 of the following 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

Fitter, A. H. and Peat, H. J., 1994, The Ecological Flora Database, J. Ecol., 82, 415-425. '<http://www.ecoflora.co.uk>'

Examples

```
## Not run:
data(traits_eco)

## End(Not run)
```

```
traits_pollen_Biolflor
      traits_pollen_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:

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLOR - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Examples

```
## Not run:
#data(traits_pollen_Biolflor)

## End(Not run)
```

```
traits_special_Biolflor
      traits_special_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:

Klotz, S., Kühn, I., Durka, W. (eds) (2002). BIOLFLORE - Eine Datenbank zu biologisch-ökologischen Merkmalen zur Flora von Deutschland. Schriftenreihe für Vegetationskunde *38*: 1-333. (Bundesamt für. Bonn, Bundesamt für Naturschutz)

Examples

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

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