

TR8: Extract traits data for plant species

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1 Rationale

The **TR8** package has been built in order to provide the user with the possibility of easily retrieving traits data for plant species from the following publicly available databases:

Biolflor <http://www2.ufz.de/biolflor/index.jsp> [7]

Ecological Flora of the British Isles <http://www.ecoflora.co.uk/> [3]

LEDA traitbase <http://www.leda-traitbase.org/LEDAportal/> [6]

Ellenberg values for Italian Flora [10]

Flowering period for Italian Flora [10] (data retrieved from <http://luirig.altervista.org/>)

Mycorrhizal intensity database [2]

MycoFlor database [4]

Catminat database [5]

BROT [8][9]

Please note that not all the traits available on the listed databases are downloaded by the package: this may change in future versions of the package (ie. some functionalities may be added and more traits will be made available).

2 Installation

The **TR8** package is available on CRAN, thus it can be easily installed through:

```
> install.packages("TR8",dependencies = TRUE)
```

The option `dependencies = TRUE` takes care of installing those packages which are needed by TR8 to work properly.

Once the package is installed, you can load it with:

```
> library(TR8)
```

Please note that:

The user is asked to always cite the data sources: the development of traits databases is a long and costly process, thus all the users of the TR8 package are asked (and reminded **every time** they load the package) to always cite the original sources of the data (see paragraph 6).

2.1 Using the development version

The devel version of the package is hosted on github at <https://github.com/GioBo/TR8>: to use this version (instead of the stable one, released from CRAN), you'll need the devtools package (<https://github.com/hadley/devtools>):

```
> ## install the package
> install.packages("devtools")
> ## load it
> library(devtools)
> ## activate dev_mode
> dev_mode(on=T)
> ## install TR8
> install_github("GioBo/TR8",ref="master")
> ## load it
> library(TR8)
> ## you can now work with TR8 functions
>
> ## if you want to go back and use the CRAN version
> ## already installed, simply deactivate dev_mode
> dev_mode(on=F)
```

3 Simple usage

Using the TR8 package is fairly simple: users just need to call the `tr8` function passing, as arguments, a vector of plant species names (**withouth authors' names!**¹) and a vector containing the codes corresponding to the traits which are to be downloaded:

¹This is needed since some traitbases do not include authors' names in the species' names.

```

> ## a vector containing a list of plant species names
> my_species<-c("Apium graveolens","Holcus mollis","Lathyrus sylvestris")
> ## a vector of traits
> to_be_downloaded<-c("reprod_B","strategy")
> ## now run tr8 and store the results in the my_traits object
> my_traits<-tr8(species_list = my_species,download_list = to_be_downloaded)

```

The codes which are accepted by TR8 are listed in the available_tr8 database:

```

> ## see the first lines of available_tr8 database
> head(available_tr8)
  short_code      description      db
1      h_max      Maximum height Ecoflora
2      h_min      Minimum height Ecoflora
3     le_area      Leaf area Ecoflora
4     le_long      Leaf longevity Ecoflora
5 phot_path Photosynthetic pathway Ecoflora
6     li_form      Life form Ecoflora

```

The database is composed of three columns:

short_code contains the codes that should be passed to the `download_list` argument of the `tr8` function.

description contains short description of each trait (please refer to the original sources for detailed descriptions).

db refers to the databases from which are providing traits data

Suppose the user is interested in downloading the *maximum height*, the *leaf area* and the *life form* (which are available through the *Ecoflora* database) for *Salix alba* and *Populus nigra* and store the resulting data in the `my_Data` object; the command should be:

```

> my_species<-c("Salix alba","Populus nigra")
> my_traits<-c("h_max","le_area","li_form")
> my_Data<-tr8(species_list = my_species, download_list = my_traits)

```

The `tr8` function will take care of downloading the data and store them in the `my_Data` object; you can see the results by printing them:

```

> ## see the downloaded data
> print(my_Data)

```

Or you can convert them to a data frame using the `extract_traits` function:

```

> traits_dataframe<-extract_traits(my_Data)

```

All the traits are now contained in a data frame with species as rows and columns as traits; where no trait data were available, you will see a **NA**.

In order to make the dataframe more readable, traits' names (i.e. columns' names) are converted to shorter codes: to see a brief explanation of the codes used to identify the traits, use the `lookup` function:

```
> lookup(my_Data)
```

The object returned by the `lookup` function can also be stored in order to be available for further elaborations:

```
> my_lookup<-lookup(my_Data)
> head(my_lookup)
```

3.1 Checking retrieved data

Several steps can go wrong during the data retrieval process (e.g. a database may contain two entries for the same species); `tr8()` will keep track of some of this problematic cases and the `issues()` function can be used to see whether any problem was faced during the process.

```
> my_species<-c("Salix alba", "Populus nigra")
> my_traits<-c("h_max", "le_area", "li_form")
> my_Data<-tr8(species_list = my_species, download_list = my_traits)
> issues(my_Data)
```

3.2 Interactive use of `tr8`

Up to now we've been using the `tr8` function in a non-interactive way. In order to help those user which are more familiar with a GUI approach, the function can also be run setting the `gui_config` parameter to **TRUE** (without providing any trait to the `download_list` parameter) and a multi-panel window will appear: the user is asked to choose those traits which are to be downloaded from the various databases ².

For a detailed explanation of each level of a trait, please refer to the original websites (all the databases listed in the references provide the users with very precise and detailed descriptions).

Typically users will have a their vegetation data in the form of a *sites*species* dataframe (or matrix), thus they may want to extract traits data for the whole dataset (this time using the GUI to select traits), i.e. :

²A note for Mac users: the GUI relies on the Tcl/Tk toolkit, thus if you want to run the GUI, please make sure that the X11 package is installed - see "Tcl/Tk" issues at <http://cran.r-project.org/bin/macosx/RMacOSX-FAQ.html>

```

> ## suppose veg_data is our dataframe with
> ## plant species as columns and sites as rows
>
> ## extract species names
> specie_names<-names(veg_data)
> ## use the tr8() function
> ## and tick those traits of interest in the pop-up window
> my_traits<-tr8(species_names,gui_config=TRUE)
> ## print the results
> print(my_traits)

```

4 Interpreting retrieved data

Please note that for many traits there is more than one entry in the original databases: in those cases, in order to obtain a single value the following strategy was adopted:

Quantitative traits the mean of all the values was calculated (e.g. when multiple values for "Seed weight mean" are available, the mean of these value is calculated)

Qualitative traits all the values are taken into account and "joined" together in a single string (the values are separated by a score "-")

Nota bene: in some cases some traits are stored as *string* in the original databases, even though they should be treated as numbers (e.g. the number *five* is stored as a string - i.e. "5", not as the numeric value 5): in those case **tr8** function is not able to interpret that entry as a numeric, thus, applying the above mentioned criteria to merge multiple traits, strange outputs may result from **tr8**, e.g. if a species has two entries for the trait **height** - day 3 and 3.5 meters - the merged value will not be the numeric mean (3.25) but the union of the two strings ("3-3.5").

Note for BROT database: BROT database contains several entries for the same trait for some species: this may be due to the fact that several sources of data were used and/or that data for different regions were reported. In the current version of **TR8** these multiple data are treated as follows:

- if there are both numeric (quantitative) and string (qualitative) entries, numeric ones are given the precedence and the mean of all numeric entries is used as the returned trait value
- if several qualitative entries are present (but no quantitative ones), only the most abundant level is reported (in case ties are present, eg. two levels are reported the same number of times, both values are reported, separated by a comma).

5 Citing the package

Please use the following citation when using TR8 package:

Bocci, G. (2015). TR8: an R package for easily retrieving plant species traits. *Methods in Ecology and Evolution*, 6(3):347-350.

Or, if you use BibTeX:

```
@Article{,
  author = {Bocci Gionata},
  title = {TR8: an R package for easily retrieving plant species traits},
  journal = {Methods in Ecology and Evolution},
  year = {2015},
  volume = {6},
  number = {3},
  pages = {347--350},
  url = {http://dx.doi.org/10.1111/2041-210X.12327},
}
```

6 Citing sources of information

Users of the TR8 package should always cite the sources of information which provided the traits data: the correct citations to be used for the retrieved data can be obtained through the `bib` method; just use:

```
> bib(my_traits)
```

7 Some notes on using tr8

A NOTE OF CAUTION

Searching the web is a time (and Internet band) consuming activity, thus the higher the number of your plant species and the traits to be retrieved, the longer it will take to `tr8()` to complete its job. Moreover, in order not to overflow the remote databases with `http` requests, the `tr8` function will always pause between one search and the following one.

A (SECOND) NOTE OF CAUTION

Some users adopt the following workflow for analysing their vegetation data:

1. insert vegetation data into a *spreadsheet file* with species as columns' and sites' as rows

2. export the spreadsheet file as a `.csv` file
3. import the `.csv` file into a **R** dataframe.

When following these steps, a dot (".") will be inserted between Genus and Species of each plant species name (i.e. column names in the **R** dataframe will not be in the form `c("Abies alba", "Salix alba")` but in the form `c("Abies.alba", "Salix.alba")`). This may cause problems for further processing of plants' species names, thus, in order to avoid this problem, please use the `check.names=F` option in `read.csv`. E.g. suppose that `my_veg_data.csv` is the `csv` file: in the **R** console, one should use:

```
> My_data<-read.csv("my_veg_data.csv",
+                   header=T,row.names=1,check.names=F)
```

8 Suggested workflow

We strongly suggest to always check plant species names with the `tnrs` function (from the `taxize` package) before using the `tr8` function; thus a typical workflow would be the following:

1. Check plant species names (e.g. with something like the following - please refer to the `taxize` package documentation[1] for further details)

```
> species_names<-names(veg_data)
> checked_names<-tnrs(species_names,source="iPlant_TNRS")
> print(checked_names)
```

Check which species (rows) in the table have a "score" value lower than 1 and check their names; if needed, correct them before using the `tr8()` function.

2. Run `tr8` (in this case using the GUI):

```
> my_traits<-tr8(species_names,gui_config = TRUE)
> print(my_traits)
```

Check whether `tr8()` had any problems in retrieving data:

```
> my_traits<-tr8(species_names,gui_config = TRUE)
> issues(my_traits)
```

3. You may want to have these traits available as a data frame: just use the `extract_traits` function which uses the results of `tr8` (in this case it's the `my_traits` objects) and returns a data frame.

```
> traits_df<-extract_traits(my_traits)
```

4. Observing a big data frame inside R could be difficult, thus users may want to save the `traits_df` data frame as a `.csv` file:

```
> save(traits_df,file="traits_df.csv")
```

and then open that file with a spreadsheet software (e.g. LibreOffice).

8.1 Dealing with synonyms

In some cases the same species may be present in different traitbases under different synonyms. In order to make it easier for the user to deal with this issue, `tr8` function has a parameter called `synonyms`: when set to `true` it forces the `tr8` to call the `tnrs` function from the `taxize` package and retrieve possible synonyms for the provided species names: in this case the retrieved trait data will have two additional columns, one called `synonyms` (for the synonyms found) and another named `original_names` which contains the original names passed by the user with the `species_list` parameter³.

```
> my_species<-c("Salix alba","Inula viscosa")
> my_traits<-c("h_max","le_area","li_form")
> my_Data<-tr8(species_list = my_species, download_list = my_traits,
+              synonyms=TRUE)
```

In the `Catminat` traitbase there are some entries which are in the form "Genus v. subspecies" (e.g. "Myrtus communis v. communis" and "Myrtus communis v. leucocarpa"); in order to allow users to search among those subspecies, the parameter `CATMINAT_ALTERNATIVES` has been introduced in the `TR8` function: when set to `TRUE` the function will search for entries which contain, in their names, the names 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").

```
> my_species<-c("Myrtus communis")
> ## some traits from Catminat
> my_traits<-c("inflorescence_fr","sex_reprod_fr","poll_vect_fr")
> my_Data<-tr8(species_list = my_species, download_list = my_traits,
+              catminat_alternatives=TRUE)
```

³**PLEASE NOTE** that when `synonyms` is set to `TRUE`, the resulting dataframe will have numbers as row.names: this is mandatory since in a few cases different species names may share a common synonym and R does not allow different rows to share the same name.

9 Further steps

The **TR8** package comes with another vignette, called **TR8_workflow**, which shows a typical workflow describing all the steps needed for retrieving and analysing traits data with **tr8**, listing the most common problems that could be faced and the possible solutions to fix them.

The vignette can be opened from within R, using:

```
> vignette("TR8_workflow")
```

Another vignette (called **Expanding_TR8**) shows to programmers how sources of data can be added to **TR8** (i.e. how functions for retrieving data should be written so that they can be easily integrated in **TR8**).

10 Local storage of remote data

The following databases are stored as files (**.txt**, **.csv** or **xlsx**) on the remote servers:

- LEDA
- Akhmetzhanova
- MycoFlor
- Catminat

These files are (quite) big in size, thus downloading them every time the **tr8()** function is used is a time consuming activity⁴. In order to make data retrieval more efficient, when **tr8** is run AND traits data from the above mentioned databases are requested for the first time, these files are downloaded and an R version (**.Rda**) copy is stored in a local directory and made available to future requests⁵.

11 Update local lookup tables

For some traitbases **tr8** uses lookup-tables which contain URLs of the species of interest (i.e. whenever the user search for traits data for some species, **tr8** searches for the corresponding URLs in such tables and then retrieve the data from the corresponding webpages); some of the traitbases queried by **tr8** are uploaded from time to time thus the function may be unable to retrieve traits

⁴The text files are not distributed together with the **TR8** package - which would save time and memory when executing the **tr8()** function - in order to avoid possible licensing conflicts between the **TR8**' GPL license and these datasets.

⁵By default these files will be installed in the directories which are commonly used for storing applications' data (which depends on the underlying operating systems; see <https://github.com/hadley/rappdirs> for details).

data for the most recently uploaded species. The `TR8_SETUP` function allows the user to download the most updated version of such tables; simply run

If the user wants to have available the most updated data,

```
> tr8_setup()
```

BEWARE: this function takes a long time to run (nearly 20 minutes are required - on a fast connection - for retrieving lookup tables for BiolFlor); it's very likely that the most recent version of TR8 contains the already up-to-date version of the data, so in most cases will never need to use this function.

References

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- [10] S. Pignatti, P. Menegoni, and S. Pietrosanti. Biondificazione attraverso le piante vascolari. Valori di indicazione secondo Ellenberg (Zeigerwerte) per le specie della Flora d’Italia. *Braun-Blanquetia*, 39:97, 2005.