

# How to expand TR8

Gionata Bocci  
Pisa (ITALY)  
boccigionata@gmail.com

November 21, 2014

This document briefly explains how users can include their functions for downloading traits in to the **TR8** package.

**Beware:** this document assumes that the reader has a good knowledge of the R programming language and has experience in writing R packages.

The best way to proceed is to clone the github repository (at <https://github.com/GioBo/TR8>) and try to work on that.

Suppose that the user has created a function called `funct_tr` which retrieves the following traits

- Height
- Dispersal type
- Clonality

from a database called `New_db` which is available on the Internet.

## 1 Adapt your function to TR8

The function should be structured in such a way that:

- it accepts the following parameters

**species\_list** the list of species names provided by the user (without authors' names);

**TRAITS** the list of traits chosen by the user among those made available by `New_db` (either passing them to the `tr8` function or choosing them through the GUI);

**rest** a number which establishes the `Sys.sleep` pause before each new query to `New_db` (**TR8** uses `Sys.sleep` in order not to overload remote servers: please always conform to this policy in writing extensions to **TR8**).

- within the function an object of class **results** is created (the definition of this S4 class is defined inside TR8)

```
> res<-new("results")
```

- if TRAIT is NULL, then **res@results** should be set to NULL (it means that these traits were not required by the user)

```
> res@results<-NULL
```

- **OR**, if TRAIT is not NULL then the selected traits for the requested species should be retrieved from **New\_db** and a dataframe **species\*trait** is created (let's call it **datatraits**); NA must be used for data which are not available (thus a plant species which is not present in **New\_db** should have all NAs in such a dataframe)

- the dataframe **species\*traits** is included in the **@result** slot of the object

```
> res@results<-datatraits
```

- a string representing the correct bibliographic citation is put in the slot **@bibliography**

```
> res@bibliography<-"Di Sarli, C. and Troilo, A., 2014.  
+   TRAITS: A new web traitbase for the flora of Argentina.  
+   http://www.pichuco.edu"
```

- **funct\_tr** returns the whole object

```
> return(res)
```

## 2 Adjust tr8() function

Then a call to **funct\_tr** should be put in TR8/R/tr8.R inside the **tr8()** definition (eg. after the call to **it\_flowering**) and its results saved into an object:

```
> it_flowering<-get_italian_flowering(species_list,  
+                                     TRAITS=traits_list$Pignatti,rest=rest)  
> my_exp<-funct_tr(species_list,TRAITS=traits_list$New_db,rest=rest)
```

please note that the variables passed as parameters are created within the **tr8** function, thus the call to **funct\_tr** should be just like it has been shown here (do not change names).

Then the **my\_exp** name should be added to those already existing in in the following cycle (toward the end of **tr8()**):

```

>         for(i in c(eco_traits,biolflor_traits,
+                   leda_traits,pignatti_traits,it_flowering,amf_traits)){
+             ## merge the dataframes only if they contain data
+             ...
+         }

```

which should become:

```

>         for(i in c(my_exp,eco_traits,biolflor_traits,
+                   leda_traits,pignatti_traits,it_flowering,amf_traits)){
+             ## merge the dataframes only if they contain data
+             ...
+         }

```

### 3 Adjust other variables

The available traits should be added to the TR8/data/column\_list.R list; this is a list of vectors in the form of

```
[[code_for_trait]] == c("short_code", "shortdescription", "Traitbase")
```

thus, in this case, we should add there the following lines:

```

> column_list<-list(
+   ## already existing traits
+   ## ...
+   ## ...
+   "height"=c("height","height of a species","New_db"),
+   "dispersal_type"=c("disp_type","Typology of dispersal","New_db"),
+   "clonality"=c("clonality","Type of clonal species","New_db")
+ )

```

This dataframe is used by tr8 to build the GUI and to pass traits to all the sub-functions which actually retrieve data from remote servers.

Convert column\_list to a dataframe (retaining the short code, the short description and the database columns) and save it as available\_tr8.Rd in TR8/data:

```

> library(plyr)
> tp<-ldply(column_list)[2:4]
> names(tp)<-c("short_code","description","db")
> save(tp,file="TR8/man/available_tr8.Rd")

```

### 4 A last remark

This workflow is working for TR8 version 0.9.xx: the inner work of the package is likely to be changed in future versions, thus users are invited to always check the latest version of the documentation.