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R packages

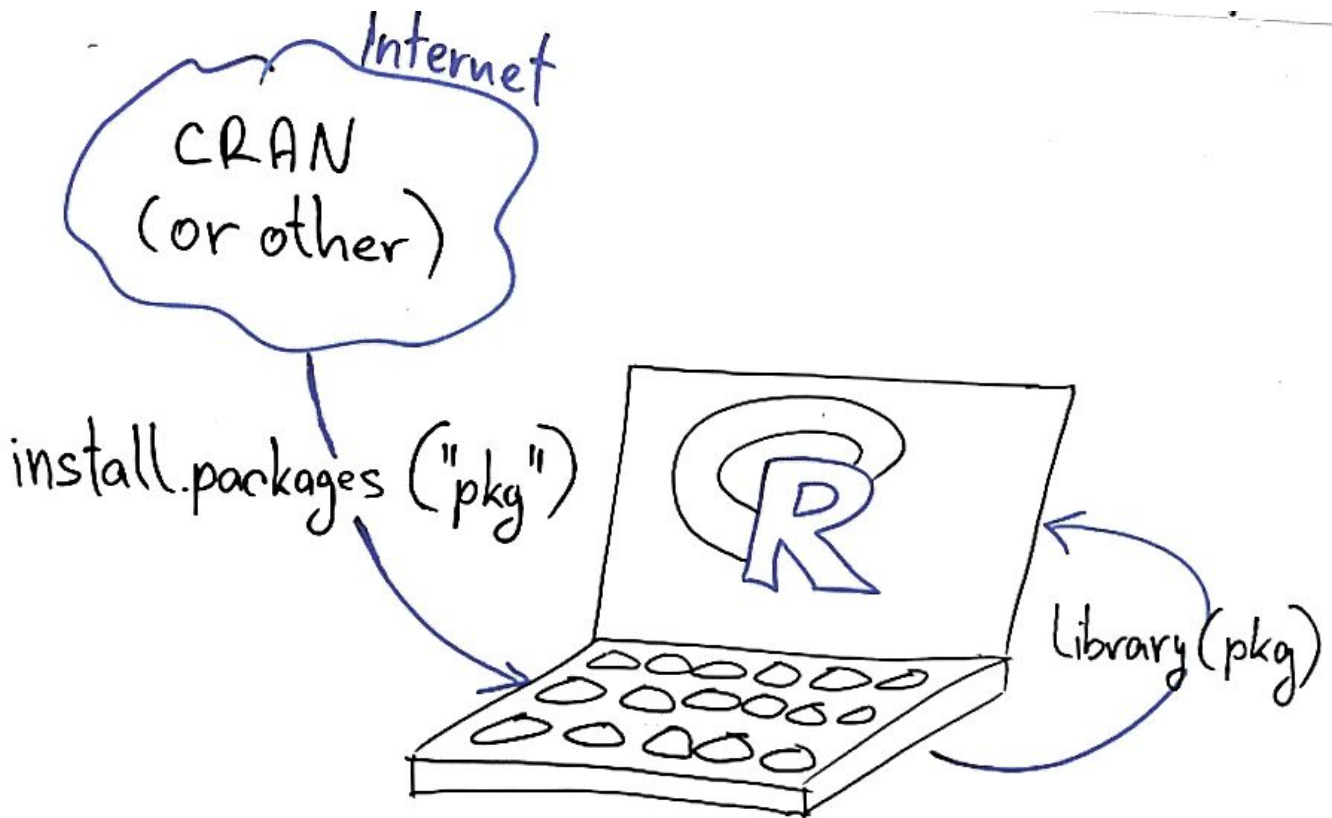
R has a great option to extend the basic functionality for other functions wrapped into packages. There are thousands of packages in central repositories like [CRAN](#) or [Bioconductor](#), and also in developers repositories like [R-Forge](#) or [GitHub](#). For an overview of documentation for packages aggregated from these repositories check the website [R Documentation](#).

Installing package is a two step process. First you need to install it from online repository (eg CRAN), and second you need to upload it into R workspace in order to use it.

1. `install.packages ("pkg")`: From the online repository, you need to install the package. You need to do this only once for given R version (unless the package needs to be updated). Installing R package will download the package somewhere into your computer, see below. Details about how to install packages from different online storage places is also below.
2. `library (pkg)`: If you want to use it in current R session, you need to upload it into R workspace. You need to do this every time you open R session and do the coding, in which you need some functionality of the package.

Note: in `install.packages`, the name of the package should be enclosed in quotation marks (`install.packages ("pkg")`), while in `library` it does not need to (both `library (pkg)` and `library ("pkg")` work).

Rule: You need to install the package on your computer before you can upload it. You need to upload the package into R before you can use it.



How to install R packages

If you have administrator rights for the computer, the packages will be installed into the `library` subfolder, usually located in `c:\Program Files\R\R-x.x.x\` ¹⁾. If you don't have administrator rights, you will be asked to install the libraries into some writeable location of the hard disc, by default into the `Documents` subfolder of your account (here, the following structure of subfolders will be created: `Documents\R\win-library\3.2`).

Installing from CRAN

Most of the commonly used R packages for analysis of ecological data are available from CRAN, and to install them, use simply `install.packages` command in R (note that the name of the package should be separated by quotation marks, and if more than one library should be installed, wrap the names into character vector):

```
install.packages ("ade4")
```

If you are using RStudio, you may use built-in function to install the packages, which is (in default setting of RStudio) located in bottom right panel, in the folder *Packages* - click the button *Install*, in *Install from* choose *Repository (CRAN)*, and in *Packages* type the name of the package.

There are, however, examples of packages which are not available from CRAN for some reason - e.g. because they are still under development, or because they do not fit rather strict CRAN rules for hosted packages. Alternative places are e.g. [R-Forge](#) or [GitHub](#).

Installing from GitHub

GitHub doesn't offer precompiled package versions - you need to compile the packages from source on your computer. However, there is a convenient R function in R package `devtools` developed by Hadley Wickham, which can help you with installing packages hosted on GitHub: `install_github`. To install some package (here called `MyPackage`, first install `devtools` from CRAN, and then apply the function `install_github`:

```
install.packages ("devtools")
devtools::install_github ("MyPackage")
```

(note that `::` means that `install_github` function will be read from the `devtools` namespace without need to actually upload the whole `devtools` library). If the GitHub package contains C/C++/Fortran code which needs to be compiled, you still need to install the set of compilation tools called [Rtools](#) on your computer.

Installing from R-Forge

R-Forge contains both source packages (files with extension `*.tar.gz` containing the original R code, which needs to be compiled during installation) and also already compiled binaries for Windows (`*.zip` files, do not need to be built). The binaries are available only for the latest R version available, so if

you are using the older version of R, you need to build the library from source. For example, to install package `packfor`²⁾ for forward selection of variables directly from R-Forge, type

```
install.packages("packfor", repos="http://R-Forge.R-project.org")
```

If you are using the latest R version, the package will probably install without problems. If not, you may receive the following warning message:

```
Warning in install.packages :  
package 'packfor' is not available (for R version 3.1.2)
```

In that case, you need to install the package from source. Manually download the binary file from R-Forge (with `*.zip` extension) to your computer, and use the command `install.packages` with argument `repos = NULL`:

```
install.packages ("C:/Users/Downloads/packfor_0.0-8.zip", repos = NULL)
```

(note that this works if your downloaded file is the version of `packfor` 0.0-8 and it is saved in Downloads folder - modify this for your current needs). If even this option doesn't work, you may need to install the package from the source - download `*.tar.gz` version to your computer and use `install.packages` function with `repos = NULL` and `type = "source"`:

```
install.packages ("C:/Users/Downloads/packfor_0.0-8.tar.gz", repos = NULL,  
type = "source")
```

However, installing R packages from source is nontrivial task and may require that your computer has installed set of compilation tools, so called [Rtools](#), because installing from source consists of several steps (compiling C/C++/Fortran codes, making documentations, checking for code errors, running examples etc.).

¹⁾

R-x.x.x stems for the R version, e.g. R-3.2.1

²⁾

Note that both forward selection function from this package have been included in the `adespatial` package available on CRAN.