Packages in R

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What are R Packages?

The package is an suitable way to organize the work and share it with others. R packages are collections of functions and data sets developed by the community. These are stored under a directory called "library"" within the R environment. By default, R installs a group of packages during installation. Once we start the R console, only the default packages are available by default. Other packages that are already installed need to be loaded explicitly to be utilized by the R program that is getting to use them.

```
.libPaths()
```

Library locations of R packages

```
## [1] "C:/Users/admin/Documents/R/win-library/4.0"
## [2] "C:/Program Files/R/R-4.0.2/library"
```

```
library()
```

List of all the packages installed

```
search()
```

All the packages currently loaded in the R environment

```
# Access the Package Description from Documentation file of the Package inside R

 packageDescription("ggplot2")

# Access the Package Help file from Package inside R.

 help(package = "ggplot2")
```

```r
# See Functions inside Packages

ls("package:stats")


# Help for Individual Functions inside Packages

help("xtabs")
help(xtabs, package = "stats")


#vignettes are documents where the authors show some functionalities of their package in a more detaile

browseVignettes()
browseVignettes(package="ggplot2")
vignette()
vignette(package = "ggplot2")
vignette("ggplot2-specs")
```

Package Description, Help and Vignettes

What are Repositories?

A repository is a place where packages are located so you can install them from it. Three of the most popular repositories for R packages are:

CRAN: The Comprehensive R Archive Network is the official repository, it is a network of ftp and web servers maintained by the R community around the world.

Bioconductor: this is a topic specific repository, intended for open source software for bioinformatics.

Github: although this is not R specific, Github is probably the most popular repository for open source projects. Its popularity comes from the unlimited space for open source, the integration with git, a version control software, and its ease to share and collaborate with others.

How to Install packages

```r
# Install Single Package from CRAN

install.packages("MASS")


# Install Multiple Packages at Same time from CRAN

install.packages(c("plyr", "dplyr"))


# Install Package from Specific CRAN Mirror

install.packages('RMySQL', repos='http://cran.us.r-project.org')
```

1. Installing Packages From CRAN

```r
install.packages("C:/Users/admin/Downloads/tidyr_1.1.2.zip", repos=NULL, type="source")
```

2. Installing Packages From Local Directory

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.12")
```

3. Installing Bioconductor Packages

4. Installing Packages Via devtools Need to Install Rtools: https://cran.rstudio.com/bin/windows/Rtools/

```r
install.packages("devtools")
```

After devtools is installed, you will be able to use the utility functions to install another packages. The options are:

install_cran() from CRAN

install_git() from a git repository

install_github() from GitHub

install_local() from a local file

install_svn() from a SVN repository

install_url() from a URL

install_bioc() from Bioconductor

install_bitbucket() from Bitbucket

install_version() from a specific version of a CRAN package.

```r
library("devtools")

# install_cran() from CRAN

  install_cran("ggplot2")
  install_cran(c("httpuv", "shiny"))


# install_git() from a git repository

  install_git("git://github.com/hadley/stringr.git")
```

```r
# install_github() from GitHub

install_github("klutometis/roxygen")


# install_local() from a local file

install_local("C:/Users/admin/Downloads/tidyr_1.1.2.zip")


# install_svn() from a SVN repository

install_svn("https://github.com/hadley/httr")


# install_url() from a URL

install_url("https://github.com/hadley/stringr/archive/master.zip")


# install_bioc() from Bioconductor

install_bioc("SummarizedExperiment")


# install_bitbucket() from Bitbucket

install_bitbucket("sulab/mygene.r@default")
```

5. Installing Packages From GitHub   Need to Install Rtools: https://cran.rstudio.com/bin/windows/Rtools/

```r
install.packages("devtools")
library(devtools)

install_github("klutometis/roxygen")
install_github("hadley/rvest")
```

How To Update, Remove And Check Installed Packages

```r
#To check what packages are installed on your computer

installed.packages()


#Uninstalling a package

remove.packages("MASS")
```
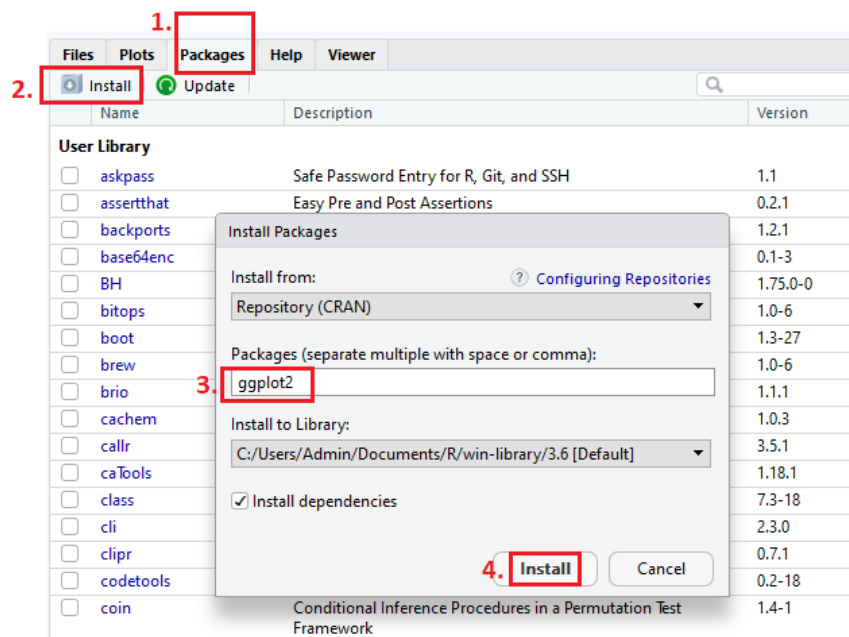
```
#Check what packages need an update

 old.packages()


#You can update all packages

 update.packages()
```

User Interfaces For Installing Packages

Load and Unload Packages

```
# Load Packages

  library(ggplot2)
  qplot(1:10,seq(1,100,by=10))


# Unload Packages

  detach(ggplot2)
```

Acces Package functions without loading Package

```
ggplot2::qplot(1:10,seq(1,100,by=10))
```