Install tutorial

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Install R

`R` is available for free for Windows, GNU/Linux and MacOS.
As for now, the latest version is `3.2.5`.

One common complain about `R` is the frequency of updates. True, but that could be sorted out by a good **package manager**

Windows

Visit the download page and choose the corresponding installer for your platform.

One way to circumvent the absence of package manager for Windows, is to install the `R` package `installr`. This package provide a function `updateR()` to takes care of updating your R installation and the migration of your installed packages whenever a major `R` release happens.

MacOS

You could either use the download page or better use the Homebrew package manager.

Once `homebrew` installed, you can install/uninstall easily with dependencies many programs and utilities. This implies to use the terminal, but worth it if you ask me. Then, installation is done with:

```
brew install r
```

and the updates will be automatically done for all your software by

```
brew update; brew upgrade
```

GNU/Linux

Any Linux distributions is bundled with a great package manager such as `dpkg` or `rpm`.

```
sudo apt-get install r-base
```

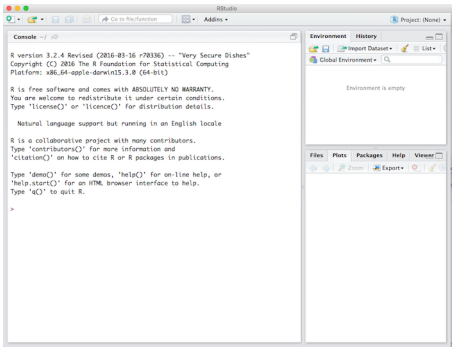
Install Rstudio

Rstudio is an Integrated Development Editor, it wraps and interface `R` but, `R` needs to installed first. The free-version contains everything you need.

Visit the download page and choose the corresponding installer for your platform. As for now, the latest version is `0.99.893`.

Open rstudio

They are 4 main panels in rstudio, but as the top-left is for scripting, the layout should looks like

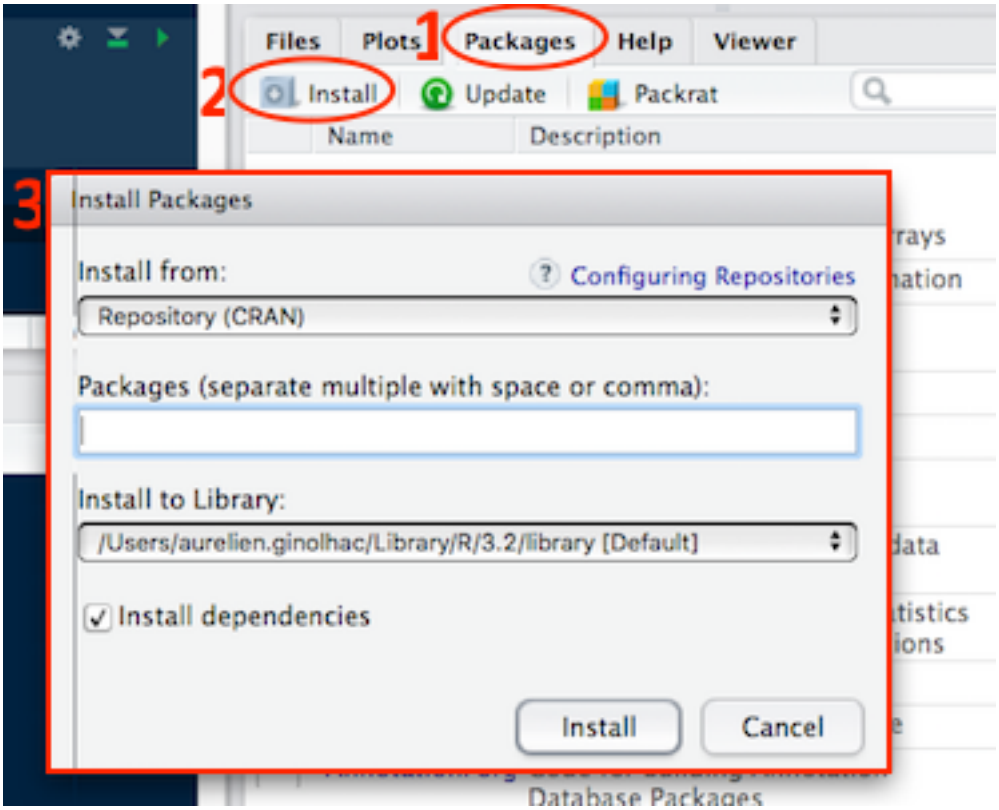


install R packages

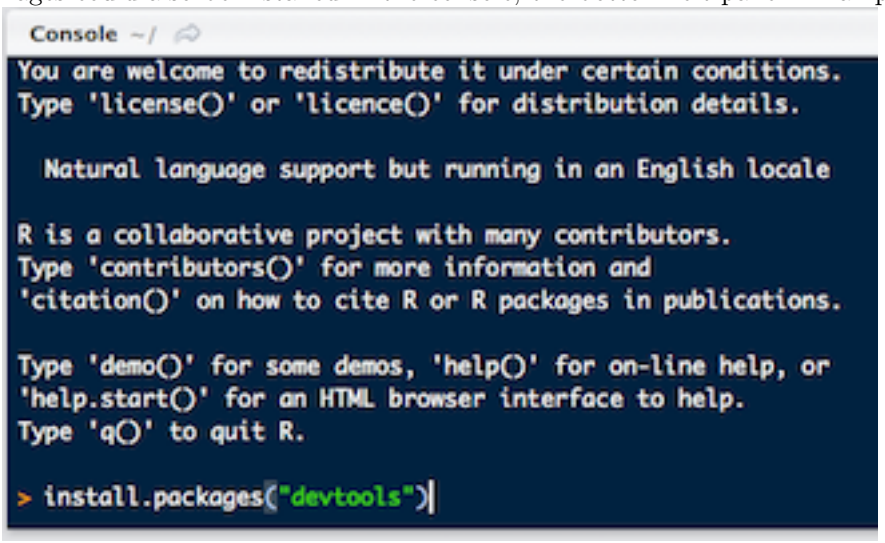
On the bottom-right panel, 5 tabs are present:

- Files
- Plots
- Packages
- Help
- Viewer

Click on the `Packages` tab (1.) and select the select the `Install` button (2.) and type `dplyr, tidyr, ggplot2, ggrepel, devtools, broom, purrr, shiny, readr, readxl, d3heatmap, stringr` in (3.)



It takes time, usually 10 seconds to 5 minutes for one package depending on its size and compilation stages. Those packages could also be installed in the console, the bottom-left panel. Example here for installing `devtools`



A note about package updates

Again, the same complain is true, updates are very frequent and when you have many packages it could be cumbersome to maintain your R up-to-date. Actually, it is as easy as

```
update.packages()
```

But, next to the `Install` button, you should use the `Update` green button in the `Packages` tab. The

advantage is that you could check the ones you want and also click on the `NEWS` links to see that was actually changed.

install bioconductor packages

The bioconductor resource will be detailed latter, but for now we could save time and install the necessary packages before the workshop.

Copy / paste the following the console.

```
source("https://bioconductor.org/biocLite.R")
biocLite(c("limma", "Biobase", "GEOquery"))
```

A note about package updates

No interface for bioconductor packages, you will need to run

```
source("https://bioconductor.org/biocLite.R")
biocLite()
```

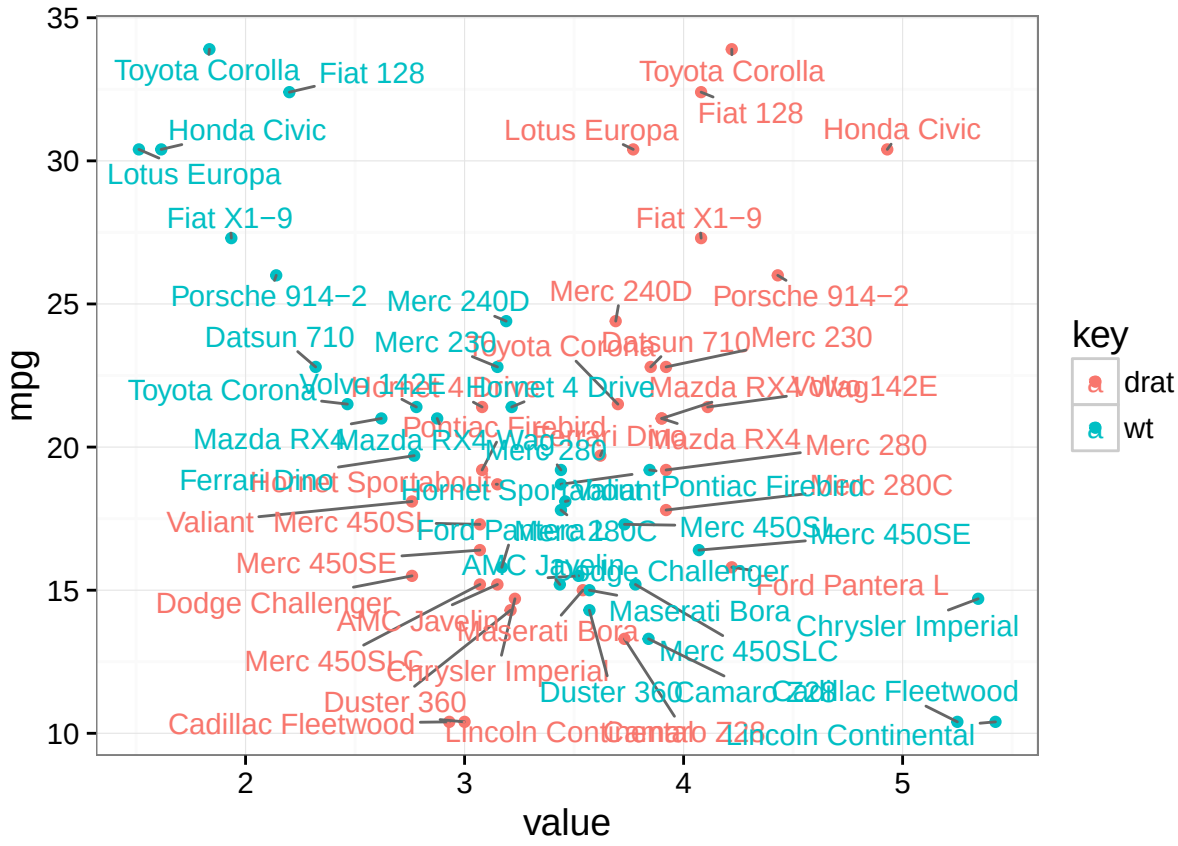
and you will be asked if you want to update some / all

Testing your installation

Copy / paste this code

```
library("ggplot2")
library("tidyr")
library("ggrepel")
library("dplyr", warn.conflicts = FALSE)
theme_set(theme_bw(14))

mtcars %>%
  add_rownames(var = "car_name") %>%
  gather(key, value, c(drat, wt)) %>%
  ggplot(aes(x = value, y = mpg, colour = key))+
  geom_point()+
  geom_text_repel(aes(label = car_name))
```


mpg
value
key
drat
wt
35
30
25
20
15
10
2
3
4
5
Toyota Corolla
Fiat 128
Honda Civic
Lotus Europa
Fiat X1−9
Porsche 914−2
Merc 240D
Datsun 710
Merc 230
Toyota Corona
Volvo 142E
Hornet 4 Drive
Mazda RX4 Wag
Pontiac Firebird
Mazda RX4
Merc 280
Ferrari Dino
Hornet Sportabout
Valiant
Merc 450SL
Ford Pantera L
Merc 280C
Merc 450SE
AMC Javelin
Dodge Challenger
Maserati Bora
Chrysler Imperial
Merc 450SLC
Duster 360
Camaro Z28
Cadillac Fleetwood
Lincoln Continental