



Package Installation

Vincent Guillemot

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OMICS

Package Installation with Fripouille



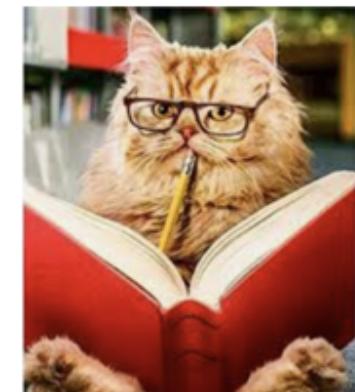
Package Installation with Fripouille



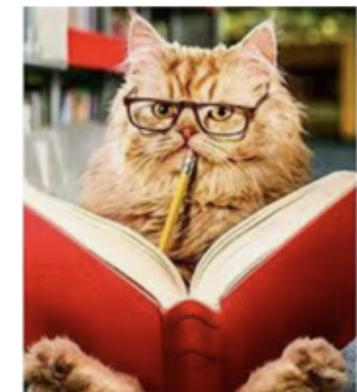
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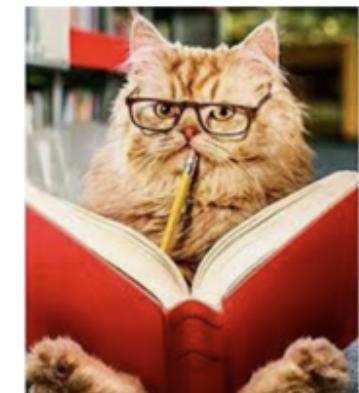
Package Installation with Fripouille



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```
install.packages("dog")
```



Package Installation with Fripouille



`install.packages("dog")`



Package Installation with Fripouille



`install.packages("dog")`



Package Installation with Fripouille



I don't remember the commands !!!



Installation : only once*

The screenshot shows the RStudio interface with the 'Packages' tab selected. A sub-menu is open under 'Install' with the option 'Install R packages' highlighted. Below it, a modal dialog titled 'Install Packages' is displayed. It has fields for 'Install from:' (set to 'Repository (CRAN)'), 'Packages (separate multiple with space or comma):' (empty), 'Install to Library:' (set to '/Library/Frameworks/R.framework/Versions/4.0/Resources/library'), and a checked checkbox for 'Install dependencies'. At the bottom are 'Install' and 'Cancel' buttons.

Load : very often!

The screenshot shows the RStudio interface with the 'Packages' tab selected and the 'Update' button highlighted. Below it, a table lists packages: 'PTCA4CATA' (unchecked), 'purrr' (checked), and 'pwr' (unchecked). At the bottom, a R console window shows the command 'library(purrr)' being run.

```
R 4.0.4 · ~/Desktop/ ↵
> library(purrr)
>
> laFonctionQueJeVoulaisUtiliser(42)
```

*except when you need to do it again

Install packages from

- Bioconductor ?
 1. First install `BiocManager` from CRAN
 2. Run the R command `BiocManager::install("package_name")`
- GitHub ?
 1. Install `devtools`
 2. Run the R command `devtools::install_github("username/repository")`.
- Source code ?
 1. Put the `source.tar.gz` in your working directory...
 2. Run the R command `install.package("source.tar.gz", repos = NULL, type = "source")`.

Exercises

Install limma

limma is the favorite package of anyone that wants to analyze gene expression data (microarray, RNA-seq, NanoString etc.)

Install it with the command:

```
BiocManager::install("limma")
```

Explore the package

1. Load : library(limma)
2. Look at the main help page

```
?`limma-package`
```

1. Look at the first vignette : vignette("intro", package = "limma")

Install the “ReMUSE” course’s package

The course’s material is in fact an R package. Install it from GitHub with the command:

```
devtools::install_github("vguillemot/ReMUSE")
```